GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 15, 2003, 03:58:02 ; Search time 5999 Seconds
(without alignments)
16639.355 Million cell updates/sec

Title: US-09-970-532-1
Perfect score: 2440
Sequence: 1 ttttttattttttttttctt.....ttaaaaaaaaaaaaaaaaaa 2440

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
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21: em_or:*
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26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2440	100.0	2440	4	BTU90937	U90937 Bos taurus
2	2440	100.0	2440	6	AR214341	AR214341 Sequence
3	960.6	39.4	2004	4	SSU19994	U19994 Sus scrofa
4	862	35.3	2171	4	AB051103	AB051103 Felis cat
5	742.2	30.4	2194	9	BC010140	BC010140 Homo sapi
6	735.8	30.2	2112	9	HUMTNFRC	M63121 Human tumor
7	728.6	29.9	2087	9	HUMTNFR	M33294 Human tumor
8	727	29.8	2175	6	A43873	A43873 Sequence 1
9	727	29.8	2175	6	A78738	A78738 Sequence 7
10	727	29.8	2175	6	AR041076	AR041076 Sequence
11	727	29.8	2175	6	I64751	I64751 Sequence 1
12	725.8	29.7	2111	6	A26412	A26412 cDNA for (5
13	725.8	29.7	2111	6	AX409713	AX409713 Sequence
14	725.8	29.7	2111	6	AX658239	AX658239 Sequence
15	725.8	29.7	2111	9	HUMTNFRB	M58286 Homo sapien
16	725.8	29.7	2161	6	AR096330	AR096330 Sequence
17	725.8	29.7	2161	6	AX700505	AX700505 Sequence
18	725.8	29.7	2161	9	HSTNFR1A	X55313 H.sapiens T
19	725.8	29.7	2176	6	A19907	A19907 Synthetic n
20	721.8	29.6	2062	6	A21522	A21522 TNF alpha g
21	718.6	29.5	2062	6	I43805	I43805 Sequence 24
22	711.4	29.2	2061	6	A20255	A20255 55kD recept
23	710.6	29.1	2109	9	AK056611	AK056611 Homo sapi
24	687.4	28.2	2050	9	HUMTNFRP	M60275 Human tumor
25	685.4	28.1	1368	6	A29098	A29098 Synthetic D
26	683.8	28.0	1368	6	AR302886	AR302886 Sequence
27	683.8	28.0	1368	6	AX530421	AX530421 Sequence
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30	592	24.3	2115	10	AF329978	AF329978 Rattus no
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35	590.4	24.2	2115	10	AF329977	AF329977 Rattus no
36	559	22.9	2154	10	MUSTNFX	L26349 Mus musculu
37	558	22.9	2179	10	MMTNFRE5	X57796 Mouse mRNA
38	555.6	22.8	1331	6	A29103	A29103 H.sapiens m
39	554	22.7	1956	10	MUSTNFR2	M59377 Murine tumo
40	554	22.7	2048	10	MUSMTNFR1	M60468 Mouse tumor
41	554	22.7	2063	10	MMP55R	X59238 Murine mRNA
42	554	22.7	2086	10	BC004599	BC004599 Mus muscu
43	554	22.7	2109	10	BC052675	BC052675 Mus muscu
44	543	22.3	543	6	AR214342	AR214342 Sequence
45	389.8	16.0	6889	6	I26928	I26928 Sequence 2

ALIGNMENTS

RESULT 1
BTU90937
LOCUS BTU90937 2440 bp mRNA linear MAM 21-JAN-2000
DEFINITION Bos taurus tumor necrosis factor-receptor I (TNF-RI) mRNA, complete cds.
ACCESSION U90937
VERSION U90937.1 GI:2290397
KEYWORDS .
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 2440)
AUTHORS Lee,E.K., Kehrli,M.E. Jr. and Taylor,M.J.

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  TITLE     Cloning and sequencing of cDNA encoding bovine tumor necrosis
            factor (TNF)-receptor I
  JOURNAL   Vet. Immunol. Immunopathol. 61 (2-4), 379-385 (1998)
  MEDLINE   98273505
   PUBMED   9613449
REFERENCE   2  (bases 1 to 2440)
  AUTHORS   Lee,E.-K., Talyor,M.J. and Kehrli,M.E.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-FEB-1997) Metabolic Disease and Immunology, National
            Animal Disease Center, 2300 Dayton Ave., Ames, IA 50010, USA
FEATURES             Location/Qualifiers
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                     /tissue_type="aorta"
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     CDS             294. .1709
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                     SRCRDEMFQVEISPCVVDRDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQE
                     RQDTICHCHMGFFLKGAKCISCHDCKNKECEKLCPTRPSTGKDSQDPGTTVLLPLVIV
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                     STPSSSPVSIPPYISCDRSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPA
                     STHLCTPGPPASTHLCTPVQKWEASAPSAPDQLADADPATLYAVVDGVPPSRWKELVR
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                     ENIEEALGGAARLASEPRLLW"
BASE COUNT      441 a    771 c    701 g    527 t
ORIGIN
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  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 2440;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTTTTATTTTTTTTTTTCTTTTTTGGGGGGGAAAGGGGTGACCCCCCTTCCCCTCCCACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TTTTTATTTTTTTTTTTCTTTTTTGGGGGGGAAAGGGGTGACCCCCCTTCCCCTCCCACC 60

Qy         61 TCCTCTCAGCTCAAGTTTTCTCGGAGCTCTCCGGGCTCTGGGCCGCAGGGCTGGCCTTCC 120
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Qy        121 GGGTTTGAGGTCCTCCGGATTGGGCTGTGTCCCCGCCCCAGTCTCAACCCTCCACTCCCC 180
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Qy        241 GCCGCCACTGCCCCAGCCCTGATGGGGGATTGAGAGGCCACAGCTGGCCGGACATGGGCC 300
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Db        301 TCCCCACCGTGCCTGGCCTGCTGCTGCCACTGGTGCTTCCAGCTCTGTTGGCAGATGTGT 360

Qy        361 ACCCCGCAGGGGTTCAGGGGCTGGTCCCTCACCCCGGGGACCTGGAGAAGAGAGAGAGTC 420
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Qy        421 CCTGTCCCCAAGGAAAATATAACCACCCGCAAAATAGCACCATTTGCTGCACCAAGTGCC 480
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Db        481 ACAAAGGTACCTATCTGTACAATGACTGTCCGGGTCCAGGGCGAGACACGGACTGCAGGG 540

Qy        541 TGTGTGCCCCTGGCACCTACACTGCCTTGGAGAACCATCTCAGACGATGCCTGAGCTGCT 600
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Db        541 TGTGTGCCCCTGGCACCTACACTGCCTTGGAGAACCATCTCAGACGATGCCTGAGCTGCT 600

Qy        601 CCAGGTGCCGGGACGAAATGTTCCAGGTGGAGATTTCGCCTTGTGTAGTGGACCGGGACA 660
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Db        601 CCAGGTGCCGGGACGAAATGTTCCAGGTGGAGATTTCGCCTTGTGTAGTGGACCGGGACA 660

Qy        661 CTGTGTGCGGCTGCAGGAAGAACCAGTACCGGGAATACTGGGGTGAAACTGGCTTCCGGT 720
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Db        661 CTGTGTGCGGCTGCAGGAAGAACCAGTACCGGGAATACTGGGGTGAAACTGGCTTCCGGT 720

Qy        721 GTCTGAACTGCAGCCTCTGTCCCAATGGCACAGTGAATATCCCCTGCCAGGAGAGACAGG 780
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Db        721 GTCTGAACTGCAGCCTCTGTCCCAATGGCACAGTGAATATCCCCTGCCAGGAGAGACAGG 780

Qy        781 ACACCATCTGCCACTGCCATATGGGCTTCTTTCTTAAAGGCGCCAAGTGCATCTCCTGTC 840
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Db        781 ACACCATCTGCCACTGCCATATGGGCTTCTTTCTTAAAGGCGCCAAGTGCATCTCCTGTC 840

Qy        841 ATGATTGTAAGAACAAGGAGTGCGAGAAGTTATGTCCAACCCGACCTTCAACTGGTAAAG 900
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Qy        901 ACTCTCAGGACCCAGGCACTACAGTACTATTACCCCTGGTGATTGTCTTCGGGCTTTGCC 960
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Qy        961 TGGCATCCTTCGCCTCTGTCGTCTTAGCATGTCGCTACCAGCGGTGGAAGCCCAAGCTCT 1020
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Db        961 TGGCATCCTTCGCCTCTGTCGTCTTAGCATGTCGCTACCAGCGGTGGAAGCCCAAGCTCT 1020

Qy       1021 ACTCCATCATTTGCGGGCAGTCGACTCTGGTAAAAGAGGGGGAGCCAGAACTCCTGGTCC 1080
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Qy       1441 CCCCGTCGCGCTGGAAGGAGTTGGTGCGGCGGCTGGGACTGAGCGAGCACGAGATCGAGC 1500
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RESULT 2
AR214341
LOCUS       AR214341               2440 bp    DNA     linear   PAT 25-SEP-2002
DEFINITION  Sequence 1 from patent US 6406907.
ACCESSION   AR214341
VERSION     AR214341.1  GI:23311975
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2440)
  AUTHORS   Taylor,M.J., Kehrli,M.E. Jr. and Lee,E.-K.
  TITLE     Bovine tumor necrosis factor receptor-1 and methods of use
  JOURNAL   Patent: US 6406907-A 1 18-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .2440
                     /organism="unknown"
BASE COUNT      441 a    771 c    701 g    527 t
ORIGIN
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Query Match 100.0%; Score 2440; DB 6; Length 2440;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2440; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 TCCTCTCAGCTCAAGTTTTCTCGGAGCTCTCCGGGCTCTGGGCCGCAGGGCTGGCCTTCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        121 GGGTTTGAGGTCCTCCGGATTGGGCTGTGTCCCCGCCCCAGTCTCAACCCTCCACTCCCC 180
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Qy        181 GACCCGAGGCCCGGGCTCCACTGGGCATACGCGAGGACCGTGTTGCTGTCACTGTCGCGG 240
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Qy        241 GCCGCCACTGCCCCAGCCCTGATGGGGGATTGAGAGGCCACAGCTGGCCGGACATGGGCC 300
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Db        301 TCCCCACCGTGCCTGGCCTGCTGCTGCCACTGGTGCTTCCAGCTCTGTTGGCAGATGTGT 360

Qy        361 ACCCCGCAGGGGTTCAGGGGCTGGTCCCTCACCCCGGGGACCTGGAGAAGAGAGAGAGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ACCCCGCAGGGGTTCAGGGGCTGGTCCCTCACCCCGGGGACCTGGAGAAGAGAGAGAGTC 420

Qy        421 CCTGTCCCCAAGGAAAATATAACCACCCGCAAAATAGCACCATTTGCTGCACCAAGTGCC 480
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Db        421 CCTGTCCCCAAGGAAAATATAACCACCCGCAAAATAGCACCATTTGCTGCACCAAGTGCC 480

Qy        481 ACAAAGGTACCTATCTGTACAATGACTGTCCGGGTCCAGGGCGAGACACGGACTGCAGGG 540
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Qy        541 TGTGTGCCCCTGGCACCTACACTGCCTTGGAGAACCATCTCAGACGATGCCTGAGCTGCT 600
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Db        841 ATGATTGTAAGAACAAGGAGTGCGAGAAGTTATGTCCAACCCGACCTTCAACTGGTAAAG 900

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Db       1921 TGAGTGTGTGTCTGTGTGTAGTGTGTGTCTGCGTGCAGTGCGTGTGTTTGTGTCTCTGTA 1980
Qy       1981 TGTGCGTCTGTGTGATGTGGAGTGTGTGTACTCGTGAGAGAGGCCGAGTGTGCCCGGAGC 2040
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Qy       2341 CTTTGCGACCCTGTGAATCGCAGGGACTTCTGTAAATACACTAAAATCTTCCAATTAAAG 2400
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Db       2401 CTCTGCCCTGGAGGGACTGGTTAAAAAAAAAAAAAAAAAA 2440
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RESULT 3
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LOCUS       SSU19994                2004 bp    mRNA    linear   MAM 30-JAN-1996
DEFINITION  Sus scrofa p55 TNF receptor mRNA, complete cds.
ACCESSION   U19994
VERSION     U19994.1  GI:1141752
KEYWORDS    .
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 2004)
  AUTHORS   Suter,B. and Pauli,U.
  TITLE     Cloning of the cDNA encoding the porcine p55 tumor necrosis factor
            receptor
  JOURNAL   Gene 163 (2), 263-266 (1995)
  MEDLINE   96011645
   PUBMED   7590278
REFERENCE   2  (bases 1 to 2004)
  AUTHORS   Pauli,U.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-JAN-1995) Urs H. Pauli, Veterinary Virology,
            University of Bern, Laenggass-Str. 122, Bern CH-3012, Switzerland
FEATURES             Location/Qualifiers
     source          1. .2004
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                     KQDTICNCHSGFFLRDKECVSCVNCKNADCKNLCPATSETRNDFQDTGTTVLLPLVIF
                     FGLCLAFFLFVGLACRYQRWKPKLYSIICGKSTPVKEGEPEPLATAPSFGPITTFSPI
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ORIGIN

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  Best Local Similarity 71.6%;  Pred. No. 4.3e-158;
  Matches 1478;  Conservative    0;  Mismatches  469;  Indels  116;  Gaps   12;

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Db         1 ATGGGCCTCTCCACCGTGCCTGGCCTGCTGCTGCCACTGGTGCTCCGGGCTCTGTTGGTG 60

Qy       354 GATGTGTACCCCGCAGGGGTTCAGGGGCTGGTCCCTCACCCCGGGGACCTGGAGAAGAGA 413
Db        61 GATGTGTACCCCGCAGGGGTCCACGGGCTGGTCCTTCACCCTGGGGACCGGGAGAAGAGA 120

Qy       414 GAGAGTCCCTGTCCCCAAGGAAAATATAACCACCCGCAAAATAGCACCATTTGCTGCACC 473
Db       121 GAGAGTTTGTGTCCCCAAGGAAAATACAGCCACCCTCAAAATAGGTCCATTTGCTGCACG 180

Qy       474 AAGTGCCACAAAGGTACCTATCTGTACAATGACTGTCCGGGTCCAGGGCGAGAGACGGAC 533
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Qy       534 TGCAGGGTGTGTGCCCCTGGCACCTACACTGCCTTGGAGAACCATCTCAGACGATGCCTG 593
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Qy       834 TCCTGTCATGATTGTAAGAACAAGGAGTGCGAGAAGTTATGTCCAACCCGACCTTCAACT 893
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Qy       894 GGTAAAGACTCTCAGGACCCAGGCACTACAGTACTATTACCCCTGGTGATTGTCTTCGGG 953
Db       601 CGTAACGACTTTCAGGACACAGGCACCACGGTGCTGTTGCCGCTGGTGATCTTCTTTGGT 660

Qy       954 CTTTGCCTGGCATCCTTCGCCTCTGTCGTCTTAGCATGTCGCTACCAGCGGTGGAAGCCC 1013
Db       661 CTTTGCCTGGCATTCTTCCTCTTCGTTGGCTTAGCTTGCCGCTACCAACGGTGGAAACCA 720

Qy      1014 AAGCTCTACTCCATCATTTGCGGGCAGTCGACTCTGGTAAAAGAGGGGGAGCCAGAACTC 1073
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Qy      1134 TCCAGTCCTGTCTCCATTCCCCCTTACATCTCCTGTGACCGGTCCAACTTCGGAGCCGTC 1193
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Qy      1610 CGTGCTCAGGGACATGGACCTGCTGGGTTGCCTGGAAAACATAGAGGAGGCGCTGGGTGG 1669
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Qy      1944 TGTGTCTGCGTGCAGTGCGTGTGTTTGTGTCTCTGTA---------------------- 1980
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Qy      1981 --TGTGCGTCTGTGTGATGTGGAGTGTGTGTACTCGTGAGAGAGGCCGAGTGTGCCCGGA 2038
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Qy      2098 TTGGAGAACTCAGCAAGGCGACTTGGGGAACCTACGTCGGTCCCTGAGCCGGTTTCGCAG 2157
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Qy      2158 TAGATAAGCCATCTTTGTATCCACTCTGCACATCCACTCATCCACTCTGTACACTAATAG 2217
Db      1864 TAGATAAGAAGTCTTTGTAACCATTATGTACACTAATAGAGACTTGGCACCCCTTTGTCT 1923

Qy      2218 AAACTTTGTTGCCCTGCCTGGACCAGCTGAACTGTCCCCAGGCAGCGGGGGAGCACAGAA 2277
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Db       1981 CAATGGGGCCTTCAGCTGGAGCT 2003

RESULT 4
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            cds.
ACCESSION   AB051103
VERSION     AB051103.1  GI:14041808
KEYWORDS    .
SOURCE      Felis catus (cat)
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
REFERENCE   1
  AUTHORS   Mizuno,T., Goto,Y., Baba,K., Masuda,K., Ohno,K. and Tsujimoto,H.
  TITLE     TNF-alpha-induced cell death in feline immunodeficiency
            virus-infected cells is mediated by the caspase cascade
  JOURNAL   Virology 287 (2), 446-455 (2001)
  MEDLINE   21425403
   PUBMED   11531421
REFERENCE   2  (bases 1 to 2171)
  AUTHORS   Mizuno,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-NOV-2000) Takuya Mizuno, The University of Tokyo,
            Department of Veterinary Internal Medicine; Yayoi 1-1-1, Bunkyo-ku,
            Tokyo 113-8657, Japan (E-mail:aa77165@mail.ecc.u-tokyo.ac.jp,
            Tel:81-3-5841-8004, Fax:81-3-5841-8178)
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ORIGIN

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Qy        301 TCCCCACCGTGCCTGGCCTGCTGCTGCCACTGGTGCTTCCAGCTCTGTTGGCAGATGTGT 360
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Qy        361 ACCCCGCAGGGGTTCAGGGGCTGGTCCCTCACCCCGGGGACCTGGAGAAGAGAGAGAGTC 420
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Qy        421 CCTGTCCCCAAGGAAAATATAACCACCCGCAAAATAGCACCATTTGCTGCACCAAGTGCC 480
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Qy        481 ACAAAGGTACCTATCTGTACAATGACTGTCCGGGTCCAGGGCGAGACACGGACTGCAGGG 540
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Qy        541 TGTGTGCCCCTGGCACCTACACTGCCTTGGAGAACCATCTCAGACGATGCCTGAGCTGCT 600
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Qy       1378 GCGCCCCCGATCAGCTCGCGGATGCCGACCCCGCGACCCTGTACGCGGTGGTGGACGGCG 1437
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Qy       1438 TGCCCCCGTCGCGCTGGAAGGAGTTGGTGCGGCGGCTGGGACTGAGCGAGCACGAGATCG 1497
Db       1269 TGCCCCCGTCGCGCTGGAAGGAGTTCGTGCGGCGGCTGGGGCTGAGCGAGCACGAGATCG 1328

Qy       1498 AGCGGCTGGAGCTGGAGAACGGGCGCCACCTGCGCGAGGCGCAGTACAGCATGCTGGCGG 1557
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Db       1329 AGCGGCTGGAGCTGCAGAACGGGCGCTGCCTGCGCGAGGCGCACTACAGCATGCTGGCGG 1388

Qy       1558 CCTGGCGGCGGCGCACGCCGCGCCGCGAGGCCACGCTGGAGCTGCTGGGCCGCGTGCTCA 1617

Db       1389 CCTGGCGGCGACGCACGCCACGACGCGAAGCCACGCTGGAGCTGCTGGGCCGCGTGCTCC 1448

Qy       1618 GGGACATGGACCTGCTGGGTTGCCTGGAAAACATAGAGGAGGCGCTGGGTGGCGCCGCCC 1677

Db       1449 GTGACATGGACCTGCTCGGCTGCCTGGAGGACATCGAGGAGGCGCTGTGCGCCCCCGCCT 1508

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Db       1566 CTGCTCTGAGGACCGCTGCCTACAGTCGGGGCGGCCCAGAAGGACGG----TGCGAGGTG 1621

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Qy       1858 CACGATCTGGCAGCCACTGACCTGGTGCTACTCACTCAGTGTACATAGCTTTTCTCAGCT 1917

Db       1667 CAGAAGCTGGCAGCCACCTACTTGGTGCTACTCCCTCAGTGTACACAGAATTTTCTCCGT 1726

Qy       1918 GCCTGAGTGTGTGTCTGTGTGTAGTGTGTGTCTGCGTGCAGTGCGTGTGTTTGTGTCTCT 1977

Db       1727 TTTCGGAGCACTGCCGGAGGGTCAGCCTTGTGTGTGTG---------------------- 1764

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Qy       2038 AGCCCAAGGCAGTGGTTGCGAAGATGAGGGGCGCCCTGCCTTATTGCCTGTTTTTTGGGC 2097

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Qy       2098 TTGGAGAACTCAGCAAGGCGACTTGGGGAACCTACGTCGGTCCCTGAGCCGGTTTCGCAG 2157

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Qy       2158 TAGATAAGCCATCTTTGTATCCACTCTGCACATCCACTCATCCACTCTGTACACTAATAG 2217

Db       1927 TAGATAAGCAATCTTTTTTATCAATTATGTTACACTAATAGAAACTGGGCACGCCTCTGC 1986

Qy       2218 AAACTTTGTTGCCCTGC-CTGGACCAGCTGAACTGTCCCCAGGCAGCGGGGGAGCACAGA 2276

Db       1987 CCCCTGCCTGGACAAGCACAGGGTGAGCTGACCTGTCCGAAGGCAGGGGCAG-GCACAGA 2045

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Db       2046 ACAATGGGGCGGCCAGCAGGAGCT 2069
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RESULT 5
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LOCUS BC010140 2194 bp mRNA linear PRI 12-JUL-2001
DEFINITION Homo sapiens, tumor necrosis factor receptor superfamily, member 1A, clone MGC:19588 IMAGE:4131360, mRNA, complete cds.
ACCESSION BC010140
VERSION BC010140.1 GI:14603367
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2194)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (02-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S., Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R., Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J., Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 27 Row: m Column: 22
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 339755.

FEATURES Location/Qualifiers
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/db_xref="taxon:9606"
/clone="MGC:19588 IMAGE:4131360"
/tissue_type="Muscle, rhabdomyosarcoma"
/clone_lib="NIH_MGC_17"
/lab_host="DH10B-R"
/note="Vector: pOTB7"
CDS 241. .1608
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/product="tumor necrosis factor receptor superfamily, member 1A"
/protein_id="AAH10140.1"
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/translation="MGLSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVC
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PSLLR"
BASE COUNT 478 a 644 c 600 g 472 t
ORIGIN

Query Match 30.4%; Score 742.2; DB 9; Length 2194;
Best Local Similarity 69.8%; Pred. No. 6.7e-120;
Matches 1176; Conservative 0; Mismatches 413; Indels 96; Gaps 9;

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Qy        182 ACCCGAGGCCCGGGCTCCACTGGGCATACGCGAGGACCGTGTTGCTGTCACTGTCGCGGG 241

Db        129 CCCAAGGCACTTGGGACGTCCTGGACAGACCGAGTCCCGGGAAGCCCCAGCACTGCCGCT 188

Qy        242 CCGCCACTGCCCC-AGCCCTGATGGGGGATTGAGAGGCCACAGCTGGCCGGACATGGGCC 300

Db        189 GCCACACTGCCCTGAGCCCAAATGGGGGAGTGAGAGGCCATAGCTGTCTGG-CATGGGCC 247
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Qy       301 TCCCCACCGTGCCTGGCCTGCTGCTGCCACTGGTGCTTCCAGCTCTGTTGGCAGATGTGT 360
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Qy       361 ACCCCGCAGGGGTTCAGGGGCTGGTCCCTCACCCCGGGGACCTGGAGAAGAGAGAGAGTC 420
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Qy       421 CCTGTCCCCAAGGAAAATATAACCACCCGCAAAATAGCACCATTTGCTGCACCAAGTGCC 480
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Qy       481 ACAAAGGTACCTATCTGTACAATGACTGTCCGGGTCCAGGGCGAGACACGGACTGCAGGG 540
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Qy       541 TGTGTGCCCCTGGCACCTACACTGCCTTGGAGAACCATCTCAGACGATGCCTGAGCTGCT 600
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Qy       601 CCAGGTGCCGGGACGAAATGTTCCAGGTGGAGATTTCGCCTTGTGTAGTGGACCGGGACA 660
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Qy       661 CTGTGTGCGGCTGCAGGAAGAACCAGTACCGGGAATACTGGGGTGAAACTGGCTTCCGGT 720
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Qy       721 GTCTGAACTGCAGCCTCTGTCCCAATGGCACAGTGAATATCCCCTGCCAGGAGAGACAGG 780
Db       668 GCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAGAAACAGA 727

Qy       781 ACACCATCTGCCACTGCCATATGGGCTTCTTTCTTAAAGGCGCCAAGTGCATCTCCTGTC 840
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Qy       841 ATGATTGTAAGAA---CAAGGAGTGCGAGAAGTTATGTCCAACCCGACCTTCAACTGGTA 897
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Qy       898 AAGACTCTCAGGACCCAGGCACTACAGTACTATTACCCCTGGTGATTGTCTTCGGGCTTT 957
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Qy       958 GCCTGGCATCCTTCGCCTCTGTCGTCTTAGCATGTCGCTACCAGCGGTGGAAGCCCAAGC 1017
Db       908 GCCTTTTATCCCTCCTCTTCATTGGTTTAATGTATCGCTACCAACGGTGGAAGTCCAAGC 967

Qy      1018 TCTACTCCATCATTTGCGGGCAGTCGACTCTGGTAAAAGAGGGGGAGCCAGAA------- 1070
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Qy      1071 --CTCCTGGTCCCGGCCCCAGGCTTCAACCCCACCACCACCATCTGCTTCAGCTCCACCC 1128
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Qy      1129 CAAGTTCCAGTCCTGTCTCCATTCCCCCTTACATCTCCTGTGACCGGTCCAACTTCGGAG 1188
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Qy      1189 ---------CCGTCGCATCTCCCTCCAGCGAGACGGCCCCGCCCCATCTAAAGGCTGGCC 1239
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Qy      1240 CCATCCTCCCGGGGGCCTCCGGCCTCCACCCACCTCTGTACCCCGGGGGCCTCCGGCCTCCA 1299
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Qy      1300 CCCACCTCTGTACCCCGGGGCCTCCGGCCTCCACCCACCTCTGCACCCCAGTTCAGAAGT 1359
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Qy      1360 GGGAAGCCAGCGCCCCCAGCGCCCCCGATCAGCTCGCGGATGCCGACCCCGCGACCCTGT 1419
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Qy      1420 ACGCGGTGGTGGACGGCGTGCCCCCGTCGCGCTGGAAGGAGTTGGTGCGGCGGCTGGGAC 1479
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Qy      1540 AGTACAGCATGCTGGCGGCCTGGCGGCGGCGCACGCCGCGCCGCGAGGCCACGCTGGAGC 1599
Db       1439 AATACAGCATGCTGGCGACCTGGAGGCGGCGCACGCCGCGGCGCGAGGCCACGCTGGAGC 1498

Qy      1600 TGCTGGGCCGCGTGCTCAGGGACATGGACCTGCTGGGTTGCCTGGAAAACATAGAGGAGG 1659
Db       1499 TGCTGGGACGCGTGCTCCGCGACATGGACCTGCTGGGCTGCCTGGAGGACATCGAGGAGG 1558

Qy      1660 CGCTGGGTGGCGCCGCCCGCCTCGCGTCCGAGCCCCGCCTTCTCTGGTGAAGCCCCGCCC 1719
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Qy      1720 CTCCG 1724
Db       1619 CTGCG 1623
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RESULT 6
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LOCUS       HUMTNFRC                2112 bp    mRNA    linear   PRI 03-AUG-1993
DEFINITION  Human tumor necrosis factor receptor (TNF receptor) mRNA, complete
            cds.
ACCESSION   M63121 M75861
VERSION     M63121.1  GI:339755
KEYWORDS    tumor necrosis factor receptor.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2112)
  AUTHORS   Himmler,A., Maurer-Fogy,I., Kronke,M., Scheurich,P.,
            Pfizenmaier,K., Lantz,M., Olsson,I., Hauptmann,R., Stratowa,C. and
            Adolf,G.R.
  TITLE     Molecular cloning and expression of human and rat tumor necrosis
            factor receptor chain (p60) and its soluble derivative, tumor
            necrosis factor-binding protein
  JOURNAL   DNA Cell Biol. 9 (10), 705-715 (1990)
  MEDLINE   91090841
   PUBMED   1702293
COMMENT     Original source text: Human cDNA to mRNA.
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Query Match 30.2%; Score 735.8; DB 9; Length 2112;
Best Local Similarity 69.9%; Pred. No. 8.9e-119;
Matches 1152; Conservative 0; Mismatches 402; Indels 95; Gaps 8;

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Qy        158 CCAGTCTCAACCCTCCACTCCCCGACCCGAGGCCCGGGCTCCACTGGGCATACGCGAGGA 217
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Qy        218 CCGTGTTGCTGTCACTGTCGCGGGCCGCCACTGCCCC-AGCCCTGATGGGGGATTGAGAG 276
Db        131 CCGGGAAGCCCCAGCACTGCCGCTGCCACACTGCCCTGAGCCCAAATGGGGGAGTGAGAG 190

Qy        277 GCCACAGCTGGCCGGACATGGGCCTCCCCACCGTGCCTGGCCTGCTGCTGCCACTGGTGC 336
Db        191 GCCATAGCTGTCTGG-CATGGGCCTCTCCACCGTGCCTGACCTGCTGCTGCCACTGGTGC 249

Qy        337 TTCCAGCTCTGTTGGCAGATGTGTACCCCGCAGGGGTTCAGGGGCTGGTCCCTCACCCCG 396
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Qy        397 GGGACCTGGAGAAGAGAGAGAGTCCCTGTCCCCAAGGAAAATATAACCACCCGCAAAATA 456
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Qy        457 GCACCATTTGCTGCACCAAGTGCCACAAAGGTACCTATCTGTACAATGACTGTCCGGGTC 516
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Qy        637 CGCCTTGTGTAGTGGACCGGGACACTGTGTGCGGCTGCAGGAAGAACCAGTACCGGGAAT 696
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Qy        697 ACTGGGGTGAAACTGGCTTCCGGTGTCTGAACTGCAGCCTCTGTCCCAATGGCACAGTGA 756
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Qy        757 ATATCCCCTGCCAGGAGAGACAGGACACCATCTGCCACTGCCATATGGGCTTCTTTCTTA 816
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Qy        817 AAGGCGCCAAGTGCATCTCCTGTCATGATTGTAAGAA---CAAGGAGTGCGAGAAGTTAT 873
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Qy        874 GTCCAACCCGACCTTCAACTGGTAAAGACTCTCAGGACCCAGGCACTACAGTACTATTAC 933
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Qy        934 CCCTGGTGATTGTCTTCGGGCTTTGCCTGGCATCCTTCGCCTCTGTCGTCTTAGCATGTC 993
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Qy        994 GCTACCAGCGGTGGAAGCCCAAGCTCTACTCCATCATTTGCGGGCAGTCGACTCTGGTAA 1053
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Qy       1165 CCTGTGACCGGTCCAACTTCGGAG---------CCGTCGCATCTCCCTCCAGCGAGACGG 1215
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Qy       1216 CCCCGCCCCATCTAAAGGCTGGCCCCATCCTCCCGGGGCCTCCGGCCTCCACCCACCTCT 1275
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Qy       1576 CGCGCCGCGAGGCCACGCTGGAGCTGCTGGGCCGCGTGCTCAGGGACATGGACCTGCTGG 1635
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Db        1501 GCTGCCTGGAGGACATCGAGGAGGCGCTTTGCGGCCCCGCCGCCCTCCCGCCCGCGCCCA 1560

Qy       1696 GCCTTCTCTGGTGAAGCCCCGCCCCTCCG 1724
Db        1561 GTCTTCTCAGATGAGGCTGCGCCCCTGCG 1589
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RESULT 7
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LOCUS       HUMTNFR                 2087 bp    mRNA    linear   PRI 10-NOV-1993
DEFINITION  Human tumor necrosis factor receptor mRNA, complete cds.
ACCESSION   M33294
VERSION     M33294.1  GI:339744
KEYWORDS    cell surface receptor; tumor necrosis factor receptor.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2087)
  AUTHORS   Schall,T.J., Lewis,M., Koller,K.J., Lee,A.L., Rice,G.C., Wong,G.H.,
            Gatanaga,T., Granger,G.A., Lentz,R., Raab,H., Kohr,W.J. and
            Goeddel,D.V.
  TITLE     Molecular cloning and expression of a receptor for human tumor
            necrosis factor
  JOURNAL   Cell 61 (2), 361-370 (1990)
  MEDLINE   90235285
   PUBMED   2158863
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COMMENT     Original source text: Human placenta, cDNA to mRNA.
            Draft entry and computer-readable sequence for [1] kindly submitted
            by T.Schall, 26-MAR-1990.
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     CDS             182. .1549
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                     /db_xref="GI:339745"
                     /translation="MGLSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVC
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BASE COUNT      433 a    624 c    581 g    449 t
ORIGIN

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Qy       208 TACGCGAGGACCGTGTTGCTGTCACTGTCGCGGGCCGCCACTGCCC-CAGCCCTGATGGG 266
Db        96 AGACCGAGTCCCGGGAAGCCCCAGCACTGCCGCTGCCACACTGCCCTGAGCCCAAATGGG 155

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DEFINITION  Sequence 1 from Patent EP0657536.
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VERSION     A43873.1  GI:2299022
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SOURCE      unidentified
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REFERENCE   1  (bases 1 to 2175)
  AUTHORS   Wallach,D., Brackebusch,C., Varfolomeev,E. and Batkin,M.
  TITLE     Proteases capable of shedding the soluble TNF-receptor and TNF-R
            derived peptides and antibodies against the proteases inhibiting
            the shedding
  JOURNAL   Patent: EP 0657536-A 1 14-JUN-1995;
            YEDA RES & DEV (IL)
COMMENT     Other publication ZA 9407962 951121
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BASE COUNT      474 a    641 c    604 g    456 t
ORIGIN

  Query Match           29.8%;  Score 727;  DB 6;  Length 2175;
  Best Local Similarity 69.6%;  Pred. No. 3.1e-117;
  Matches 1129;  Conservative    0;  Mismatches  400;  Indels   92;  Gaps    7;

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Qy     1044 ACTCTGGTAAAAGAGGGGGAGCCAGAA---------CTCCTGGTCCCGGCCCCAGGCTTC 1094
Db     1009 ACACCTGAAAAAGAGGGGGAGCTTGAAGGAACTACTACTAAGCCCCTGGCCCCAAACCCA 1068

Qy     1095 AACCCCACCACCACCATCTGCTTCAGCTCCACCCCAAGTTCCAGTCCTGTCTCCATTCCC 1154
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RESULT 9
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DEFINITION  Sequence 7 from Patent EP0568925.
ACCESSION   A78738
VERSION     A78738.1  GI:6090341
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 2175)
  AUTHORS   Brakebusch,C. and Wallach,D.
  TITLE     TNF RECEPTOR ACTION MODULATION
  JOURNAL   Patent: EP 0568925-A 7 10-NOV-1993;
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  Query Match           29.8%;  Score 727;  DB 6;  Length 2175;
  Best Local Similarity 69.6%;  Pred. No. 3.1e-117;
  Matches 1129;  Conservative    0;  Mismatches  400;  Indels   92;  Gaps    7;

Qy        148 TGTCCCCGCCCCAGTCTCAACCCTCCACTCCCCGACCCGAGGCCCGGGCTCCACTGGGCA 207
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Qy        208 TACGCGAGGACCGTGTTGCTGTCACTGTCGCGGGCCGCCACTGCCC-CAGCCCTGATGGG 266
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Qy        387 CCTCACCCCGGGGACCTGGAGAAGAGAGAGAGTCCCTGTCCCCAAGGAAAATATAACCAC 446
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Qy       1044 ACTCTGGTAAAAGAGGGGGAGCCAGAA---------CTCCTGGTCCCGGCCCCAGGCTTC 1094
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Qy       1095 AACCCCACCACCACCATCTGCTTCAGCTCCACCCCAAGTTCCAGTCCTGTCTCCATTCCC 1154
Db       1069 AGCTTCAGTCCCACTCCAGGCTTCACCCCCACCCTGGGCTTCAGTCCCGTGCCCAGTTCC 1128

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Qy       1206 AGCGAGACGGCCCCGCCCCATCTAAAGGCTGGCCCCATCCTCCCGGGGCCTCCGGCCTCC 1265
Db       1189 AGAGAGGTGGCACCACCCTATCAGGGGGCTGACCCCATCCT------------------- 1229

Qy       1266 ACCCACCTCTGTACCCCGGGGCCTCCGGCCTCCACCCACCTCTGTACCCCGGGGCCTCCG 1325
Db       1230 ----------------------------------------------TGCGACAGCCCTC 1242

Qy       1326 GCCTCCACCCACCTCTGCACCCCAGTTCAGAAGTGGGAAGCCAGCGCCCCCAGCGCCCCC 1385
Db       1243 GCCTCCGACCCCATCCCCAACCCCCTTCAGAAGTGGGAGGACAGCGCCCACA---AGCCA 1299

Qy       1386 GATCAGCTCGCGGATGCCGACCCCGCGACCCTGTACGCGGTGGTGGACGGCGTGCCCCCG 1445
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            Aderka,D.
  TITLE     Expression of the recombinant tumor necrosis factor binding protein
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  JOURNAL   Patent: US 5811261-A 1 22-SEP-1998;
FEATURES             Location/Qualifiers
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BASE COUNT      474 a    641 c    604 g    456 t
ORIGIN

  Query Match           29.8%;  Score 727;  DB 6;  Length 2175;
  Best Local Similarity  69.6%;  Pred. No. 3.1e-117;
  Matches 1129;  Conservative    0;  Mismatches  400;  Indels   92;  Gaps    7;

Qy        148 TGTCCCCGCCCCAGTCTCAACCCTCCACTCCCCGACCCGAGGCCCGGGCTCCACTGGGCA 207
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Db        170 AGACCGAGTCCCGGGAAGCCCCAGCACTGCCGCTGCCACACTGCCCTGAGCCCAAATGGG 229

Qy        267 GGATTGAGAGGCCACAGCTGGCCGGACATGGGCCTCCCCACCGTGCCTGGCCTGCTGCTG 326
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Qy       1044 ACTCTGGTAAAAGAGGGGGAGCCAGAA---------CTCCTGGTCCCGGCCCCAGGCTTC 1094
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Db       1069 AGCTTCAGTCCCACTCCAGGCTTCACCCCCACCCTGGGCTTCAGTCCCGTGCCCAGTTCC 1128

Qy       1155 CCTTACATCTCCTGTGACCGGTCCAACTTCGGAG---------CCGTCGCATCTCCCTCC 1205
Db       1129 ACCTTCACCTCCAGCTCCACCTATACCCCCGGTGACTGTCCCAACTTTGCGGCTCCCCGC 1188

Qy       1206 AGCGAGACGGCCCCGCCCCATCTAAAGGCTGGCCCCATCCTCCCGGGGCCTCCGGCCTCC 1265
Db       1189 AGAGAGGTGGCACCACCCTATCAGGGGGCTGACCCCATCCT------------------- 1229

Qy       1266 ACCCACCTCTGTACCCCGGGGCCTCCGGCCTCCACCCACCTCTGTACCCCGGGGCCTCCG 1325
Db       1230 ----------------------------------------------TGCGACAGCCCTC 1242

Qy       1326 GCCTCCACCCACCTCTGCACCCCAGTTCAGAAGTGGGAAGCCAGCGCCCCCAGCGCCCCC 1385
Db       1243 GCCTCCGACCCCATCCCCAACCCCCTTCAGAAGTGGGAGGACAGCGCCCACA---AGCCA 1299

Qy       1386 GATCAGCTCGCGGATGCCGACCCCGCGACCCTGTACGCGGTGGTGGACGGCGTGCCCCCG 1445
Db       1300 CAGAGCCTAGACACTGATGACCCCGCGACGCTGTACGCCGTGGTGGAGAACGTGCCCCCG 1359

Qy       1446 TCGCGCTGGAAGGAGTTGGTGCGGCGGCTGGGACTGAGCGAGCACGAGATCGAGCGGCTG 1505
Db       1360 TTGCGCTGGAAGGAATTCGTGCGGCGCCTAGGGCTGAGCGACCACGAGATCGATCGGCTG 1419

Qy       1506 GAGCTGGAGAACGGGCGCCACCTGCGCGAGGCGCAGTACAGCATGCTGGCGGCCTGGCGG 1565
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Qy       1566 CGGCGCACGCCGCGCCGCGAGGCCACGCTGGAGCTGCTGGGCCGCGTGCTCAGGGACATG 1625
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Qy       1626 GACCTGCTGGGTTGCCTGGAAAACATAGAGGAGGCGCTGGGTGGCGCCGCCCGCCTCGCG 1685
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Qy       1686 TCCGAGCCCCGCCTTCTCTGGTGAAGCCCCGCCCCTCCGACTGCGGGCCTCCCCGCCCTG 1745
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Qy       1746 C 1746
Db       1660 C 1660


RESULT 11
I64751
LOCUS       I64751                  2175 bp    DNA     linear   PAT 07-OCT-1997
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DEFINITION  Sequence 1 from patent US 5665859.
ACCESSION   I64751
VERSION     I64751.1  GI:2481645
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2175)
  AUTHORS   Wallach,D., Brakebusch,C., Varfolomeev,E. and Batkin,M.
  TITLE     Molecules influencing the shedding of the TNF receptor, their
            preparation and their use
  JOURNAL   Patent: US 5665859-A 1 09-SEP-1997;
FEATURES             Location/Qualifiers
     source          1. .2175
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BASE COUNT      474 a    641 c    604 g    456 t
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Query Match 29.8%; Score 727; DB 6; Length 2175;
Best Local Similarity 69.6%; Pred. No. 3.1e-117;
Matches 1129; Conservative 0; Mismatches 400; Indels 92; Gaps 7;

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Qy        148 TGTCCCCGCCCCAGTCTCAACCCTCCACTCCCCGACCCGAGGCCCGGGCTCCACTGGGCA 207
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Qy        208 TACGCGAGGACCGTGTTGCTGTCACTGTCGCGGGCCGCCACTGCCC-CAGCCCTGATGGG 266
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Qy        507 TGTCCGGGTCCAGGGCGAGACACGGACTGCAGGGTGTGTGCCCCTGGCACCTACACTGCC 566
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Db        589 GTGGAGATCTCTTCTTGCACAGTGGACCGGGACACCGTGTGTGGCTGCAGGAAGAACCAG 648

Qy        687 TACCGGGAATACTGGGGTGAAACTGGCTTCCGGTGTCTGAACTGCAGCCTCTGTCCCAAT 746
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Qy       1044 ACTCTGGTAAAAGAGGGGGAGCCAGAA---------CTCCTGGTCCCGGCCCCAGGCTTC 1094
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Db       1069 AGCTTCAGTCCCACTCCAGGCTTCACCCCCACCCTGGGCTTCAGTCCCGTGCCCAGTTCC 1128

Qy       1155 CCTTACATCTCCTGTGACCGGTCCAACTTCGGAG---------CCGTCGCATCTCCCTCC 1205
Db       1129 ACCTTCACCTCCAGCTCCACCTATACCCCCGGTGACTGTCCCAACTTTGCGGCTCCCCGC 1188

Qy       1206 AGCGAGACGGCCCCGCCCCATCTAAAGGCTGGCCCCATCCTCCCGGGGCCTCCGGCCTCC 1265
Db       1189 AGAGAGGTGGCACCACCCTATCAGGGGGCTGACCCCATCCT------------------- 1229

Qy       1266 ACCCACCTCTGTACCCCGGGGCCTCCGGCCTCCACCCACCTCTGTACCCCGGGGCCTCCG 1325
Db       1230 -*----------------------------------------------TGCGACAGCCCTC 1242

Qy       1326 GCCTCCACCCACCTCTGCACCCCAGTTCAGAAGTGGGAAGCCAGCGCCCCCAGCGCCCCC 1385
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Qy       1386 GATCAGCTCGCGGATGCCGACCCCGCGACCCTGTACGCGGTGGTGGACGGCGTGCCCCCG 1445
Db       1300 CAGAGCCTAGACACTGATGACCCCGCGACGCTGTACGCCGTGGTGGAGAACGTGCCCCCG 1359

Qy       1446 TCGCGCTGGAAGGAGTTGGTGCGGCGGCTGGGACTGAGCGAGCACGAGATCGAGCGGCTG 1505
Db       1360 TTGCGCTGGAAGGAATTCGTGCGGCGCCTAGGGCTGAGCGACCACGAGATCGATCGGCTG 1419

Qy       1506 GAGCTGGAGAACGGGCGCCACCTGCGCGAGGCGCAGTACAGCATGCTGGCGGCCTGGCGG 1565
Db       1420 GAGCTGCAGAACGGGCGCTGCCTGCGCGAGGCGCAATACAGCATGCTGGCGACCTGGAGG 1479

Qy       1566 CGGCGCACGCCGCGCCGCGAGGCCACGCTGGAGCTGCTGGGCCGCGTGCTCAGGGACATG 1625
Db       1480 CGGCGCACGCCGCGGCGCGAGGCCACGCTGGAGCTGCTGGGACGCGTGCTCCGCGACATG 1539

Qy       1626 GACCTGCTGGGTTGCCTGGAAAACATAGAGGAGGCGCTGGGTGGCGCCGCCCGCCTCGCG 1685
Db       1540 GACCTGCTGGGCTGCCTGGAGGACATCGAGGAGGCGCTTTGCGGCCCCGCCGCCCTCCCG 1599

Qy       1686 TCCGAGCCCCGCCTTCTCTGGTGAAGCCCCGCCCCTCCGACTGCGGGCCTCCCCGCCCTG 1745
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Qy       1746 C 1746
Db       1660 C 1660
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RESULT 12
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LOCUS       A26412                 2111 bp    DNA     linear   PAT 26-APR-1995
DEFINITION  cDNA for (55kD TNF-BP) tumor necrosis factor binding protein from
            patent EP0417563.
ACCESSION   A26412
VERSION     A26412.1  GI:904968
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
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REFERENCE   1  (bases 1 to 2111)
  AUTHORS   Brockhaus,M., Dembic,Z., Gentz,R., Lesslauer,W., Loetscher,H. and
            Schlaeger,E.J.
  TITLE     TNF-binding proteins
  JOURNAL   Patent: EP 0417563-A 24 20-MAR-1991;
            F. HOFFMANN-LA ROCHE AG
FEATURES             Location/Qualifiers
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BASE COUNT      445 a    629 c    587 g    450 t
ORIGIN

  Query Match           29.7%;  Score 725.8;  DB 6;  Length 2111;
  Best Local Similarity  70.0%;  Pred. No. 5e-117;
  Matches 1120;  Conservative    0;  Mismatches  387;  Indels   92;  Gaps    7;

Qy       148 TGTCCCCGCCCCAGTCTCAACCCTCCACTCCCCGACCCGAGGCCCGGGCTCCACTGGGCA 207
Db        41 TCTCTATGCCCGAGTCTCAACCCTCAACTGTCACCCCAAGGCACTTGGGACGTCCTGGAC 100

Qy       208 TACGCGAGGACCGTGTTGCTGTCACTGTCGCGGGCCGCCACTGCCC-CAGCCCTGATGGG 266
Db       101 AGACCGAGTCCCGGGAAGCCCCAGCACTGCCGCTGCCACACTGCCCTGAGCCCAAATGGG 160

Qy       267 GGATTGAGAGGCCACAGCTGGCCGGACATGGGCCTCCCCACCGTGCCTGGCCTGCTGCTG 326
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Qy       387 CCTCACCCCGGGGACCTGGAGAAGAGAGAGAGTCCCTGTCCCCAAGGAAAATATAACCAC 446
Db       280 CCTCACCTAGGGGACAGGGAGAAGAGAGATAGTGTGTGTCCCCAAGGAAAATATATCCAC 339

Qy       447 CCGCAAAATAGCACCATTTGCTGCACCAAGTGCCACAAAGGTACCTATCTGTACAATGAC 506
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Qy       507 TGTCCGGGTCCAGGGCGAGACACGGACTGCAGGGTGTGTGCCCCTGGCACCTACACTGCC 566
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Qy       567 TTGGAGAACCATCTCAGACGATGCCTGAGCTGCTCCAGGTGCCGGGACGAAATGTTCCAG 626
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Qy       627 GTGGAGATTTCGCCTTGTGTAGTGGACCGGGACACTGTGTGCGGCTGCAGGAAGAACCAG 686
Db       520 GTGGAGATCTCTTCTTGCACAGTGGACCGGGACACCGTGTGTGGCTGCAGGAAGAACCAG 579

Qy       687 TACCGGGAATACTGGGGTGAAACTGGCTTCCGGTGTCTGAACTGCAGCCTCTGTCCCAAT 746
Db       580 TACCGGCATTATTGGAGTGAAAACCTTTTCCAGTGCTTCAATTGCAGCCTCTGCCTCAAT 639

Qy       747 GGCACAGTGAATATCCCCTGCCAGGAGAGACAGGACACCATCTGCCACTGCCATATGGGC 806
Db       640 GGGACCGTGCACCTCTCCTGCCAGGAGAAACAGAACACCGTGTGCACCTGCCATGCAGGT 699

Qy       807 TTCTTTCTTAAAGGCGCCAAGTGCATCTCCTGTCATGATTGTAAGAA---CAAGGAGTGC 863
Db       700 TTCTTTCTAAGAGAAAACGAGTGTGTCTCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGC 759

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Qy      1044 ACTCTGGTAAAAGAGGGGGAGCCAGAA---------CTCCTGGTCCCGGCCCCAGGCTTC 1094
Db       940 ACACCTGAAAAAGAGGGGGAGCTTGAAGGAACTACTACTAAGCCCCTGGCCCCAAACCCA 999

Qy      1095 AACCCCACCACCACCATCTGCTTCAGCTCCACCCCAAGTTCCAGTCCTGTCTCCATTCCC 1154
Db      1000 AGCTTCAGTCCCACTCCAGGCTTCACCCCCACCCTGGGCTTCAGTCCCGTGCCCAGTTCC 1059

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Db      1060 ACCTTCACCTCCAGCTCCACCTATACCCCCGGTGACTGTCCCAACTTTGCGGCTCCCCGC 1119

Qy      1206 AGCGAGACGGCCCCGCCCCATCTAAAGGCTGGCCCCATCCTCCCGGGGGCCTCCGGCCTCC 1265
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Qy      1326 GCCTCCACCCACCTCTGCACCCCAGTTCAGAAGTGGGAAGCCAGCGCCCCCAGCGCCCCC 1385
Db      1174 GCCTCCGACCCCATCCCCAACCCCCTTCAGAAGTGGGAGGACAGCGCCCACA---AGCCA 1230

Qy      1386 GATCAGCTCGCGGATGCCGACCCCGCGACCCTGTACGCGGTGGTGGACGGCGTGCCCCCG 1445
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Qy      1446 TCGCGCTGGAAGGAGTTGGTGCGGCGGCTGGGACTGAGCGAGCACGAGATCGAGCGGCTG 1505
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Qy      1506 GAGCTGGAGAACGGGCGCCACCTGCGCGAGGCGCAGTACAGCATGCTGGCGGCCTGGCGG 1565
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Qy      1626 GACCTGCTGGGTTGCCTGGAAAACATAGAGGAGGCGCTGGGTGGCGCCGCCCGCCTCGCG 1685
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RESULT 13
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LOCUS       AX409713               2111 bp    DNA     linear   PAT 14-JUN-2002
DEFINITION  Sequence 2360 from Patent WO0229103.
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ACCESSION   AX409713
VERSION     AX409713.1  GI:21442418
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Alvares,C., Horne,D., Peres-da-Silva,S. and Vockley,J.G.
  TITLE     Gene expression profiles in liver cancer
  JOURNAL   Patent: WO 0229103-A 2360 11-APR-2002;
            GENE LOGIC INC (US)
FEATURES             Location/Qualifiers
     source          1..2111
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                     /db_xref="taxon:9606"
                     /note="EMBL/GenBank Accession No. M58286"
BASE COUNT      445 a    629 c    587 g    450 t
ORIGIN

  Query Match             29.7%;  Score 725.8;  DB 6;  Length 2111;
  Best Local Similarity   70.0%;  Pred. No. 5e-117;
  Matches 1120;  Conservative    0;  Mismatches  387;  Indels   92;  Gaps    7;

Qy        148 TGTCCCCGCCCCAGTCTCAACCCTCCACTCCCCGACCCGAGGCCCGGGCTCCACTGGGCA 207
Db         41 TCTCTATGCCCGAGTCTCAACCCTCAACTGTCACCCCAAGGCACTTGGGACGTCCTGGAC 100

Qy        208 TACGCGAGGACCGTGTTGCTGTCACTGTCGCGGGCCGCCACTGCCC-CAGCCCTGATGGG 266
Db        101 AGACCGAGTCCCGGGAAGCCCCAGCACTGCCGCTGCCACACTGCCCTGAGCCCAAATGGG 160

Qy        267 GGATTGAGAGGCCACAGCTGGCCGGACATGGGCCTCCCCACCGTGCCTGGCCTGCTGCTG 326
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Qy        327 CCACTGGTGCTTCCAGCTCTGTTGGCAGATGTGTACCCCGCAGGGGTTCAGGGGCTGGTC 386
Db        220 CCGCTGGTGCTCCTGGAGCTGTTGGTGGGAATATACCCCTCAGGGGTTATTGGACTGGTC 279

Qy        387 CCTCACCCCGGGGACCTGGAGAAGAGAGAGAGTCCCTGTCCCCAAGGAAAATATAACCAC 446
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Qy        687 TACCGGGAATACTGGGGTGAAACTGGCTTCCGGTGTCTGAACTGCAGCCTCTGTCCCAAT 746
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Qy        747 GGCACAGTGAATATCCCCTGCCAGGAGAGACAGGACACCATCTGCCACTGCCATATGGGC 806
Db        640 GGGACCGTGCACCTCTCCTGCCAGGAGAAACAGAACACCGTGTGCACCTGCCATGCAGGT 699

Qy        807 TTCTTTCTTAAAGGCGCCAAGTGCATCTCCTGTCATGATTGTAAGAA---CAAGGAGTGC 863
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Qy        864 GAGAAGTTATGTCCAACCGGACCTTCAACTGGTAAAGACTCTCAGGACCCAGGCACTACA 923
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Qy        924 GTACTATTACCCCTGGTGATTGTCTTCGGGCTTTGCCTGGCATCCTTCGCCTCTGTCGTC 983
Db        820 GTGCTGTTGCCCCTGGTCATTTTCTTTGGTCTTTGCCTTTTATCCCTCCTCTTCATTGGT 879

Qy        984 TTAGCATGTCGCTACCAGCGGTGGAAGCCCAAGCTCTACTCCATCATTTGCGGGCAGTCG 1043
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Qy       1044 ACTCTGGTAAAAGAGGGGGAGCCAGAA---------CTCCTGGTCCCGGCCCCAGGCTTC 1094
Db        940 ACACCTGAAAAAGAGGGGGAGCTTGAAGGAACTACTACTAAGCCCCTGGCCCCAAACCCA 999

Qy       1095 AACCCCACCACCACCATCTGCTTCAGCTCCACCCCAAGTTCCAGTCCTGTCTCCATTCCC 1154
Db       1000 AGCTTCAGTCCCACTCCAGGCTTCACCCCCACCCTGGGCTTCAGTCCCGTGCCCAGTTCC 1059

Qy       1155 CCTTACATCTCCTGTGACCGGTCCAACTTCGGAG---------CCGTCGCATCTCCCTCC 1205
Db       1060 ACCTTCACCTCCAGCTCCACCTATACCCCCGGTGACTGTCCCAACTTTGCGGCTCCCCGC 1119

Qy       1206 AGCGAGACGGCCCCGCCCCATCTAAAGGCTGGCCCCATCCTCCCGGGGCCTCCGGCCTCC 1265
Db       1120 AGAGAGGTGGCACCACCCTATCAGGGGGCTGACCCCATCCT------------------- 1160

Qy       1266 ACCCACCTCTGTACCCCGGGGCCTCCGGCCTCCACCCACCTCTGTACCCCGGGGCCTCCG 1325
Db       1161 ---------------------------------------------TGCGACAGCCCTC 1173

Qy       1326 GCCTCCACCCACCTCTGCACCCCAGTTCAGAAGTGGGAAGCCAGCGCCCCCAGCGCCCCC 1385
Db       1174 GCCTCCGACCCCATCCCCAACCCCCTTCAGAAGTGGGAGGACAGCGCCCACA---AGCCA 1230

Qy       1386 GATCAGCTCGCGGATGCCGACCCCGCGACCCTGTACGCGGTGGTGGACGGCGTGCCCCCG 1445
Db       1231 CAGAGCCTAGACACTGATGACCCCGCGACGCTGTACGCCGTGGTGGAGAACGTGCCCCCG 1290

Qy       1446 TCGCGCTGGAAGGAGTTGGTGCGGCGGCTGGGACTGAGCGAGCACGAGATCGAGCGGCTG 1505
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Qy       1686 TCCGAGCCCCGCCTTCTCTGGTGAAGCCCCGCCCCTCCG 1724
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RESULT 14
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LOCUS       AX658239                2111 bp    DNA     linear   PAT 22-MAR-2003
DEFINITION  Sequence 155 from Patent WO03000928.
ACCESSION   AX658239
VERSION     AX658239.1  GI:29160775
KEYWORDS    .
SOURCE      Homo sapiens (human)
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
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  AUTHORS   Poulsen,H.S., Pedersen,N., Mortensen,S., Sorensen,S.B.,
            Petersen,M.W. and Elsner,H.I.
  TITLE     Methods for identification of cancer cell surface molecules and
            cancer specific promoters, and therapeutic uses thereof
  JOURNAL   Patent: WO 03000928-A 155 03-JAN-2003;
            Odin Medical A/S (DK)
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BASE COUNT      445 a    629 c    587 g    450 t
ORIGIN

  Query Match           29.7%;  Score 725.8;  DB 6;  Length 2111;
  Best Local Similarity   70.0%;  Pred. No. 5e-117;
  Matches 1120;  Conservative    0;  Mismatches  387;  Indels   92;  Gaps    7;

Qy        148 TGTCCCCGCCCCAGTCTCAACCCTCCACTCCCCGACCCGAGGCCCGGGCTCCACTGGGCA 207
Db         41 TCTCTATGCCCGAGTCTCAACCCTCAACTGTCACCCCAAGGCACTTGGGACGTCCTGGAC 100

Qy        208 TACGCGAGGACCGTGTTGCTGTCACTGTCGCGGGCCGCCACTGCCC-CAGCCCTGATGGG 266
Db        101 AGACCGAGTCCCGGGAAGCCCCAGCACTGCCGCTGCCACACTGCCCTGAGCCCAAATGGG 160

Qy        267 GGATTGAGAGGCCACAGCTGGCCGGACATGGGCCTCCCCACCGTGCCTGGCCTGCTGCTG 326
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Qy        447 CCGCAAAATAGCACCATTTGCTGCACCAAGTGCCACAAAGGTACCTATCTGTACAATGAC 506
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Qy        627 GTGGAGATTTCGCCTTGTGTAGTGGACCGGGACACTGTGTGCGGCTGCAGGAAGAACCAG 686
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Qy        687 TACCGGGAATACTGGGGTGAAACTGGCTTCCGGTGTCTGAACTGCAGCCTCTGTCCCAAT 746
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Qy        924 GTACTATTACCCCTGGTGATTGTCTTCGGGCTTTGCCTGGCATCCTTCGCCTCTGTCGTC 983
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Qy       1206 AGCGAGACGGCCCCGCCCCATCTAAAGGCTGGCCCCATCCTCCCGGGGCCTCCGGCCTCC 1265
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Db       1531 CCCGCGCCCAGTCTTCTCAGATGAGGCTGCGCCCCTGCG 1569


RESULT 15
HUMTNFRB
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DEFINITION  Homo sapiens tumor necrosis factor receptor mRNA, complete cds.
ACCESSION   M58286 M33480
VERSION     M58286.1  GI:339753
KEYWORDS    tumor necrosis factor receptor.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2111)
  AUTHORS   Loetscher,H., Pan,Y.C., Lahm,H.W., Gentz,R., Brockhaus,M.,
            Tabuchi,H. and Lesslauer,W.
  TITLE     Molecular cloning and expression of the human 55 kd tumor necrosis
            factor receptor
  JOURNAL   Cell 61 (2), 351-359 (1990)
  MEDLINE   90235284
   PUBMED   2158862
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COMMENT     Original source text: Human cell line HL60,·cDNA to mRNA.
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BASE COUNT      445 a    629 c    587 g    450 t
ORIGIN

  Query Match           29.7%;  Score 725.8;  DB 9;  Length 2111;
  Best Local Similarity  70.0%;  Pred. No. 5e-117;
  Matches 1120;  Conservative    0;  Mismatches  387;  Indels   92;  Gaps    7;

Qy        148 TGTCCCCGCCCCAGTCTCAACCCTCCACTCCCCGACCCGAGGCCCGGGCTCCACTGGGCA 207
Db         41 TCTCTATGCCCGAGTCTCAACCCTCAACTGTCACCCCAAGGCACTTGGGACGTCCTGGAC 100

Qy        208 TACGCGAGGACCGTGTTGCTGTCACTGTCGCGGGCCGCCACTGCCC-CAGCCCTGATGGG 266
Db        101 AGACCGAGTCCCGGGAAGCCCCAGCACTGCCGCTGCCACACTGCCCTGAGCCCAAATGGG 160

Qy        267 GGATTGAGAGGCCACAGCTGGCCGGACATGGGCCTCCCCACCGTGCCTGGCCTGCTGCTG 326
Db        161 GGAGTGAGAGGCCATAGCTGTCTGG-CATGGGCCTCTCCACCGTGCCTGACCTGCTGCTG 219

Qy        327 CCACTGGTGCTTCCAGCTCTGTTGGCAGATGTGTACCCCGCAGGGGTTCAGGGGCTGGTC 386
Db        220 CCGCTGGTGCTCCTGGAGCTGTTGGTGGGAATATACCCCTCAGGGGTTATTGGACTGGTC 279

Qy        387 CCTCACCCCGGGGACCTGGAGAAGAGAGAGAGTCCCTGTCCCCAAGGAAAATATAACCAC 446
Db        280 CCTCACCTAGGGGACAGGGAGAAGAGAGATAGTGTGTGTCCCCAAGGAAAATATATCCAC 339

Qy        447 CCGCAAAATAGCACCATTTGCTGCACCAAGTGCCACAAAGGTACCTATCTGTACAATGAC 506
Db        340 CCTCAAAATAATTCGATTTGCTGTACCAAGTGCCACAAAGGAACCTACTTGTACAATGAC 399

Qy        507 TGTCCGGGTCCAGGGCGAGACACGGACTGCAGGGTGTGTGCCCCTGGCACCTACACTGCC 566
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Qy        567 TTGGAGAACCATCTCAGACGATGCCTGAGCTGCTCCAGGTGCCGGGACGAAATGTTCCAG 626
Db        460 TCAGAAAACCACCTCAGACACTGCCTCAGCTGCTCCAAATGCCGAAAGGAAATGGGTCAG 519

Qy        627 GTGGAGATTTCGCCTTGTGTAGTGGACCGGGACACTGTGTGCGGCTGCAGGAAGAACCAG 686
Db        520 GTGGAGATCTCTTCTTGCACAGTGGACCGGGACACCGTGTGTGGCTGCAGGAAGAACCAG 579

Qy        687 TACCGGGAATACTGGGGTGAAACTGGCTTCCGGTGTCTGAACTGCAGCCTCTGTCCCAAT 746
Db        580 TACCGGCATTATTGGAGTGAAAACCTTTTCCAGTGCTTCAATTGCAGCCTCTGCCTCAAT 639

Qy        747 GGCACAGTGAATATCCCCTGCCAGGAGAGACAGGACACCATCTGCCACTGCCATATGGGC 806
Db        640 GGGACCGTGCACCTCTCCTGCCAGGAGAAACAGAACACCGTGTGCACCTGCCATGCAGGT 699

Qy        807 TTCTTTCTTAAAGGCGCCAAGTGCATCTCCTGTCATGATTGTAAGAA---CAAGGAGTGC 863
Db        700 TTCTTTCTAAGAGAAAACGAGTGTGTCTCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGC 759

Qy        864 GAGAAGTTATGTCCAACCCGACCTTCAACTGGTAAAGACTCTCAGGACCCAGGCACTACA 923
Db        760 ACGAAGTTGTGCCTACCCCAGATTGAGAATGTTAAGGGCACTGAGGACTCAGGCACCACA 819

Qy        924 GTACTATTACCCCTGGTGATTGTCTTCGGGCTTTGCCTGGCATCCTTCGCCTCTGTCGTC 983
Db        820 GTGCTGTTGCCCCTGGTCATTTTCTTTGGTCTTTGCCTTTTATCCCTCCTCTTCATTGGT 879

Qy        984 TTAGCATGTCGCTACCAGCGGTGGAAGCCCAAGCTCTACTCCATCATTTGCGGGCAGTCG 1043
Db        880 TTAATGTATCGCTACCAACGGTGGAAGTCCAAGCTCTACTCCATTGTTTGTGGGAAATCG 939

Qy       1044 ACTCTGGTAAAAGAGGGGGAGCCAGAA---------CTCCTGGTCCCGGCCCCAGGCTTC 1094
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Qy       1095 AACCCCACCACCACCATCTGCTTCAGCTCCACCCCAAGTTCCAGTCCTGTCTCCATTCCC 1154
Db       1000 AGCTTCAGTCCCACTCCAGGCTTCACCCCCACCCTGGGCTTCAGTCCCGTGCCCAGTTCC 1059

Qy       1155 CCTTACATCTCCTGTGACCGGTCCAACTTCGGAG---------CCGTCGCATCTCCCTCC 1205
Db       1060 ACCTTCACCTCCAGCTCCACCTATACCCCCGGTGACTGTCCCAACTTTGCGGCTCCCCGC 1119

Qy       1206 AGCGAGACGGCCCCGCCCCATCTAAAGGCTGGCCCCATCCTCCCGGGGCCTCCGGCCTCC 1265
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Qy       1266 ACCCACCTCTGTACCCCGGGGCCTCCGGCCTCCACCCACCTCTGTACCCCGGGGCCTCCG 1325
Db       1161 ----------------------------------------------TGCGACAGCCCTC 1173

Qy       1326 GCCTCCACCCACCTCTGCACCCCAGTTCAGAAGTGGGAAGCCAGCGCCCCCAGCGCCCCC 1385
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Qy       1386 GATCAGCTCGCGGATGCCGACCCCGCGACCCTGTACGCGGTGGTGGACGGCGTGCCCCCG 1445
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Qy       1446 TCGCGCTGGAAGGAGTTGGTGCGGCGGCTGGGACTGAGCGAGCACGAGATCGAGCGGCTG 1505
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Db       1351 GAGCTGCAGAACGGGCGCTGCCTGCGCGAGGCGCAATACAGCATGCTGGCGACCTGGAGG 1410

Qy       1566 CGGCGCACGCCGCGCCGCGAGGCCACGCTGGAGCTGCTGGGCCGCGTGCTCAGGGACATG 1625
Db       1411 CGGCGCACGCCGCGGCGCGAGGCCACGCTGGAGCTGCTGGGACGCGTGCTCCGCGACATG 1470

Qy       1626 GACCTGCTGGGTTGCCTGGAAAACATAGAGGAGGCGCTGGGTGGCGCCGCCCGCCTCGCG 1685
Db       1471 GACCTGCTGGGCTGCCTGGAGGACATCGAGGAGGCGCTTTGCGGCCCCGCCGCCCTCCCG 1530

Qy       1686 TCCGAGCCCCGCCTTCTCTGGTGAAGCCCCGCCCCTCCG 1724
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Job time : 6022 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 15, 2003, 03:56:42 ; Search time 465 Seconds
(without alignments)
14164.793 Million cell updates/sec

Title: US-09-970-532-1
Perfect score: 2440
Sequence: 1 ttttttattttttttttctt.....ttaaaaaaaaaaaaaaaaaa 2440

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2440	100.0	2440	24	AAD42477	Bovine tumour necr
2	2440	100.0	2440	24	ABQ79378	Bovine tumour necr
3	735.8	30.2	2141	11	ABQ77487	Human TNF-R DNA hu
4	729.4	29.9	2141	11	AAQ06285	Human Tumour Necro
5	725.8	29.7	2088	12	AAQ10883	30kD TNF inhibitor
6	725.8	29.7	2088	22	AAC83946	Human 30 kDa TNF i
7	725.8	29.7	2111	20	AAZ09170	Human tumour necro
8	725.8	29.7	2111	22	AAH48859	Human TNFBP-associ
9	725.8	29.7	2111	24	ABK84039	Human cDNA differe
10	725.8	29.7	2111	24	ABN95862	Gene #2360 used to
11	725.8	29.7	2161	21	AAZ48475	Human tumour necro
12	725.8	29.7	2161	24	ABT04971	Cytokine tumour ne
13	725.8	29.7	2161	24	ABK13194	Human tumour necro
14	725.4	29.7	2175	16	AAQ90513	p55 TNF-R gene. H
15	724.2	29.7	2111	12	AAQ10955	Encodes human 55kD
16	721.8	29.6	2062	13	AAQ20973	TNF-alpha binding
17	721.8	29.6	2062	13	AAQ24440	Encodes TNF-alpha
18	721	29.5	2176	12	AAQ12215	Type I TNF recepto
19	719	29.5	2170	14	AAQ50870	p55 Tumour necrosi
20	683.8	28.0	1368	11	ABQ77479	Human TNF receptor
21	683.8	28.0	1368	14	AAQ49932	Lambda-derived TNF
22	683.8	28.0	1368	21	AAA95105	Human TNFR1 coding
23	599.2	24.6	2130	24	ABK63694	Rat sequence diffe
24	592.8	24.3	2173	11	ABQ77486	Rat TNF-R DNA raTN
25	592.4	24.3	2173	11	AAQ06284	Rat Tumour Necrosi
26	558	22.9	2179	24	ABT05130	Cytokine tumour ne
27	552.6	22.6	1334	11	ABQ77484	Human TNF-BP DNA d
28	551	22.6	1334	11	AAQ06282	Plasmid Tumour Nec
29	543	22.3	543	24	AAD42478	Bovine tumour necr
30	543	22.3	543	24	ABQ79379	Soluble bovine tum
31	399.2	16.4	413	25	ABX37720	Bovine EST associa
32	389.8	16.0	6889	17	AAT15931	DHFR/intron (WTras
33	388.6	15.9	6926	18	AAV04431	Vector pcDNA3-IgG1
34	388	15.9	1335	25	ABT32041	Concatameric immun
35	377.8	15.5	1887	25	ABT32043	Concatameric immun
36	371.8	15.2	608	13	AAQ24441	Encodes truncated
37	366.8	15.0	1827	25	ABT32045	Concatameric immun
38	336.6	13.8	504	13	AAQ24445	Encodes truncated
39	307.2	12.6	1478	20	AAX58150	CadC-fusion polype
40	304.4	12.5	507	24	ABL99490	Target canine gene
41	304.4	12.5	1301	18	AAT94022	cDNA for TBP(20-19
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43	286.4	11.7	483	11	ABQ77480	Human secretory TN
44	286.4	11.7	483	19	AAV41548	Human soluble tumo
45	286.4	11.7	483	19	AAV19801	Soluble tumour nec

ALIGNMENTS

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RESULT 1
AAD42477
ID   AAD42477 standard; cDNA; 2440 BP.
XX
AC   AAD42477;
XX
DT   15-NOV-2002  (first entry)
XX
DE   Bovine tumour necrosis factor receptor-I (TNF-RI) cDNA.
XX
KW   Bovine; cattle; coliform mastitis; inflammatory disease; receptor;
KW   tumour necrosis factor receptor-I; TNF-RI; antiinflammatory; gene; ss.
XX
OS   Bos taurus.
XX
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PD   18-JUN-2002.
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PF   25-FEB-2000; 2000US-0513007.
XX
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PR 26-FEB-1999; 99US-122156P.
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PA (IOWA) UNIV IOWA STATE RES FOUND INC.
PA (USDA) US SEC OF AGRIC.
XX
PI Taylor MJ, Kehrli ME, Lee E;
XX
DR WPI; 2002-588816/63.
DR P-PSDB; AAE25816.
XX
PT Novel nucleic acid molecule encoding bovine tumor necrosis factor
PT receptor-I which is a potent inhibitor of tumor necrosis factor-alpha
PT useful for treating coliform mastitis or other inflammatory disease in
PT cattle -
XX
PS Claim 1; Column 11-16; 16pp; English.
XX
CC The invention relates to an isolated nucleic acid encoding a polypeptide
CC that binds bovine tumour necrosis factor (TNF). The invention is useful
CC for expressing bovine TNF-RI or soluble bovine TNF-RI which is useful as
CC an inhibitor of TNF in cattle suffering from coliform mastitis or other
CC inflammatory disease. The nucleic acids and polypeptide or their
CC fragments are useful for treating mastitis. The present sequence is
CC bovine tumour necrosis factor receptor-I (TNF-RI) cDNA.
XX
SQ Sequence 2440 BP; 441 A; 771 C; 701 G; 527 T; 0 other;

Query Match 100.0%; Score 2440; DB 24; Length 2440;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2440; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 TCCTCTCAGCTCAAGTTTTCTCGGAGCTCTCCGGGCTCTGGGCCGCAGGGCTGGCCTTCC 120
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Qy        181 GACCCGAGGCCCGGGCTCCACTGGGCATACGCGAGGACCGTGTTGCTGTCACTGTCGCGG 240
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Db        181 GACCCGAGGCCCGGGCTCCACTGGGCATACGCGAGGACCGTGTTGCTGTCACTGTCGCGG 240

Qy        241 GCCGCCACTGCCCCAGCCCTGATGGGGGATTGAGAGGCCACAGCTGGCCGGACATGGGCC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCCGCCACTGCCCCAGCCCTGATGGGGGATTGAGAGGCCACAGCTGGCCGGACATGGGCC 300

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ACCCCGCAGGGGTTCAGGGGCTGGTCCCTCACCCCGGGGACCTGGAGAAGAGAGAGAGTC 420

Qy        421 CCTGTCCCCAAGGAAAATATAACCACCCGCAAAATAGCACCATTTGCTGCACCAAGTGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCTGTCCCCAAGGAAAATATAACCACCCGCAAAATAGCACCATTTGCTGCACCAAGTGCC 480

Qy        481 ACAAAGGTACCTATCTGTACAATGACTGTCCGGGTCCAGGGCGAGACACGGACTGCAGGG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ACAAAGGTACCTATCTGTACAATGACTGTCCGGGTCCAGGGCGAGACACGGACTGCAGGG 540

Qy        541 TGTGTGCCCCTGGCACCTACACTGCCTTGGAGAACCATCTCAGACGATGCCTGAGCTGCT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TGTGTGCCCCTGGCACCTACACTGCCTTGGAGAACCATCTCAGACGATGCCTGAGCTGCT 600

Qy        601 CCAGGTGCCGGGACGAAATGTTCCAGGTGGAGATTTCGCCTTGTGTAGTGGACCGGGACA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCAGGTGCCGGGACGAAATGTTCCAGGTGGAGATTTCGCCTTGTGTAGTGGACCGGGACA 660

Qy        661 CTGTGTGCGGCTGCAGGAAGAACCAGTACCGGGAATACTGGGGTGAAACTGGCTTCCGGT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CTGTGTGCGGCTGCAGGAAGAACCAGTACCGGGAATACTGGGGTGAAACTGGCTTCCGGT 720

Qy        721 GTCTGAACTGCAGCCTCTGTCCCAATGGCACAGTGAATATCCCCTGCCAGGAGAGACAGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTCTGAACTGCAGCCTCTGTCCCAATGGCACAGTGAATATCCCCTGCCAGGAGAGACAGG 780

Qy        781 ACACCATCTGCCACTGCCATATGGGCTTCTTTCTTAAAGGCGCCAAGTGCATCTCCTGTC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ACACCATCTGCCACTGCCATATGGGCTTCTTTCTTAAAGGCGCCAAGTGCATCTCCTGTC 840

Qy        841 ATGATTGTAAGAACAAGGAGTGCGAGAAGTTATGTCCAACCCGACCTTCAACTGGTAAAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ATGATTGTAAGAACAAGGAGTGCGAGAAGTTATGTCCAACCCGACCTTCAACTGGTAAAG 900

Qy        901 ACTCTCAGGACCCAGGCACTACAGTACTATTACCCCTGGTGATTGTCTTCGGGCTTTGCC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ACTCTCAGGACCCAGGCACTACAGTACTATTACCCCTGGTGATTGTCTTCGGGCTTTGCC 960

Qy        961 TGGCATCCTTCGCCTCTGTCGTCTTAGCATGTCGCTACCAGCGGTGGAAGCCCAAGCTCT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TGGCATCCTTCGCCTCTGTCGTCTTAGCATGTCGCTACCAGCGGTGGAAGCCCAAGCTCT 1020

Qy       1021 ACTCCATCATTTGCGGGCAGTCGACTCTGGTAAAAGAGGGGGAGCCAGAACTCCTGGTCC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ACTCCATCATTTGCGGGCAGTCGACTCTGGTAAAAGAGGGGGAGCCAGAACTCCTGGTCC 1080

Qy       1081 CGGCCCCAGGCTTCAACCCCACCACCACCATCTGCTTCAGCTCCACCCCAAGTTCCAGTC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CGGCCCCAGGCTTCAACCCCACCACCACCATCTGCTTCAGCTCCACCCCAAGTTCCAGTC 1140

Qy       1141 CTGTCTCCATTCCCCCTTACATCTCCTGTGACCGGTCCAACTTCGGAGCCGTCGCATCTC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 CTGTCTCCATTCCCCCTTACATCTCCTGTGACCGGTCCAACTTCGGAGCCGTCGCATCTC 1200

Qy       1201 CCTCCAGCGAGACGGCCCCGCCCCATCTAAAGGCTGGCCCCATCCTCCCGGGGCCTCCGG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CCTCCAGCGAGACGGCCCCGCCCCATCTAAAGGCTGGCCCCATCCTCCCGGGGCCTCCGG 1260

Qy       1261 CCTCCACCCACCTCTGTACCCCGGGGCCTCCGGCCTCCACCCACCTCTGTACCCCGGGGC 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CCTCCACCCACCTCTGTACCCCGGGGCCTCCGGCCTCCACCCACCTCTGTACCCCGGGGC 1320

Qy       1321 CTCCGGCCTCCACCCACCTCTGCACCCCAGTTCAGAAGTGGGAAGCCAGCGCCCCCAGCG 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 CTCCGGCCTCCACCCACCTCTGCACCCCAGTTCAGAAGTGGGAAGCCAGCGCCCCCAGCG 1380

Qy       1381 CCCCCGATCAGCTCGCGGATGCCGACCCCGCGACCCTGTACGCGGTGGTGGACGGCGTGC 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CCCCCGATCAGCTCGCGGATGCCGACCCCGCGACCCTGTACGCGGTGGTGGACGGCGTGC 1440

Qy       1441 CCCCGTCGCGCTGGAAGGAGTTGGTGCGGCGGCTGGGACTGAGCGAGCACGAGATCGAGC 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CCCCGTCGCGCTGGAAGGAGTTGGTGCGGCGGCTGGGACTGAGCGAGCACGAGATCGAGC 1500

Qy       1501 GGCTGGAGCTGGAGAACGGGCGCCACCTGCGCGAGGCGCAGTACAGCATGCTGGCGGCCT 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GGCTGGAGCTGGAGAACGGGCGCCACCTGCGCGAGGCGCAGTACAGCATGCTGGCGGCCT 1560

Qy       1561 GGCGGCGGCGCACGCCGCGCCGCGAGGCCACGCTGGAGCTGCTGGGCCGCGTGCTCAGGG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 GGCGGCGGCGCACGCCGCGCCGCGAGGCCACGCTGGAGCTGCTGGGCCGCGTGCTCAGGG 1620

Qy       1621 ACATGGACCTGCTGGGTTGCCTGGAAAACATAGAGGAGGCGCTGGGTGGCGCCGCCCGCC 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 ACATGGACCTGCTGGGTTGCCTGGAAAACATAGAGGAGGCGCTGGGTGGCGCCGCCCGCC 1680

Qy       1681 TCGCGTCCGAGCCCCGCCTTCTCTGGTGAAGCCCCGCCCCTCCGACTGCGGGCCTCCCCG 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 TCGCGTCCGAGCCCCGCCTTCTCTGGTGAAGCCCCGCCCCTCCGACTGCGGGCCTCCCCG 1740
```

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Qy       1741 CCCTGCAGACGGCTGCTTCCTTCCTGTGCCAGGCAGCCCGGAAGGATCTGCGAGATGCCC 1800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 CCCTGCAGACGGCTGCTTCCTTCCTGTGCCAGGCAGCCCGGAAGGATCTGCGAGATGCCC 1800

Qy       1801 TGTGGACCTCCTGTTTTGTTTTGTTTTTTTCTGGAGAGGAAGTCTTGGAGGAGCAGGCAC 1860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 TGTGGACCTCCTGTTTTGTTTTGTTTTTTTCTGGAGAGGAAGTCTTGGAGGAGCAGGCAC 1860

Qy       1861 GATCTGGCAGCCACTGACCTGGTGCTACTCACTCAGTGTACATAGCTTTTCTCAGCTGCC 1920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 GATCTGGCAGCCACTGACCTGGTGCTACTCACTCAGTGTACATAGCTTTTCTCAGCTGCC 1920

Qy       1921 TGAGTGTGTGTCTGTGTGTAGTGTGTGTCTGCGTGCAGTGCGTGTGTTTGTGTCTCTGTA 1980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 TGAGTGTGTGTCTGTGTGTAGTGTGTGTCTGCGTGCAGTGCGTGTGTTTGTGTCTCTGTA 1980

Qy       1981 TGTGCGTCTGTGTGATGTGGAGTGTGTGTACTCGTGAGAGAGGCCGAGTGTGCCCGGAGC 2040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 TGTGCGTCTGTGTGATGTGGAGTGTGTGTACTCGTGAGAGAGGCCGAGTGTGCCCGGAGC 2040

Qy       2041 CCAAGGCAGTGGTTGCGAAGATGAGGGGCGCCCTGCCTTATTGCCTGTTTTTTGGGCTTG 2100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 CCAAGGCAGTGGTTGCGAAGATGAGGGGCGCCCTGCCTTATTGCCTGTTTTTTGGGCTTG 2100

Qy       2101 GAGAACTCAGCAAGGCGACTTGGGGAACCTACGTCGGTCCCTGAGCCGGTTTCGCAGTAG 2160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 GAGAACTCAGCAAGGCGACTTGGGGAACCTACGTCGGTCCCTGAGCCGGTTTCGCAGTAG 2160

Qy       2161 ATAAGCCATCTTTGTATCCACTCTGCACATCCACTCATCCACTCTGTACACTAATAGAAA 2220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 ATAAGCCATCTTTGTATCCACTCTGCACATCCACTCATCCACTCTGTACACTAATAGAAA 2220

Qy       2221 CTTTGTTGCCCTGCCTGGACCAGCTGAACTGTCCCCAGGCAGCGGGGGAGCACAGAAAAA 2280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 CTTTGTTGCCCTGCCTGGACCAGCTGAACTGTCCCCAGGCAGCGGGGGAGCACAGAAAAA 2280

Qy       2281 TGGGGCCTCCCAAGGGAGCTAGCTGTTCAGTTCAGTTCAGTCGCTCAGTCGTGTCCGACT 2340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 TGGGGCCTCCCAAGGGAGCTAGCTGTTCAGTTCAGTTCAGTCGCTCAGTCGTGTCCGACT 2340

Qy       2341 CTTTGCGACCCTGTGAATCGCAGGGACTTCTGTAAATACACTAAAATCTTCCAATTAAAG 2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 CTTTGCGACCCTGTGAATCGCAGGGACTTCTGTAAATACACTAAAATCTTCCAATTAAAG 2400

Qy       2401 CTCTGCCCTGGAGGGACTGGTTAAAAAAAAAAAAAAAAAA 2440
             ||||||||||||||||||||||||||||||||||||||||
Db       2401 CTCTGCCCTGGAGGGACTGGTTAAAAAAAAAAAAAAAAAA 2440
```

RESULT 2
ABQ79378
ID ABQ79378 standard; cDNA; 2440 BP.
XX
AC ABQ79378;
XX
DT 05-NOV-2002 (first entry)
XX
DE Bovine tumour necrosis factor receptor-I cDNA.
XX
KW Bovine; tumour necrosis factor receptor-I; TNF-RI; antiinflammatory;
KW TNF cytotoxicity; mastitis; tumour necrosis factor-alpha; TNF-alpha;
KW monoclonal antibody BC9; TNF-beta; gene; ss.
XX
OS Bos taurus.
XX
FH Key   Location/Qualifiers
FT CDS   294..1709
FT   /*tag= a
FT   /product= "Bovine TNF-RI"
FT sig_peptide   294..383
FT   /*tag= b
FT   /label= signal_peptide
FT mat_peptide   384..1706
FT   /*tag= c
FT   /label= mature_bovine_TNF-RI
XX
PN US2002076765-A1.
XX
PD 20-JUN-2002.
XX
PF 03-OCT-2001; 2001US-0970532.
XX
PR 26-FEB-1999; 99US-122156P.
PR 25-FEB-2000; 2000US-0513007.
XX
PA (IOWA) UNIV IOWA STATE RES FOUND INC.
XX
PI Taylor MJ, Kehrli ME, Lee E, Mwangi S;
XX
DR WPI; 2002-557247/59.
DR P-PSDB; ABB98169.
XX
PT New isolated, soluble, bovine tumour necrosis factor receptor I, useful
PT for inhibiting tumour necrosis factor cytotoxicity for treating
PT mastitis, is a better inhibitor of tumour necrosis factor compared to
PT monoclonal antibody BC9 -
XX
PS Claim 1(a); Fig 1; 17pp; English.
XX
CC The invention relates to an isolated nucleic acid encoding bovine tumour
CC necrosis factor receptor-I (TNF-RI). The activity of polynucleotides of
CC the invention may be described as antiinflammatory. Polypeptides of the
CC invention are useful for inhibiting TNF cytotoxicity in a bovine. This is
CC useful for treating mastitis and other inflammatory disease. Soluble
CC bovine TNF-RI is a better inhibitor of bovine TNF-alpha than monoclonal
CC antibody BC9 (an antibody directed towards TNF-alpha), and can bind both
CC TNF-alpha and TNF-beta. The current sequence represents bovine tumour
CC necrosis factor receptor-I cDNA.
XX
SQ Sequence 2440 BP; 441 A; 771 C; 701 G; 527 T; 0 other;

```
  Query Match             100.0%;  Score 2440;  DB 24;  Length 2440;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2440;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTTTTATTTTTTTTTTTCTTTTTTGGGGGGGAAAGGGGTGACCCCCCTTCCCCTCCCACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TTTTTATTTTTTTTTTTCTTTTTTGGGGGGGAAAGGGGTGACCCCCCTTCCCCTCCCACC 60

Qy         61 TCCTCTCAGCTCAAGTTTTCTCGGAGCTCTCCGGGCTCTGGGCCGCAGGGCTGGCCTTCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCTCTCAGCTCAAGTTTTCTCGGAGCTCTCCGGGCTCTGGGCCGCAGGGCTGGCCTTCC 120

Qy        121 GGGTTTGAGGTCCTCCGGATTGGGCTGTGTCCCCGCCCCAGTCTCAACCCTCCACTCCCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGTTTGAGGTCCTCCGGATTGGGCTGTGTCCCCGCCCCAGTCTCAACCCTCCACTCCCC 180

Qy        181 GACCCGAGGCCCGGGCTCCACTGGGCATACGCGAGGACCGTGTTGCTGTCACTGTCGCGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GACCCGAGGCCCGGGCTCCACTGGGCATACGCGAGGACCGTGTTGCTGTCACTGTCGCGG 240

Qy        241 GCCGCCACTGCCCCAGCCCTGATGGGGGATTGAGAGGCCACAGCTGGCCGGACATGGGCC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCCGCCACTGCCCCAGCCCTGATGGGGGATTGAGAGGCCACAGCTGGCCGGACATGGGCC 300

Qy        301 TCCCCACCGTGCCTGGCCTGCTGCTGCCACTGGTGCTTCCAGCTCTGTTGGCAGATGTGT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCCCACCGTGCCTGGCCTGCTGCTGCCACTGGTGCTTCCAGCTCTGTTGGCAGATGTGT 360

Qy        361 ACCCCGCAGGGGTTCAGGGGCTGGTCCCTCACCCCGGGGACCTGGAGAAGAGAGAGAGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ACCCCGCAGGGGTTCAGGGGCTGGTCCCTCACCCCGGGGACCTGGAGAAGAGAGAGAGTC 420

Qy        421 CCTGTCCCCAAGGAAAATATAACCACCCGCAAAATAGCACCATTTGCTGCACCAAGTGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        421 CCTGTCCCCAAGGAAAATATAACCACCCGCAAAATAGCACCATTTGCTGCACCAAGTGCC 480
Qy        481 ACAAAGGTACCTATCTGTACAATGACTGTCCGGGTCCAGGGCGAGACACGGACTGCAGGG 540
Db        481 ACAAAGGTACCTATCTGTACAATGACTGTCCGGGTCCAGGGCGAGACACGGACTGCAGGG 540
Qy        541 TGTGTGCCCCTGGCACCTACACTGCCTTGGAGAACCATCTCAGACGATGCCTGAGCTGCT 600
Db        541 TGTGTGCCCCTGGCACCTACACTGCCTTGGAGAACCATCTCAGACGATGCCTGAGCTGCT 600
Qy        601 CCAGGTGCCGGGACGAAATGTTCCAGGTGGAGATTTCGCCTTGTGTAGTGGACCGGGACA 660
Db        601 CCAGGTGCCGGGACGAAATGTTCCAGGTGGAGATTTCGCCTTGTGTAGTGGACCGGGACA 660
Qy        661 CTGTGTGCGGCTGCAGGAAGAACCAGTACCGGGAATACTGGGGTGAAACTGGCTTCCGGT 720
Db        661 CTGTGTGCGGCTGCAGGAAGAACCAGTACCGGGAATACTGGGGTGAAACTGGCTTCCGGT 720
Qy        721 GTCTGAACTGCAGCCTCTGTCCCAATGGCACAGTGAATATCCCCTGCCAGGAGAGACAGG 780
Db        721 GTCTGAACTGCAGCCTCTGTCCCAATGGCACAGTGAATATCCCCTGCCAGGAGAGACAGG 780
Qy        781 ACACCATCTGCCACTGCCATATGGGCTTCTTTCTTAAAGGCGCCAAGTGCATCTCCTGTC 840
Db        781 ACACCATCTGCCACTGCCATATGGGCTTCTTTCTTAAAGGCGCCAAGTGCATCTCCTGTC 840
Qy        841 ATGATTGTAAGAACAAGGAGTGCGAGAAGTTATGTCCAACCCGACCTTCAACTGGTAAAG 900
Db        841 ATGATTGTAAGAACAAGGAGTGCGAGAAGTTATGTCCAACCCGACCTTCAACTGGTAAAG 900
Qy        901 ACTCTCAGGACCCAGGCACTACAGTACTATTACCCCTGGTGATTGTCTTCGGGCTTTGCC 960
Db        901 ACTCTCAGGACCCAGGCACTACAGTACTATTACCCCTGGTGATTGTCTTCGGGCTTTGCC 960
Qy        961 TGGCATCCTTCGCCTCTGTCGTCTTAGCATGTCGCTACCAGCGGTGGAAGCCCAAGCTCT 1020
Db        961 TGGCATCCTTCGCCTCTGTCGTCTTAGCATGTCGCTACCAGCGGTGGAAGCCCAAGCTCT 1020
Qy       1021 ACTCCATCATTTGCGGGCAGTCGACTCTGGTAAAAGAGGGGGAGCCAGAACTCCTGGTCC 1080
Db       1021 ACTCCATCATTTGCGGGCAGTCGACTCTGGTAAAAGAGGGGGAGCCAGAACTCCTGGTCC 1080
Qy       1081 CGGCCCCAGGCTTCAACCCCACCACCACCATCTGCTTCAGCTCCACCCCAAGTTCCAGTC 1140
Db       1081 CGGCCCCAGGCTTCAACCCCACCACCACCATCTGCTTCAGCTCCACCCCAAGTTCCAGTC 1140
Qy       1141 CTGTCTCCATTCCCCCTTACATCTCCTGTGACCGGTCCAACTTCGGAGCCGTCGCATCTC 1200
Db       1141 CTGTCTCCATTCCCCCTTACATCTCCTGTGACCGGTCCAACTTCGGAGCCGTCGCATCTC 1200
Qy       1201 CCTCCAGCGAGACGGCCCCGCCCCATCTAAAGGCTGGCCCCATCCTCCCGGGGGCCTCCGG 1260
Db       1201 CCTCCAGCGAGACGGCCCCGCCCCATCTAAAGGCTGGCCCCATCCTCCCGGGGGCCTCCGG 1260
Qy       1261 CCTCCACCCACCTCTGTACCCCGGGGCCTCCGGCCTCCACCCACCTCTGTACCCCGGGGC 1320
Db       1261 CCTCCACCCACCTCTGTACCCCGGGGCCTCCGGCCTCCACCCACCTCTGTACCCCGGGGC 1320
Qy       1321 CTCCGGCCTCCACCCACCTCTGCACCCCAGTTCAGAAGTGGGAAGCCAGCGCCCCCAGCG 1380
Db       1321 CTCCGGCCTCCACCCACCTCTGCACCCCAGTTCAGAAGTGGGAAGCCAGCGCCCCCAGCG 1380
Qy       1381 CCCCCGATCAGCTCGCGGATGCCGACCCCGCGACCCTGTACGCGGTGGTGGACGGCGTGC 1440
Db       1381 CCCCCGATCAGCTCGCGGATGCCGACCCCGCGACCCTGTACGCGGTGGTGGACGGCGTGC 1440
Qy       1441 CCCCGTCGCGCTGGAAGGAGTTGGTGCGGCGGCTGGGACTGAGCGAGCACGAGATCGAGC 1500
Db       1441 CCCCGTCGCGCTGGAAGGAGTTGGTGCGGCGGCTGGGACTGAGCGAGCACGAGATCGAGC 1500
Qy       1501 GGCTGGAGCTGGAGAACGGGCGCCACCTGCGCGAGGCGCAGTACAGCATGCTGGCGGCCT 1560
Db       1501 GGCTGGAGCTGGAGAACGGGCGCCACCTGCGCGAGGCGCAGTACAGCATGCTGGCGGCCT 1560
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Qy       1561 GGCGGCGGCGCACGCCGCGCCGCGAGGCCACGCTGGAGCTGCTGGGCCGCGTGCTCAGGG 1620
Db       1561 GGCGGCGGCGCACGCCGCGCCGCGAGGCCACGCTGGAGCTGCTGGGCCGCGTGCTCAGGG 1620
Qy       1621 ACATGGACCTGCTGGGTTGCCTGGAAAACATAGAGGAGGCGCTGGGTGGCGCCGCCCGCC 1680
Db       1621 ACATGGACCTGCTGGGTTGCCTGGAAAACATAGAGGAGGCGCTGGGTGGCGCCGCCCGCC 1680
Qy       1681 TCGCGTCCGAGCCCCGCCTTCTCTGGTGAAGCCCCGCCCCTCCGACTGCGGGCCTCCCCG 1740
Db       1681 TCGCGTCCGAGCCCCGCCTTCTCTGGTGAAGCCCCGCCCCTCCGACTGCGGGCCTCCCCG 1740
Qy       1741 CCCTGCAGACGGCTGCTTCCTTCCTGTGCCAGGCAGCCCGGAAGGATCTGCGAGATGCCC 1800
Db       1741 CCCTGCAGACGGCTGCTTCCTTCCTGTGCCAGGCAGCCCGGAAGGATCTGCGAGATGCCC 1800
Qy       1801 TGTGGACCTCCTGTTTTGTTTTGTTTTTTTCTGGAGAGGAAGTCTTGGAGGAGCAGGCAC 1860
Db       1801 TGTGGACCTCCTGTTTTGTTTTGTTTTTTTCTGGAGAGGAAGTCTTGGAGGAGCAGGCAC 1860
Qy       1861 GATCTGGCAGCCACTGACCTGGTGCTACTCACTCAGTGTACATAGCTTTTCTCAGCTGCC 1920
Db       1861 GATCTGGCAGCCACTGACCTGGTGCTACTCACTCAGTGTACATAGCTTTTCTCAGCTGCC 1920
Qy       1921 TGAGTGTGTGTCTGTGTGTAGTGTGTGTCTGCGTGCAGTGCGTGTGTTTGTGTCTCTGTA 1980
Db       1921 TGAGTGTGTGTCTGTGTGTAGTGTGTGTCTGCGTGCAGTGCGTGTGTTTGTGTCTCTGTA 1980
Qy       1981 TGTGCGTCTGTGTGATGTGGAGTGTGTGTACTCGTGAGAGAGGCCGAGTGTGCCCGGAGC 2040
Db       1981 TGTGCGTCTGTGTGATGTGGAGTGTGTGTACTCGTGAGAGAGGCCGAGTGTGCCCGGAGC 2040
Qy       2041 CCAAGGCAGTGGTTGCGAAGATGAGGGGCGCCCTGCCTTATTGCCTGTTTTTTGGGCTTG 2100
Db       2041 CCAAGGCAGTGGTTGCGAAGATGAGGGGCGCCCTGCCTTATTGCCTGTTTTTTGGGCTTG 2100
Qy       2101 GAGAACTCAGCAAGGCGACTTGGGGAACCTACGTCGGTCCCTGAGCCGGTTTCGCAGTAG 2160
Db       2101 GAGAACTCAGCAAGGCGACTTGGGGAACCTACGTCGGTCCCTGAGCCGGTTTCGCAGTAG 2160
Qy       2161 ATAAGCCATCTTTGTATCCACTCTGCACATCCACTCATCCACTCTGTACACTAATAGAAA 2220
Db       2161 ATAAGCCATCTTTGTATCCACTCTGCACATCCACTCATCCACTCTGTACACTAATAGAAA 2220
Qy       2221 CTTTGTTGCCCTGCCTGGACCAGCTGAACTGTCCCCAGGCAGCGGGGGAGCACAGAAAAA 2280
Db       2221 CTTTGTTGCCCTGCCTGGACCAGCTGAACTGTCCCCAGGCAGCGGGGGAGCACAGAAAAA 2280
Qy       2281 TGGGGCCTCCCAAGGGAGCTAGCTGTTCAGTTCAGTTCAGTCGCTCAGTCGTGTCCGACT 2340
Db       2281 TGGGGCCTCCCAAGGGAGCTAGCTGTTCAGTTCAGTTCAGTCGCTCAGTCGTGTCCGACT 2340
Qy       2341 CTTTGCGACCCTGTGAATCGCAGGGACTTCTGTAAATACACTAAAATCTTCCAATTAAAG 2400
Db       2341 CTTTGCGACCCTGTGAATCGCAGGGACTTCTGTAAATACACTAAAATCTTCCAATTAAAG 2400
Qy       2401 CTCTGCCCTGGAGGGACTGGTTAAAAAAAAAAAAAAAAAA 2440
Db       2401 CTCTGCCCTGGAGGGACTGGTTAAAAAAAAAAAAAAAAAA 2440
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RESULT 3
ABQ77487
ID   ABQ77487 standard; DNA; 2141 BP.
XX
AC   ABQ77487;
XX
DT   14-MAY-2003  (first entry)
XX
DE   Human TNF-R DNA huTNF-R.
XX
KW   TNF; human; tumour necrosis factor; tumour necrosis factor receptor;
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KW   TNF-R; tumour necrosis factor binding protein; TNF-BP; tumour; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             213..1580
FT                   /*tag=  a
FT                   /product= "huTNF-R"
XX
PN   EP393438-A.
XX
PD   24-OCT-1990.
XX
PF   06-APR-1990;    90EP-0106624.
XX
PR   21-APR-1989;    89DE-3913101.
PR   21-JUN-1989;    89DE-3920282.
XX
PA   (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
PA   (SYND ) SYNERGEN INC.
XX
PI   Hauptmann R,  Himmler A,  Maurer-Fogy I,  Stratowa C;
XX
DR   WPI; 1990-321987/43.
DR   P-PSDB; ABG74755.
XX
PT   DNA encoding TNF binding protein and TNF- receptor - used in tumour
PT   treatment and to understand mechanisms to TNF action
XX
PS   Example 9; Fig 9; 51pp; German.
XX
CC   This invention describes novel polynucleotide sequences encoding tumour
CC   necrosis factor (TNF) receptor (TNF-R) or TNF binding protein (TNF-BP).
CC   The products of the invention are useful in pharmaceutical compositions
CC   for prophylaxis or treatment of human tumours and to understand the
CC   mechanisms of TNF action. This sequence encodes the human TNF-R,
CC   huTNF-R described in the disclosure of the invention.
XX
SQ   Sequence 2141 BP; 455 A; 634 C; 592 G; 460 T; 0 other;

  Query Match             30.2%;  Score 735.8;  DB 11;  Length 2141;
  Best Local Similarity   69.9%;  Pred. No. 4.5e-141;
  Matches 1152;  Conservative    0;  Mismatches  402;  Indels   95;  Gaps    8;

Qy       101 GGCCGCAGGGCTGGCCTTCCGGGTTTGAGGTCCTCCGGATTGGGCTGTG---TCCCCGCC 157
Db        17 GGCTCCAGTTCTGGCCTTTGGGGTTCAAGATCACTGGGACCAGGCCGTGATCTCTATGCC  76

Qy       158 CCAGTCTCAACCCTCCACTCCCCGACCCGAGGCCCGGGCTCCACTGGGCATACGCGAGGA 217
Db        77 CGAGTCTCAACCCTCAACTGTCACCCCAAGGCACTTGGGACGTCCTGGACAGACCGAGTC 136

Qy       218 CCGTGTTGCTGTCACTGTCGCGGGCCGCCACTGCCCC-AGCCCTGATGGGGGATTGAGAG 276
Db       137 CCGGGAAGCCCCAGCACTGCCGCTGCCACACTGCCCTGAGCCCAAATGGGGGAGTGAGAG 196

Qy       277 GCCACAGCTGGCCGGACATGGGCCTCCCCACCGTGCCTGGCCTGCTGCTGCCACTGGTGC 336
Db       197 GCCATAGCTGTCTGG-CATGGGCCTCTCCACCGTGCCTGACCTGCTGCTGCCACTGGTGC 255

Qy       337 TTCCAGCTCTGTTGGCAGATGTGTACCCCGCAGGGGTTCAGGGGCTGGTCCCTCACCCCG 396
Db       256 TCCTGGAGCTGTTGGTGGGAATATACCCCTCAGGGGTTATTGGACTGGTCCCTCACCTAG 315

Qy       397 GGGACCTGGAGAAGAGAGAGAGTCCCTGTCCCCAAGGAAAATATAACCACCCGCAAAATA 456
Db       316 GGGACAGGGAGAAGAGAGATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATA 375

Qy       457 GCACCATTTGCTGCACCAAGTGCCACAAAGGTACCTATCTGTACAATGACTGTCCGGGTC 516
Db       376 ATTCGATTTGCTGTACCAAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCC 435

Qy       517 CAGGGCGAGACACGGACTGCAGGGTGTGTGCCCCTGGCACCTACACTGCCTTGGAGAACC 576

Db       436 CGGGGCAGGATACGGACTGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACC 495

Qy       577 ATCTCAGACGATGCCTGAGCTGCTCCAGGTGCCGGGACGAAATGTTCCAGGTGGAGATTT 636
Db       496 ACCTCAGACACTGCCTCAGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCT 555

Qy       637 CGCCTTGTGTAGTGGACCGGGACACTGTGTGCGGCTGCAGGAAGAACCAGTACCGGGAAT 696
Db       556 CTTCTTGCACAGTGGACCGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATT 615

Qy       697 ACTGGGGTGAAACTGGCTTCCGGTGTCTGAACTGCAGCCTCTGTCCCAATGGCACAGTGA 756
Db       616 ATTGGAGTGAAAACCTTTTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGC 675

Qy       757 ATATCCCCTGCCAGGAGAGACAGGACACCATCTGCCACTGCCATATGGGCTTCTTTCTTA 816
Db       676 ACCTCTCCTGCCAGGAGAAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAA 735

Qy       817 AAGGCGCCAAGTGCATCTCCTGTCATGATTGTAAGAA---CAAGGAGTGCGAGAAGTTAT 873
Db       736 GAGAAAACGAGTGTGTCTCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGT 795

Qy       874 GTCCAACCCGACCTTCAACTGGTAAAGACTCTCAGGACCCAGGCACTACAGTACTATTAC 933
Db       796 GCCTACCCCAGATTGAGAATGTTAAGGGCACTGAGGACTCAGGCACCACAGTGCTGTTGC 855

Qy       934 CCCTGGTGATTGTCTTCGGGCTTTGCCTGGCATCCTTCGCCTCTGTCGTCTTAGCATGTC 993
Db       856 CCCTGGTCATTTTCTTTGGTCTTTGCCTTTATCCCTCCTCTTCATTGGTTTAATGTATC 915

Qy       994 GCTACCAGCGGTGGAAGCCCAAGCTCTACTCCATCATTTGCGGGCAGTCGACTCTGGTAA 1053
Db       916 GCTACCAACGGTGGAAGTCCAAGCTCTACTCCATTGTTTGTGGGAAATCGACACCTGAAA 975

Qy      1054 AAGAGGGGGAGCCAGAA---------CTCCTGGTCCCGGCCCCAGGCTTCAACCCCACCA 1104
Db       976 AAGAGGGGGAGCTTGAAGGAACTACTACTAAGCCCCTGGCCCCAAACCCAAGCTTCAGTC 1035

Qy      1105 CCACCATCTGCTTCAGCTCCACCCCAAGTTCCAGTCCTGTCTCCATTCCCCCTTACATCT 1164
Db      1036 CCACTCCAGGCTTCACCCCCACCCTGGGCTTCAGTCCCGTGCCCAGTTCCACCTTCACCT 1095

Qy      1165 CCTGTGACCGGTCCAACTTCGGAG---------CCGTCGCATCTCCCTCCAGCGAGACGG 1215
Db      1096 CCAGCTCCACCTATACCCCCGGTGACTGTCCCAACTTTGCGGCTCCCCGCAGAGAGGTGG 1155

Qy      1216 CCCCGCCCCATCTAAAGGCTGGCCCCATCCTCCCGGGGCCTCCGGCCTCCACCCACCTCT 1275
Db      1156 CACCACCCTATCAGGGGGCTGACCCCATCCT---------------------------- 1186

Qy      1276 GTACCCCGGGGCCTCCGGCCTCCACCCACCTCTGTACCCCGGGGCCTCCGGCCTCCACCC 1335
Db      1187 ------------------------------------TGCGACAGCCCTCGCCTCCGACC 1209

Qy      1336 ACCTCTGCACCCCAGTTCAGAAGTGGGAAGCCAGCGCCCCCAGCGCCCCCGATCAGCTCG 1395
Db      1210 CCATCCCCAACCCCCTTCAGAAGTGGGAGGACAGCGCCCACA---AGCCACAGAGCCTAG 1266

Qy      1396 CGGATGCCGACCCCGCGACCCTGTACGCGGTGGTGGACGGCGTGCCCCCGTCGCGCTGGA 1455
Db      1267 ACACTGATGACCCCGCGACGCTGTACGCCGTGGTGGAGAACGTGCCCCCGTTGCGCTGGA 1326

Qy      1456 AGGAGTTGGTGCGGCGGCTGGGACTGAGCGAGCACGAGATCGAGCGGCTGGAGCTGGAGA 1515
Db      1327 AGGAATTCGTGCGGCGCCTAGGGCTGAGCGACCACGAGATCGATCGGCTGGAGCTGCAGA 1386

Qy      1516 ACGGGCGCCACCTGCGCGAGGCGCAGTACAGCATGCTGGCGGCCTGGCGGCGGCGCACGC 1575
Db      1387 ACGGGCGCTGCCTGCGCGAGGCGCAATACAGCATGCTGGCGACCTGGAGGCGGCGCACGC 1446

Qy      1576 CGCGCCGCGAGGCCACGCTGGAGCTGCTGGGCCGCGTGCTCAGGGACATGGACCTGCTGG 1635
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Db       1447 CGCGGCGCGAGGCCACGCTGGAGCTGCTGGGACGCGTGCTCCGCGACATGGACCTGCTGG 1506

Qy       1636 GTTGCCTGGAAAACATAGAGGAGGCGCTGGGTGGCGCCGCCCGCCTCGCGTCCGAGCCCC 1695

Db       1507 GCTGCCTGGAGGACATCGAGGAGGCGCTTTGCGGCCCCGCCGCCCTCCCGCCCGCGCCCA 1566

Qy       1696 GCCTTCTCTGGTGAAGCCCCGCCCCTCCG 1724

Db       1567 GTCTTCTCAGATGAGGCTGCGCCCCTGCG 1595


RESULT 4
AAQ06285
ID   AAQ06285 standard; DNA; 2141 BP.
XX
AC   AAQ06285;
XX
DT   25-MAR-2003  (updated)
DT   29-JAN-1991  (first entry)
XX
DE   Human Tumour Necrosis Factor-Receptor cDNA insert.
XX
KW   Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;
KW   lambdaTNF-R2; raTNF-R8; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             213..1577
FT                   /*tag= a
FT                   /label=huTNF-R
XX
PN   EP393438-A.
XX
PD   24-OCT-1990.
XX
PF   06-APR-1990;   90EP-0106624.
XX
PR   21-JUN-1989;   89DE-3920282.
PR   21-APR-1989;   89DE-3913101.
XX
PA   (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
PA   (SYND ) SYNERGEN INC.
XX
PI   Hauptmann R,  Himmler A,  Maurerfogy I,  Stratowa C;
XX
DR   WPI; 1990-321987/43.
DR   P-PSDB; AAR07451.
XX
PT   DNA encoding TNF binding protein and TNF- receptor - used in
PT   tumour treatment and to understand mechanismsm to TNF action
XX
PS   Disclosure; Fig 91(1-2); 51pp; German.
XX
CC   raTNF-R8 (AAQ06284) was used to screen the HS913T cDNA library.
CC   LambdaTNF-R2 encodes the complete human TNF-R2 and was used to
CC   construct a plasmid (pADTNF-R) expressing the product the same way
CC   as pADTNF-BP (see AAQ06282).
CC   See also AAQ06282-Q06285.
CC   (Updated on 25-MAR-2003 to correct PA field.)
CC   (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ   Sequence 2141 BP; 455 A; 633 C; 593 G; 460 T; 0 other;

  Query Match             29.9%;  Score 729.4;  DB 11;  Length 2141;
  Best Local Similarity   69.6%;  Pred. No. 9.1e-140;
  Matches 1148;  Conservative    0;  Mismatches  406;  Indels   95;  Gaps    8;

Qy        101 GGCCGCAGGGCTGGCCTTCCGGGTTTGAGGTCCTCCGGATTGGGCTGTG---TCCCCGCC 157

Db         17 GGCTCCAGTTCTGGCCTTTGGGGTTCAAGATCACTGGGACCAGGCCGTGATCTCTATGCC 76

Qy        158 CCAGTCTCAACCCTCCACTCCCCGACCCGAGGCCCGGGCTCCACTGGGCATACGCGAGGA 217

Db         77 CGAGTCTCAACCCTCAACTGTCACCCCAAGGCACTTGGGACGTCCTGGACAGACCGAGTC 136

Qy        218 CCGTGTTGCTGTCACTGTCGCGGGCCGCCACTGCCCC-AGCCCTGATGGGGGATTGAGAG 276

Db        137 CCGGGAAGCCCCAGCACTGCCGCTGCCACACTGCCCTGAGCCCAAATGGGGGAGTGAGAG 196

Qy        277 GCCACAGCTGGCCGGACATGGGCCTCCCCACCGTGCCTGGCCTGCTGCTGCCACTGGTGC 336

Db        197 GCGATAGCTGTCTGG-CATGGGCCTCTCCAGCGTGCCTGACCTGCTGCTGCCACTGGTGC 255

Qy        337 TTCCAGCTCTGTTGGCAGATGTGTACCCCGCAGGGGTTCAGGGGCTGGTCCCTCACCCCG 396

Db        256 TCGTGGAGCTGTTGGTGGGAATATACCCCTCAGCGGTTATTGGACTGGTCCCTCACCTAG 315

Qy        397 GGGACCTGGAGAAGAGAGAGAGTCCCTGTCCCCAAGGAAAATATAACCACCCGCAAAATA 456

Db        316 GGGACAGGGAGAAGAGAGATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATA 375

Qy        457 GCACCATTTGCTGCACCAAGTGCCACAAAGGTACCTATCTGTACAATGACTGTCCGGGTC 516

Db        376 ATTCGATTTGCTGTACCAAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCC 435

Qy        517 CAGGGCGAGACACGGACTGCAGGGTGTGTGCCCCTGGCACCTACACTGCCTTGGAGAACC 576

Db        436 CGGGGCAGGATACGGACTGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACC 495

Qy        577 ATCTCAGACGATGCCTGAGCTGCTCCAGGTGCCGGGACGAAATGTTCCAGGTGGAGATTT 636

Db        496 ACCTCAGACACTGCCTCAGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCT 555

Qy        637 CGCCTTGTGTAGTGGACCGGGACACTGTGTGCGGCTGCAGGAAGAACCAGTACCGGGAAT 696

Db        556 CTTCTTGCACAGTGGACCGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATT 615

Qy        697 ACTGGGGTGAAACTGGCTTCCGGTGTCTGAACTGCAGCCTCTGTCCCAATGGCACAGTGA 756

Db        616 ATTGGAGTGAAAACCTTTTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGC 675

Qy        757 ATATCCCCTGCCAGGAGAGACAGGACACCATCTGCCACTGCCATATGGGCTTCTTTCTTA 816

Db        676 ACCTCTCCTGCCAGGAGAAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAA 735

Qy        817 AAGGCGCCAAGTGCATCTCCTGTCATGATTGTAAGAA---CAAGGAGTGCGAGAAGTTAT 873

Db        736 GAGAAAACGAGTGTGTCTCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGT 795

Qy        874 GTCCAACCCGACCTTCAACTGGTAAAGACTCTCAGGACCCAGGCACTACAGTACTATTAC 933

Db        796 GCCTACCCCAGATTCAGAATGTTAAGGGCACTGAGGACTCAGGCACCACAGTGCTGTTGC 855

Qy        934 CCCTGGTGATTGTCTTCGGGCTTTGCCTGGCATCCTTCGCCTCTGTCGTCTTAGCATGTC 993

Db        856 CCCTGGTCATTTTCTTTGGTCTTTGCCTTTTATCCCTCCTCTTCATTGGTTTAATGTATC 915

Qy        994 GCTACCAGCGGTGGAAGCCCAAGCTCTACTCCATCATTTGCGGGCAGTCGACTCTGGTAA 1053

Db        916 GCTACCAACGGTGGAAGTCCAAGCTCTACTCCATTGTTTGTGGGAAATCGACACCTGAAA 975

Qy       1054 AAGAGGGGGAGCCAGAA---------CTCCTGGTCCCGGCCCCAGGCTTCAACCCCACCA 1104

Db        976 AAGAGGGGGAGCTTGAAGGAACTACTACTAAGCCCCTGGCCCCAAACCCAAGCTTCAGTC 1035

Qy       1105 CCACCATCTGCTTCAGCTCCACCCCAAGTTCCAGTCCTGTCTCCATTCCCCCTTACATCT 1164

Db       1036 CCACTCCAGGCTTCACCCCCACCCTGGGCTTCAGTCCCGTGCCCAGTTCCACCTTCACCT 1095

Qy       1165 CCTGTGACCGGTCCAACTTCGGAG---------CCGTCGCATCTCCCTCCAGCGAGACGG 1215

Db       1096 CCAGCTCCACCTATACCCCCGGTGACTGTCCCAACTTTGCGGCTCCCCGCAGAGAGGTGG 1155

Qy       1216 CCCCGCCCCATCTAAAGGCTGGCCCCATCCTCCCGGGGCCTCCGGCCTCCACCCACCTCT 1275
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Db       1156 CACCACCCTATCAGGGGGCTGACCCCATCCT---------------------------- 1186

Qy       1276 GTACCCCGGGGCCTCCGGCCTCCACCCACCTCTGTACCCCGGGGCCTCCGGCCTCCACCC 1335
                                                ||    | |  ||||||  ||
Db       1187 ------------------------------------TGCGACAGCCCTCGCCTCCGACC 1209

Qy       1336 ACCTCTGCACCCCAGTTCAGAAGTGGGAAGCCAGCGCCCCCAGCGCCCCCGATCAGCTCG 1395
              | ||  || |||  |||||||||||||| | |||||||| ||     ||  |    || |
Db       1210 CCATCCCCAACCCCCTTCAGAAGTGGGAGGACAGCGCCCACA---AGCCACAGAGCCTAG 1266

Qy       1396 CGGATGCCGACCCCGCGACCCTGTACGCGGTGGTGGACGGCGTGCCCCCGTCGCGCTGGA 1455
                ||  |||||||||||| |||||||| ||||||||   |||||||||||| ||||||||
Db       1267 ACACTGATGACCCCGCGACGCTGTACGCCGTGGTGGAGAACGTGCCCCCGTTGCGCTGGA 1326

Qy       1456 AGGAGTTGGTGCGGCGGCTGGGACTGAGCGAGCACGAGATCGAGCGGCTGGAGCTGGAGA 1515
              |||| || |||||||| || || |||||||| |||||||||| |||||||||| |||
Db       1327 AGGAATTCGTGCGGCGCCTAGGGCTGAGCGACCACGAGATCGATCGGCTGGAGCTGCAGA 1386

Qy       1516 ACGGGCGCCACCTGCGCGAGGCGCAGTACAGCATGCTGGCGGCCTGGCGGCGGCGCACGC 1575
              |||||||| |||||||||||||| |||||||||||||| ||||| ||||||||||||
Db       1387 ACGGGCGCTGCCTGCGCGAGGCGCAATACAGCATGCTGGCGACCTGGAGGCGGCGCACGC 1446

Qy       1576 CGCGCCGCGAGGCCACGCTGGAGCTGCTGGGCCGCGTGCTCAGGGACATGGACCTGCTGG 1635
              |||| |||||||||||||||||||||||| |||||||| | ||||||||||||||||
Db       1447 CGCGGCGCGAGGCCACGCTGGAGCTGCTGGGACGCGTGCTCCGCGACATGGACCTGCTGG 1506

Qy       1636 GTTGCCTGGAAAACATAGAGGAGGCGCTGGGTGGCGCCGCCCGCCTCGCGTCCGAGCCCC 1695
              | |||||||| |||| |||||||||| | ||| ||||| |||| || ||| ||||
Db       1507 GCTGCCTGGAGGACATCGAGGAGGCGCTTTGCGGCCCCGCCGCCCTCCCGCCCGCGCCCA 1566

Qy       1696 GCCTTCTCTGGTGAAGCCCCGCCCCTCCG 1724
              | |||||| | ||| ||  ||||||| ||
Db       1567 GTCTTCTCAGATGAGGCTGCGCCCCTGCG 1595


RESULT 5
AAQ10883
ID   AAQ10883 standard; cDNA; 2088 BP.
XX
AC   AAQ10883;
XX
DT   25-MAR-2003  (updated)
DT   13-MAY-1991  (first entry)
XX
DE   30kD TNF inhibitor precursor gene in lambda-gt10-7ctnfbp.
XX
KW   Tumour necrosis factor; inhibitor; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             171..1536
FT                   /*tag= a
XX
PN   AU9058976-A.
XX
PD   24-JAN-1991.
XX
PF   16-JUL-1990;   90AU-0058976.
XX
PR   07-FEB-1990;   90US-0479661.
PR   18-JUL-1989;   89US-0381080.
PR   11-DEC-1989;   89US-0450329.
XX
PA   (SYND ) SYNERGEN INC.
XX
DR   WPI; 1991-073847/11.
DR   P-PSDB; AAR10986.
XX
PT   Tumour necrosis factor inhibitor - for suppression of TNF-alpha
PT   and -beta, useful as therapeutic agent.
XX
PS   Disclosure; Fig 21; 142pp; English.
XX
CC   The sequence encodes the entire 30 kD TNF inhibitor. The clone from
CC   which the sequence was obtd. was isolated from a cDNA library
CC   prepd. from RNA form U937 cells treated with PMA/PHA.   The whole
CC   gene can be inserted into expression vectors for prepn. of TNF
CC   inhibitor for use in the treatment of inflammatory and degenerative
CC   diseases.
CC   See also AAQ10878, AAQ10884 and AAQ10907.
CC   (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ   Sequence 2088 BP; 439 A; 626 C; 578 G; 445 T; 0 other;

  Query Match          29.7%;  Score 725.8;  DB 12;  Length 2088;
  Best Local Similarity   70.0%;  Pred. No. 5e-139;
  Matches 1120;  Conservative    0;  Mismatches  387;  Indels   92;  Gaps    7;

Qy        148 TGTCCCCGCCCCAGTCTCAACCCTCCACTCCCCGACCCGAGGCCCGGGCTCCACTGGGCA 207
              | ||   |||| ||||||||||||| |||  |   ||   |  |  ||  |  |  ||
Db         23 TCTCTATGCCCGAGTCTCAACCCTCAACTGTCACCCCAAGGCACTTGGGACGTCCTGGAC 82

Qy        208 TACGCGAGGACCGTGTTGCTGTCACTGTCGCGGGCCGCCACTGCCC-CAGCCCTGATGGG 266
                  |||| ||| |  ||       |  |  ||   |  |||||||  |||||  |||||
Db         83 AGACCGAGTCCCGGGAAGCCCCAGCACTGCCGCTGCCACACTGCCCTGAGCCCAAATGGG 142

Qy        267 GGATTGAGAGGCCACAGCTGGCCGGACATGGGCCTCCCCACCGTGCCTGGCCTGCTGCTG 326
              ||| |||||||||| ||||| | || |||||||||| |||||||||| ||||||||||
Db        143 GGAGTGAGAGGCCATAGCTGTCTGG-CATGGGCCTCTCCACCGTGCCTGACCTGCTGCTG 201

Qy        327 CCACTGGTGCTTCCAGCTCTGTTGGCAGATGTGTACCCCGCAGGGGTTCAGGGGCTGGTC 386
              || |||||||| |  | |||||||  |   | ||||||  |||||||    || ||||||
Db        202 CCGCTGGTGCTCCTGGAGCTGTTGGTGGGAATATACCCCTCAGGGGTTATTGGACTGGTC 261

Qy        387 CCTCACCCCGGGGACCTGGAGAAGAGAGAGAGTCCCTGTCCCCAAGGAAAATATAACCAC 446
              |||||||  ||||||  |||||||||||| |||  ||||||||||||||||||| ||||
Db        262 CCTCACCTAGGGGACAGGGAGAAGAGAGATAGTGTGTGTCCCCAAGGAAAATATATCCAC 321

Qy        447 CCGCAAAATAGCACCATTTGCTGCACCAAGTGCCACAAAGGTACCTATCTGTACAATGAC 506
              || |||||||  | |||||||| |||||||||||||||| |||||  ||||||||||
Db        322 CCTCAAAATAATTCGATTTGCTGTACCAAGTGCCACAAAGGAACCTACTTGTACAATGAC 381

Qy        507 TGTCCGGGTCCAGGGCGAGACACGGACTGCAGGGTGTGTGCCCCTGGCACCTACACTGCC 566
              ||||| || || ||||  || |||||||||||||| |||||      ||| ||| ||| ||
Db        382 TGTCCAGGCCCGGGGCAGGATACGGACTGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCT 441

Qy        567 TTGGAGAACCATCTCAGACGATGCCTGAGCTGCTCCAGGTGCCGGGACGAAATGTTCCAG 626
              |  || ||||| |||||||  ||||| ||||||||||  |||||  | ||||||   |||
Db        442 TCAGAAAACCACCTCAGACACTGCCTCAGCTGCTCCAAATGCCGAAAGGAAATGGGTCAG 501

Qy        627 GTGGAGATTTCGCCTTGTGTAGTGGACCGGGACACTGTGTGCGGCTGCAGGAAGAACCAG 686
              |||||||| ||  ||||  |||||||||||||||| |||||  |||||||||||||||||
Db        502 GTGGAGATCTCTTCTTGCACAGTGGACCGGGACACCGTGTGTGGCTGCAGGAAGAACCAG 561

Qy        687 TACCGGGAATACTGGGGTGAAACTGGCTTCCGGTGTCTGAACTGCAGCCTCTGTCCCAAT 746
              ||||||  | || ||| ||||||      |||| |||  | || ||||||||||| | ||||
Db        562 TACCGGCATTATTGGAGTGAAAACCTTTTCCAGTGCTTCAATTGCAGCCTCTGCCTCAAT 621

Qy        747 GGCACAGTGAATATCCCCTGCCAGGAGAGACAGGACACCATCTGCCACTGCCATATGGGC 806
              || || ||| |  || |||||||||||| |||| ||||| | |||  |||||||   ||
Db        622 GGGACCGTGCACCTCTCCTGCCAGGAGAAACAGAACACCGTGTGCACCTGCCATGCAGGT 681

Qy        807 TTCTTTCTTAAAGGCGCCAAGTGCATCTCCTGTCATGATTGTAAGAA---CAAGGAGTGC 863
              |||||||| | ||   | |||| ||||||||  | | ||||||    | ||||||||
Db        682 TTCTTTCTAAGAGAAAACGAGTGTGTCTCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGC 741

Qy        864 GAGAAGTTATGTCCAACCCGACCTTCAACTGGTAAAGACTCTCAGGACCCAGGCACTACA 923
              |||||| || | | |||     |  | || ||| | | || ||||| ||||||| |||
Db        742 ACGAAGTTGTGCCTACCCCAGATTGAGAATGTTAAGGGCACTGAGGACTCAGGCACCACA 801

Qy        924 GTACTATTACCCCTGGTGATTGTCTTCGGGCTTTGCCTGGCATCCTTCGCCTCTGTCGTC 983
              || || ||  |||||||| ||| |||| || ||||||||   |||| ||  ||   | |
Db        802 GTGCTGTTGCCCCTGGTCATTTTCTTTGGTCTTTGCCTTTTATCCCTCCTCTTCATTGGT 861

Qy        984 TTAGCATGTCGCTACCAGCGGTGGAAGCCCAAGCTCTACTCCATCATTTGCGGGCAGTCG 1043
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Db        862 TTAATGTATCGCTACCAACGGTGGAAGTCCAAGCTCTACTCCATTGTTTGTGGGAAATCG 921

Qy       1044 ACTCTGGTAAAAGAGGGGGAGCCAGAA---------CTCCTGGTCCCGGCCCCAGGCTTC 1094

Db        922 ACACCTGAAAAAGAGGGGGAGCTTGAAGGAACTACTACTAAGCCCCTGGCCCCAAACCCA 981

Qy       1095 AACCCCACCACCACCATCTGCTTCAGCTCCACCCCAAGTTCCAGTCCTGTCTCCATTCCC 1154

Db        982 AGCTTCAGTCCCACTCCAGGCTTCACCCCCACCCTGGGCTTCAGTCCCGTGCCCAGTTCC 1041

Qy       1155 CCTTACATCTCCTGTGACCGGTCCAACTTCGGAG---------CCGTCGCATCTCCCTCC 1205

Db       1042 ACCTTCACCTCCAGCTCCACCTATACCCCCGGTGACTGTCCCAACTTTGCGGCTCCCCGC 1101

Qy       1206 AGCGAGACGGCCCCGCCCCATCTAAAGGCTGGCCCCATCCTCCCGGGGCCTCCGGCCTCC 1265

Db       1102 AGAGAGGTGGCACCACCCTATCAGGGGGCTGACCCCATCCT------------------- 1142

Qy       1266 ACCCACCTCTGTACCCCGGGGCCTCCGGCCTCCACCCACCTCTGTACCCCGGGGCCTCCG 1325

Db       1143 ----------------------------------------------TGCGACAGCCCTC 1155

Qy       1326 GCCTCCACCCACCTCTGCACCCCAGTTCAGAAGTGGGAAGCCAGCGCCCCCAGCGCCCCC 1385

Db       1156 GCCTCCGACCCCATCCCCAACCCCCTTCAGAAGTGGGAGGACAGCGCCCACA---AGCCA 1212

Qy       1386 GATCAGCTCGCGGATGCCGACCCCGCGACCCTGTACGCGGTGGTGGACGGCGTGCCCCCG 1445

Db       1213 CAGAGCCTAGACACTGATGACCCCGCGACGCTGTACGCCGTGGTGGAGAACGTGCCCCCG 1272

Qy       1446 TCGCGCTGGAAGGAGTTGGTGCGGCGGCTGGGACTGAGCGAGCACGAGATCGAGCGGCTG 1505

Db       1273 TTGCGCTGGAAGGAATTCGTGCGGCGCCTAGGGCTGAGCGACCACGAGATCGATCGGCTG 1332

Qy       1506 GAGCTGGAGAACGGGCGCCACCTGCGCGAGGCGCAGTACAGCATGCTGGCGGCCTGGCGG 1565

Db       1333 GAGCTGCAGAACGGGCGCTGCCTGCGCGAGGCGCAATACAGCATGCTGGCGACCTGGAGG 1392

Qy       1566 CGGCGCACGCCGCGCCGCGAGGCCACGCTGGAGCTGCTGGGCCGCGTGCTCAGGGACATG 1625

Db       1393 CGGCGCACGCCGCGGCGCGAGGCCACGCTGGAGCTGCTGGGACGCGTGCTCCGCGACATG 1452

Qy       1626 GACCTGCTGGGTTGCCTGGAAAACATAGAGGAGGCGCTGGGTGGCGCCGCCCGCCTCGCG 1685

Db       1453 GACCTGCTGGGCTGCCTGGAGGACATCGAGGAGGCGCTTTGCGGCCCCGCCGCCCTCCCG 1512

Qy       1686 TCCGAGCCCCGCCTTCTCTGGTGAAGCCCCGCCCCTCCG 1724

Db       1513 CCCGCGCCCAGTCTTCTCAGATGAGGCTGCGCCCCTGCG 1551
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RESULT 6
AAC83946
ID   AAC83946 standard; DNA; 2088 BP.
XX
AC   AAC83946;
XX
DT   02-MAR-2001  (first entry)
XX
DE   Human 30 kDa TNF inhibitor precursor coding sequence.
XX
KW   TNF inhibitor; antiinflammatory; Tumour Necrosis Factor; interleukin;
KW   IL-1; inflammatory disease; degenerative disease; human; ss.
XX
OS   Homo sapiens.
XX
PN   US6143866-A.
XX
PD   07-NOV-2000.
XX
PF   19-JAN-1995; 95US-0375242.
XX
PR   19-JUL-1990; 90US-0555274.
PR   09-JUL-1993; 93US-0090366.
PR   18-JUL-1989; 89US-0381080.
PR   11-DEC-1989; 89US-0450329.
PR   07-FEB-1990; 90US-0479661.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Squires C, King MW, Hale KK, Brewer MT, Thompson RC;
PI   Vanderslice RW, Vannice J, Kohno T;
XX
DR   WPI; 2001-006443/01.
DR   P-PSDB; AAB37677.
XX
PT   Novel 30 kDa tumor necrosis factor inhibitor analog comprising a
PT   non-native cysteine residue cross-linked with polyethylene glycol,
PT   useful for treating inflammatory and degenerative diseases mediated by
PT   TNF -
XX
PS   Example 6; Fig 21; 82pp; English.
XX
CC   The present invention relates to Tumour Necrosis Factor (TNF) inhibitors
CC   (see AAB37676 and AAB37685), which have TNF inhibitory activity. The
CC   novel TNF inhibitors of the present invention are useful as therapeutic
CC   agents for inhibiting the activity of TNF and interleukin (IL-1), and
CC   for treating inflammatory and degenerative diseases mediated by TNF. The
CC   present sequence is the coding sequence for the precursor of 30 kDa TNF
CC   inhibitor. The 30 kDa TNF inhibitor can inhibit TNF alpha.
XX
SQ   Sequence 2088 BP; 439 A; 626 C; 578 G; 445 T; 0 other;

  Query Match            29.7%;  Score 725.8;  DB 22;  Length 2088;
  Best Local Similarity  70.0%;  Pred. No. 5e-139;
  Matches 1120;  Conservative    0;  Mismatches  387;  Indels   92;  Gaps    7;

Qy        148 TGTCCCCGCCCCAGTCTCAACCCTCCACTCCCCGACCCGAGGCCCGGGCTCCACTGGGCA 207

Db         23 TCTCTATGCCCGAGTCTCAACCCTCAACTGTCACCCCAAGGCACTTGGGACGTCCTGGAC 82

Qy        208 TACGCGAGGACCGTGTTGCTGTCACTGTCGCGGGCCGCCACTGCCC-CAGCCCTGATGGG 266

Db         83 AGACCGAGTCCCGGGAAGCCCCAGCACTGCCGCTGCCACACTGCCCTGAGCCCAAATGGG 142

Qy        267 GGATTGAGAGGCCACAGCTGGCCGGACATGGGCCTCCCCACCGTGCCTGGCCTGCTGCTG 326

Db        143 GGAGTGAGAGGCCATAGCTGTCTGG-CATGGGCCTCTCCACCGTGCCTGACCTGCTGCTG 201

Qy        327 CCACTGGTGCTTCCAGCTCTGTTGGCAGATGTGTACCCCGCAGGGGTTCAGGGGCTGGTC 386

Db        202 CCGCTGGTGCTCCTGGAGCTGTTGGTGGGAATATACCCCTCAGGGGTTATTGGACTGGTC 261

Qy        387 CCTCACCCCGGGGACCTGGAGAAGAGAGAGAGTCCCTGTCCCCAAGGAAAATATAACCAC 446

Db        262 CCTCACCTAGGGGACAGGGAGAAGAGAGATAGTGTGTGTCCCCAAGGAAAATATATCCAC 321

Qy        447 CCGCAAAATAGCACCATTTGCTGCACCAAGTGCCACAAAGGTACCTATCTGTACAATGAC 506

Db        322 CCTCAAAATAATTCGATTTGCTGTACCAAGTGCCACAAAGGAACCTACTTGTACAATGAC 381

Qy        507 TGTCCGGGTCCAGGGCGAGACACGGACTGCAGGGTGTGTGCCCCTGGCACCTACACTGCC 566

Db        382 TGTCCAGGCCCGGGGCAGGATACGGACTGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCT 441

Qy        567 TTGGAGAACCATCTCAGACGATGCCTGAGCTGCTCCAGGTGCCGGGACGAAATGTTCCAG 626

Db        442 TCAGAAAACCACCTCAGACACTGCCTCAGCTGCTCCAAATGCCGAAAGGAAATGGGTCAG 501

Qy        627 GTGGAGATTTCGCCTTGTGTAGTGGACCGGGACACTGTGTGCGGCTGCAGGAAGAACCAG 686

Db        502 GTGGAGATCTCTTCTTGCACAGTGGACCGGGACACCGTGTGTGGCTGCAGGAAGAACCAG 561

Qy        687 TACCGGGAATACTGGGGTGAAACTGGCTTCCGGTGTCTGAACTGCAGCCTCTGTCCCAAT 746
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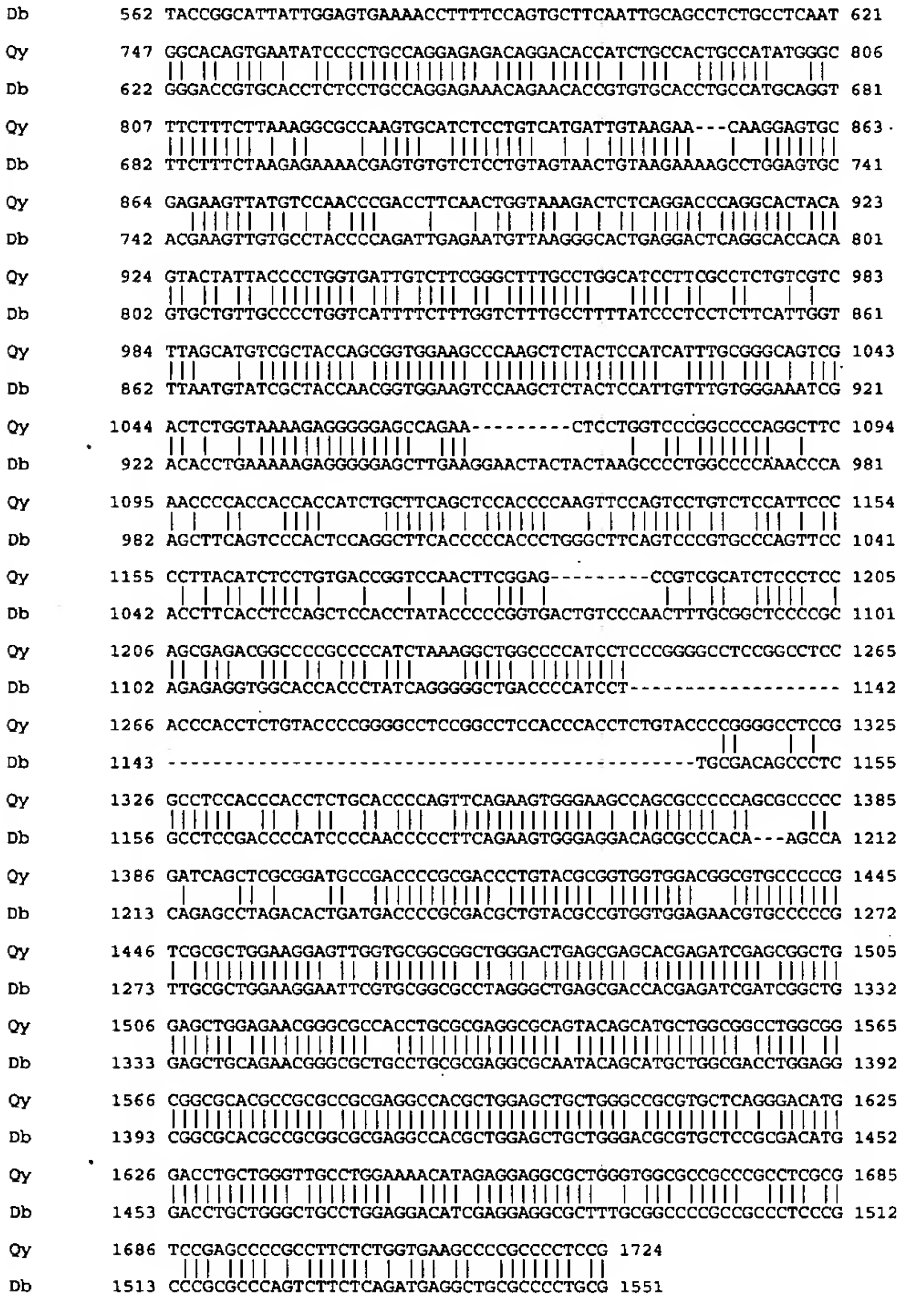
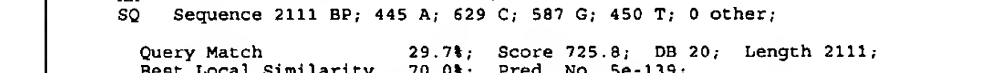
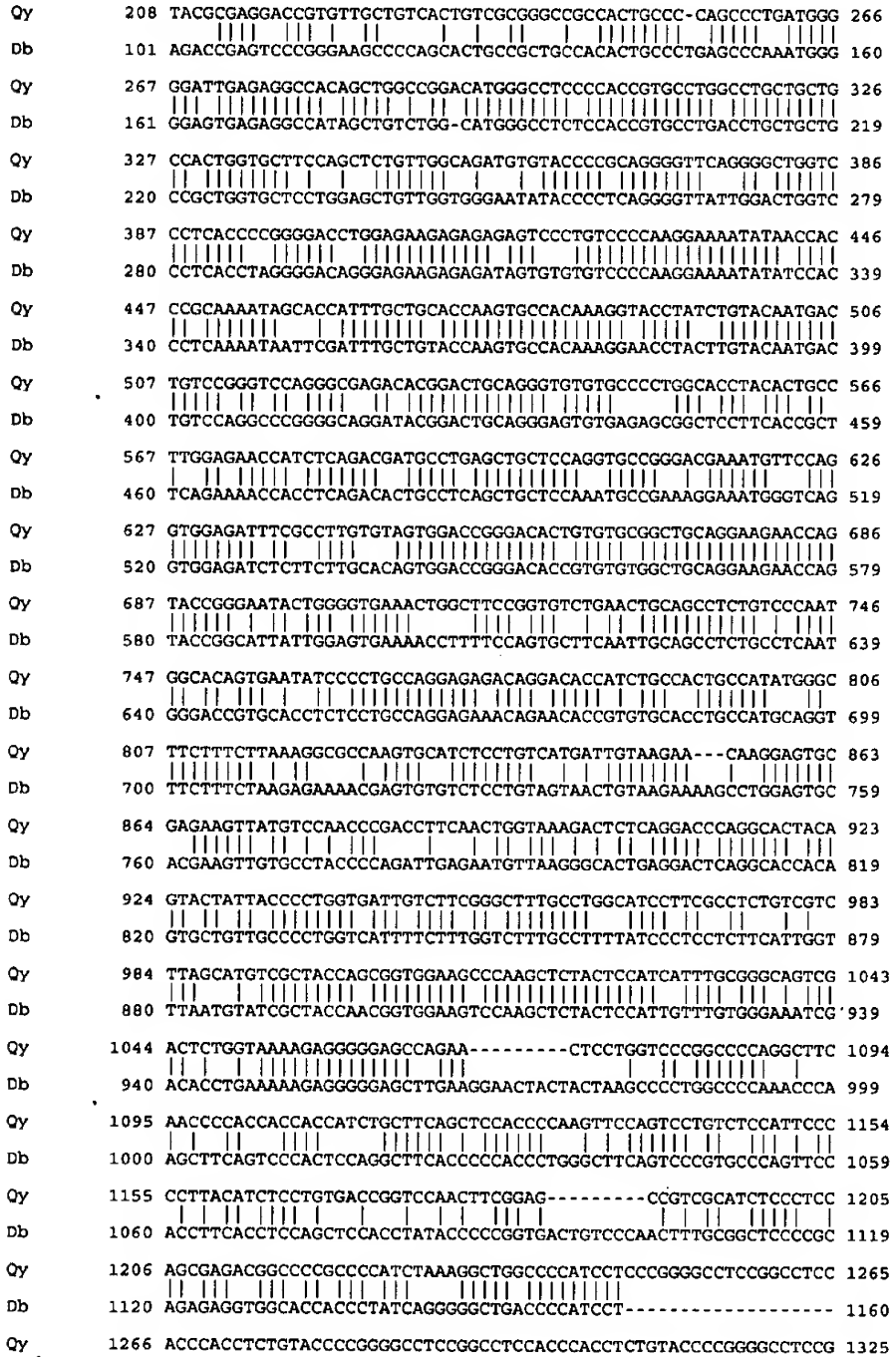


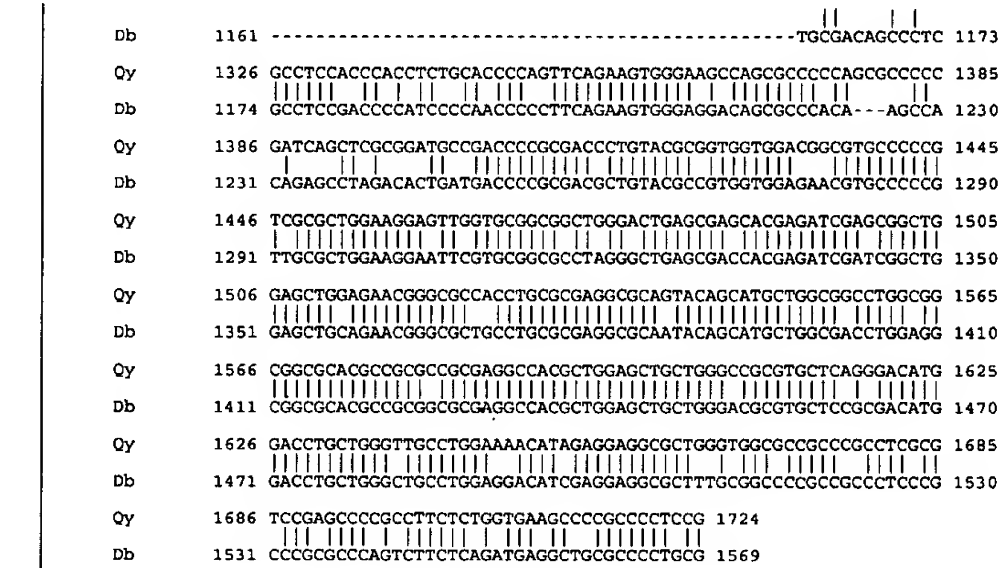
RESULT 7
AAZ09170

ID AAZ09170 standard; cDNA; 2111 BP.
XX
AC AAZ09170;
XX
DT 20-MAR-2003 (updated)
DT 18-OCT-1999 (first entry)
XX
DE Human tumour necrosis factor binding protein cDNA.
XX
KW Tumour necrosis factor binding protein; TNF; insoluble protein; agonist;
KW anti-inflammatory; antimalarial; treatment; septic shock; inflammation;
KW autoimmune glomerulonephritis; cerebral malaria; immune response;
KW antagonist; diagnosis; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 187..1554
FT /*tag= a
FT /product= "TNF binding protein"
FT sig_peptide 187..273
FT /*tag= b
FT mat_peptide 274..1551
FT /*tag= c
XX
PN EP939121-A2.
XX
PD 01-SEP-1999.
XX
PF 31-AUG-1990; 99EP-0100703.
XX
PR 12-SEP-1989; 89CH-0003319.
PR 08-MAR-1990; 90CH-0000746.
PR 20-APR-1990; 90CH-0001347.
PR 31-AUG-1990; 90EP-0116707.
XX
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
PI Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Loetscher H;
PI Schlaeger E;
XX
DR WPI; 1999-480840/41.
DR P-PSDB; AAY30934.
XX
PT New insoluble proteins, and fragments, that bind to tumor necrosis
PT factor, used to treat e.g. septic shock or cerebral malaria
XX
PS Claim 4; Fig 1; 25pp; German.
XX
CC This invention describes novel homogeneous insoluble proteins (I),
CC their (in)soluble fragments (Ia) and their salts that can bind tumour
CC necrosis factor (TNF). The products of the invention have
CC anti-inflammatory and antimalarial activity. (I) and (Ia) are used (i)
CC to treat diseases in which TNF is involved (e.g. septic shock, autoimmune
CC glomerulonephritis, cerebral malaria, immune responses and inflammation),
CC (ii) to purify TNF, (iii) to identify TNF (ant)agonists and (iv) for
CC diagnostic determination of TNF in body fluids. Antibodies raised against
CC (I) are used for affinity purification of (I). This sequence encodes
CC a tumour necrosis factor binding protein described in the method of
CC the invention.
CC (Updated on 20-MAR-2003 to correct PF field.)
CC (Updated on 20-MAR-2003 to correct PR field.)
XX
SQ Sequence 2111 BP; 445 A; 629 C; 587 G; 450 T; 0 other;

Query Match 29.7%; Score 725.8; DB 20; Length 2111;
Best Local Similarity 70.0%; Pred. No. 5e-139;
Matches 1120; Conservative 0; Mismatches 387; Indels 92; Gaps 7;







RESULT 8
AAH48859
ID AAH48859 standard; DNA; 2111 BP.
XX
AC AAH48859;
XX
DT 12-NOV-2001 (first entry)
XX
DE Human TNFBP-associated DNA #1.
XX
KW TNF; tumor necrosis factor binding protein; TNFBP; treatment;
KW insoluble protein; antiinflammatory; immunosuppressive; antibacterial;
KW antiprotozoal; treatment; meningococcal sepsis; cerebral malaria;
KW autoimmune glomerulonephritis; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 187..1554
FT /*tag= a
FT /product= "TNFBP-associated protein"
FT sig_peptide 187..270
FT /*tag= b
FT mat_peptide 271..1551
FT /*tag= c
XX
PN EP1132471-A2.
XX
PD 12-SEP-2001.
XX
PF 31-AUG-1990; 2001EP-0108117.
XX
PR 12-SEP-1989; 89CH-0003319.
PR 08-MAR-1990; 90CH-0000746.
PR 20-APR-1990; 90CH-0001347.
PR 31-AUG-1990; 90EP-0116707.
PR 31-AUG-1990; 99EP-0100703.
XX
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
PI Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Loetscher H;

PI Schlaeger E;
XX
DR WPI; 2001-559312/63.
DR P-PSDB; AAB86817.
XX
PT New homogeneous, insoluble proteins that bind tumor necrosis factor
PT (TNF), useful for treating TNF-mediated disorders, e.g. inflammation -
XX
PS Claim 4a; Fig 1; 26pp; German.
XX
CC This invention describes novel insoluble proteins (I), also their
CC (in)soluble fragments and pharmaceutically acceptable salts, able to bind
CC tumor necrosis factor (TNF) and in homogeneous form. The products of the
CC invention have antiinflammatory, immunosuppressive, antibacterial,
CC antiprotozoal activity. (I), and related recombinant proteins, are used
CC to treat diseases mediated by TNF, e.g. shock in cases of meningococcal
CC sepsis; development of autoimmune glomerulonephritis and cerebral
CC malaria. Also (I), or antibodies specific for them, are used for
CC diagnostic determination of TNF in body fluids, for affinity purification
CC of TNF and for identifying (ant)agonists of TNF. This sequence encodes a
CC human TNF binding protein described in the method of the invention.
XX
SQ Sequence 2111 BP; 447 A; 627 C; 587 G; 450 T; 0 other;

Query Match 29.7%; Score 725.8; DB 22; Length 2111;
Best Local Similarity 70.0%; Pred. No. 5e-139;
Matches 1120; Conservative 0; Mismatches 387; Indels 92; Gaps 7;

```
Qy      148 TGTCCCCGCCCCAGTCTCAACCCTCCACTCCCCGACCCGAGGCCCGGGCTCCACTGGGCA 207
Db       41 TCTCTATGCCCGAGTCTCAACCCTCAACTGTCACCCCAAGGCACTTGGGACGTCCTGGAC 100

Qy      208 TACGCGAGGACCGTGTTGCTGTCACTGTCGCGGGCCGCCACTGCCC-CAGCCCTGATGGG 266
Db      101 AGACCGAGTCCCGGGAAGCCCCAGCACTGCCGCTGCCACACTGCCCTGAGCCCAAATGGG 160

Qy      267 GGATTGAGAGGCCACAGCTGGCCGGACATGGGCCTCCCCACCGTGCCTGGCCTGCTGCTG 326
Db      161 GGAGTGAGAGGCCATAGCTGTCTGG-CATGGGCCTCTCCACCGTGCCTGACCTGCTGCTG 219

Qy      327 CCACTGGTGCTTCCAGCTCTGTTGGCAGATGTGTACCCCGCAGGGGTTCAGGGGCTGGTC 386
Db      220 CCGCTGGTGCTCCTGGAGCTGTTGGTGGGAATATACCCCTCAGGGGTTATTGGACTGGTC 279

Qy      387 CCTCACCCCGGGGACCTGGAGAAGAGAGAGAGTCCCTGTCCCCAAGGAAAATATAACCAC 446
Db      280 CCTCACCTAGGGGACAGGGAGAAGAGAGATAGTGTGTGTCCCCAAGGAAAATATATCCAC 339

Qy      447 CCGCAAAATAGCACCATTTGCTGCACCAAGTGCCACAAAGGTACCTATCTGTACAATGAC 506
Db      340 CCTCAAAATAATTCGATTTGCTGTACCAAGTGCCACAAAGGAACCTACTTGTACAATGAC 399

Qy      507 TGTCCGGGTCCAGGGCGAGACACGGACTGCAGGGTGTGTGCCCCTGGCACCTACACTGCC 566
Db      400 TGTCCAGGCCCGGGGCAGGATACGGACTGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCT 459

Qy      567 TTGGAGAACCATCTCAGACGATGCCTGAGCTGCTCCAGGTGCCGGGACGAAATGTTCCAG 626
Db      460 TCAGAAAACCACCTCAGACACTGCCTCAGCTGCTCCAAATGCCGAAAGGAAATGGGTCAG 519

Qy      627 GTGGAGATTTCGCCTTGTGTAGTGGACCGGGACACTGTGTGCGGCTGCAGGAAGAACCAG 686
Db      520 GTGGAGATCTCTTCTTGCACAGTGGACCGGGACACCGTGTGTGGCTGCAGGAAGAACCAG 579

Qy      687 TACCGGGAATACTGGGGTGAAACTGGCTTCCGGTGTCTGAACTGCAGCCTCTGTCCCAAT 746
Db      580 TACCGGCATTATTGGAGTGAAAACCTTTTCCAGTGCTTCAATTGCAGCCTCTGCCTCAAT 639

Qy      747 GGCACAGTGAATATCCCCTGCCAGGAGAGACAGGACACCATCTGCCACTGCCATATGGGC 806
Db      640 GGGACCGTGCACCTCTCCTGCCAGGAGAAACAGAACACCGTGTGCACCTGCCATGCAGGT 699

Qy      807 TTCTTTCTTAAAGGCGCCAAGTGCATCTCCTGTCATGATTGTAAGAA---CAAGGAGTGC 863

Db      700 TTCTTTCTAAGAGAAAACGAGTGTGTCTCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGC 759

Qy      864 GAGAAGTTATGTCCAACCCGACCTTCAACTGGTAAAGACTCTCAGGACCCAGGCACTACA 923
Db      760 ACGAAGTTGTGCCTACCCCAGATTGAGAATGTTAAGGGCACTGAGGACTCAGGCACCACA 819

Qy      924 GTACTATTACCCCTGGTGATTGTCTTCGGGCTTTGCCTGGCATCCTTCGCCTCTGTCGTC 983
Db      820 GTGCTGTTGCCCCTGGTCATTTTCTTTGGTCTTTGCCTTTTATCCCTCCTCTTCATTGGT 879

Qy      984 TTAGCATGTCGCTACCAGCGGTGGAAGCCCAAGCTCTACTCCATCATTTGCGGGCAGTCG 1043
Db      880 TTAATGTATCGCTACCAACGGTGGAAGTCCAAGCTCTACTCCATTGTTTGTGGGAAATCG 939

Qy     1044 ACTCTGGTAAAAGAGGGGGAGCCAGAA---------CTCCTGGTCCCGGCCCCAGGCTTC 1094
Db      940 ACACCTGAAAAAGAGGGGGAGCTTGAAGGAACTACTACTAAGCCCCTGGCCCCAAACCCA 999

Qy     1095 AACCCCACCACCACCATCTGCTTCAGCTCCACCCCAAGTTCCAGTCCTGTCTCCATTCCC 1154
Db     1000 AGCTTCAGTCCCACTCCAGGCTTCACCCCCACCCTGGGCTTCAGTCCCGTGCCCAGTTCC 1059

Qy     1155 CCTTACATCTCCTGTGACCGGTCCAACTTCGGAG---------CCGTCGCATCTCCCTCC 1205
Db     1060 ACCTTCACCTCCAGCTCCACCTATACCCCCGGTGACTGTCCCAACTTTGCGGCTCCCCGC 1119

Qy     1206 AGCGAGACGGCCCCGCCCCATCTAAAGGCTGGCCCCATCCTCCCGGGGCCTCCGGCCTCC 1265
Db     1120 AGAGAGGTGGCACCACCCTATCAGGGGGCTGACCCCATCCT------------------- 1160

Qy     1266 ACCCACCTCTGTACCCCGGGGCCTCCGGCCTCCACCCACCTCTGTACCCCGGGGCCTCCG 1325
Db     1161 ----------------------------------------------TGCGACAGCCCTC 1173

Qy     1326 GCCTCCACCCACCTCTGCAGCCCAGTTCAGAAGTGGGAAGCCAGCGCCCCCAGCGCCCCC 1385
Db     1174 GCCTCCGACCCCATCCCCAACCCCCTTCAGAAGTGGGAGGACAGCGCCCACA---AGCCA 1230

Qy     1386 GATCAGCTCGCGGATGCCGACCCCGCGACCCTGTACGCGGTGGTGGACGGCGTGCCCCCG 1445
Db     1231 CAGAGCCTAGACACTGATGACCCCGCGACGCTGTACGCCGTGGTGGAGAACGTGCCCCCG 1290

Qy     1446 TCGCGCTGGAAGGAGTTGGTGCGGCGGCTGGGACTGAGCGAGCACGAGATCGAGCGGCTG 1505
Db     1291 TTGCGCTGGAAGGAATTCGTGCGGCGCCTAGGGCTGAGCGACCACGAGATCGATCGGCTG 1350

Qy     1506 GAGCTGGAGAACGGGCGCCACCTGCGCGAGGCGCAGTACAGCATGCTGGCGGCCTGGCGG 1565
Db     1351 GAGCTGCAGAACGGGCGCTGCCTGCGCGAGGCGCAATACAGCATGCTGGCGACCTGGAGG 1410

Qy     1566 CGGCGCACGCCGCGCCGCGAGGCCACGCTGGAGCTGCTGGGCCGCGTGCTCAGGGACATG 1625
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Qy     1626 GACCTGCTGGGTTGCCTGGAAAACATAGAGGAGGCGCTGGGTGGCGCCGCCCGCCTCGCG 1685
Db     1471 GACCTGCTGGGCTGCCTGGAGGACATCGAGGAGGCGCTTTGCGGCCCCGCCGCCCTCCCG 1530

Qy     1686 TCCGAGCCCCGCCTTCTCTGGTGAAGCCCCGCCCCTCCG 1724
Db     1531 CCCGCGCCCAGTCTTCTCAGATGAGGCTGCGCCCCTGCG 1569
```

RESULT 9
ABK84039
ID ABK84039 standard; cDNA; 2111 BP.
XX
AC ABK84039;
XX
DT 14-AUG-2002 (first entry)
XX
DE Human cDNA differentially expressed in granulocytic cells #610.

XX
KW Human; ss; granulocytic cell; DNA chip; bacterial infection;
KW viral infection; parasitic infection; protozoal infection;
KW fungal infection; sterile inflammatory disease; psoriasis;
KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
KW cardiac reperfusion injury; renal reperfusion injury; ARDS;
KW adult respiratory distress syndrome; inflammatory bowel disease;
KW Crohn's disease; ulcerative colitis; periodontal disease;
KW granulocyte activation; chronic inflammation; allergy.
XX
OS Homo sapiens.
XX
PN WO200228999-A2.
XX
PD 11-APR-2002.
XX
PF 03-OCT-2001; 2001WO-US30821.
XX
PR 03-OCT-2000; 2000US-237189P.
XX
PA (GENE-) GENE LOGIC INC.
XX
PI Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;
XX
DR WPI; 2002-435328/46.
XX
PT Detecting granulocyte activation by detecting differential expression
PT of genes associated with granulocyte activation, which serves as
PT diagnostic markers that is useful for monitoring disease states and
PT drug toxicity -
XX
PS Claim 1; SEQ ID No 610; 114pp; English.
XX
CC The invention relates to detecting (M1) granulocyte (GC) activation
CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by
CC DNA chip analysis as given in the specification, and comparing
CC the expression level to an expression level in an unactivated
CC GC, where differential expression of Gs is indicative of GCA.
CC Also included are modulating (M2) GA by contacting GC with an agent
CC that alters the expression of at least one gene in Gs; (2) screening (M3)
CC for an agent capable of modulating GCA or an inflammation (especially
CC chronic) in a tissue, an allergic response in a subject, exposure of a
CC subject to a pathogen or sterile inflammatory disease using the
CC gene expression profile; (3) detecting (M4) an inflammation (especially
CC chronic) in a tissue, an allergic response in a subject, exposure of a
CC subject to a pathogen or sterile inflammatory disease, by detecting the
CC level of expression in a sample of the tissue of gene(s) from Gs, where
CC the level of expression of the gene is indicative of inflammation;
CC (4) treating (M5) an inflammation (especially chronic) or in a tissue,
CC an allergic response in a subject, exposure of a subject to a pathogen
CC or sterile inflammatory disease, by contacting a tissue having
CC inflammation with an agent that modulates the expression of gene(s)
CC from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for
CC modulating GA; M3 is useful for screening an agent capable of modulating
CC GCA preferably in an inflammation in a tissue; M4 is useful for
CC detecting an inflammation (especially chronic) in a tissue, an allergic
CC response in a subject, exposure of a subject to a pathogen or sterile
CC inflammatory disease (e.g. psoriasis, rheumatoid arthritis,
CC glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal
CC reperfusion injury, ARDS, adult respiratory distress syndrome,
CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,
CC periodontal disease; also bacterial infection, viral infection,
CC parasitic infection, protozoal infection, fungal infection and M5 is
CC useful for treating one of the above conditions. The present
CC sequence represents a gene differentially expressed in granulocytes.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 2111 BP; 445 A; 629 C; 587 G; 450 T; 0 other;

Query Match 29.7%; Score 725.8; DB 24; Length 2111;

Best Local Similarity 70.0%; Pred. No. 5e-139;
Matches 1120; Conservative 0; Mismatches 387; Indels 92; Gaps 7;

```
Qy      148 TGTCCCCGCCCCAGTCTCAACCCTCCACTCCCCGACCCGAGGCCCGGGCTCCACTGGGCA 207
Db       41 TCTCTATGCCCGAGTCTCAACCCTCAACTGTCACCCCAAGGCACTTGGGACGTCCTGGAC 100

Qy      208 TACGCGAGGACCGTGTTGCTGTCACTGTCGCGGGCCGCCACTGCCC-CAGCCCTGATGGG 266
Db      101 AGACCGAGTCCCGGGAAGCCCCAGCACTGCCGCTGCCACACTGCCCTGAGCCCAAATGGG 160

Qy      267 GGATTGAGAGGCCACAGCTGGCCGGACATGGGCCTCCCCACCGTGCCTGGCCTGCTGCTG 326
Db      161 GGAGTGAGAGGCCATAGCTGTCTGG-CATGGGCCTCTCCACCGTGCCTGACCTGCTGCTG 219

Qy      327 CCACTGGTGCTTCCAGCTCTGTTGGCAGATGTGTACCCCGCAGGGGTTCAGGGGCTGGTC 386
Db      220 CCGCTGGTGCTCCTGGAGCTGTTGGTGGGAATATACCCCTCAGGGGTTATTGGACTGGTC 279

Qy      387 CCTCACCCCGGGGACCTGGAGAAGAGAGAGAGTCCCTGTCCCCAAGGAAAATATAACCAC 446
Db      280 CCTCACCTAGGGGACAGGGAGAAGAGAGATAGTGTGTGTCCCCAAGGAAAATATATCCAC 339

Qy      447 CCGCAAAATAGCACCATTTGCTGCACCAAGTGCCACAAAGGTACCTATCTGTACAATGAC 506
Db      340 CCTCAAAATAATTCGATTTGCTGTACCAAGTGCCACAAAGGAACCTACTTGTACAATGAC 399

Qy      507 TGTCCGGGTCCAGGGCGAGACACGGACTGCAGGGTGTGTGCCCCTGGCACCTACACTGCC 566
Db      400 TGTCCAGGCCCGGGGCAGGATACGGACTGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCT 459

Qy      567 TTGGAGAACCATCTCAGACGATGCCTGAGCTGCTCCAGGTGCCGGGACGAAATGTTCCAG 626
Db      460 TCAGAAAACCACCTCAGACACTGCCTCAGCTGCTCCAAATGCCGAAAGGAAATGGGTCAG 519

Qy      627 GTGGAGATTTCGCCTTGTGTAGTGGACCGGGACACTGTGTGCGGCTGCAGGAAGAACCAG 686
Db      520 GTGGAGATCTCTTCTTGCACAGTGGACCGGGACACCGTGTGTGGCTGCAGGAAGAACCAG 579

Qy      687 TACCGGGAATACTGGGGTGAAACTGGCTTCCGGTGTCTGAACTGCAGCCTCTGTCCCAAT 746
Db      580 TACCGGCATTATTGGAGTGAAAACCTTTTCCAGTGCTTCAATTGCAGCCTCTGCCTCAAT 639

Qy      747 GGCACAGTGAATATCCCCTGCCAGGAGAGACAGGACACCATCTGCCACTGCCATATGGGC 806
Db      640 GGGACCGTGCACCTCTCCTGCCAGGAGAAACAGAACACCGTGTGCACCTGCCATGCAGGT 699

Qy      807 TTCTTTCTTAAAGGCGCCAAGTGCATCTCCTGTCATGATTGTAAGAA---CAAGGAGTGC 863
Db      700 TTCTTTCTAAGAGAAAACGAGTGTGTCTCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGC 759

Qy      864 GAGAAGTTATGTCCAACCCGACCTTCAACTGGTAAAGACTCTCAGGACCCAGGCACTACA 923
Db      760 ACGAAGTTGTGCCTACCCCAGATTGAGAATGTTAAGGGCACTGAGGACTCAGGCACCACA 819

Qy      924 GTACTATTACCCCTGGTGATTGTCTTCGGGCTTTGCCTGGCATCCTTCGCCTCTGTCGTC 983
Db      820 GTGCTGTTGCCCCTGGTCATTTTCTTTGGTCTTTGCCTTTTATCCCTCCTCTTCATTGGT 879

Qy      984 TTAGCATGTCGCTACCAGCGGTGGAAGCCCAAGCTCTACTCCATCATTTGCGGGCAGTCG 1043
Db      880 TTAATGTATCGCTACCAACGGTGGAAGTCCAAGCTCTACTCCATTGTTTGTGGGAAATCG 939

Qy     1044 ACTCTGGTAAAAGAGGGGGAGCCAGAA---------CTCCTGGTCCCGGCCCCAGGCTTC 1094
Db      940 ACACCTGAAAAAGAGGGGGAGCTTGAAGGAACTACTACTAAGCCCCTGGCCCCAAACCCA 999

Qy     1095 AACCCCACCACCACCATCTGCTTCAGCTCCACCCCAAGTTCCAGTCCTGTCTCCATTCCC 1154
Db     1000 AGCTTCAGTCCCACTCCAGGCTTCACCCCCACCCTGGGCTTCAGTCCCGTGCCCAGTTCC 1059

Qy     1155 CCTTACATCTCCTGTGACCGGTCCAACTTCGGAG---------CCGTCGCATCTCCCTCC 1205
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Db       1060 ACCTTCACCTCCAGCTCCACCTATACCCCCGGTGACTGTCCCAACTTTGCGGCTCCCCGC 1119

Qy       1206 AGCGAGACGGCCCCGCCCCATCTAAAGGCTGGCCCCATCCTCCCGGGGGCCTCCGGCCTCC 1265
              || ||| ||| || ||| |||    ||||| |||||||||
Db       1120 AGAGAGGTGGCACCACCCTATCAGGGGGCTGACCCCATCCT------------------- 1160

Qy       1266 ACCCACCTCTGTACCCCGGGGCCTCCGGCCTCCACCCACCTCTGTACCCCGGGGCCTCCG 1325
                                                              ||   | ||
Db       1161 ----------------------------------------------TGCGACAGCCCTC 1173

Qy       1326 GCCTCCACCCACCTCTGCACCCCAGTTCAGAAGTGGGAAGCCAGCGCCCCCAGCGCCCCC 1385
              ||||||  || | ||  || ||| |||||||||||||| | |||||||| ||     ||
Db       1174 GCCTCCGACCCCATCCCCAACCCCCTTCAGAAGTGGGAGGACAGCGCCCACA---AGCCA 1230

Qy       1386 GATCAGCTCGCGGATGCCGACCCCGCGACCCTGTACGCGGTGGTGGACGGCGTGCCCCCG 1445
                |   || |   ||  |||||||||||| |||||||| ||||||||   ||||||||||
Db       1231 CAGAGCCTAGACACTGATGACCCCGCGACGCTGTACGCCGTGGTGGAGAACGTGCCCCCG 1290

Qy       1446 TCGCGCTGGAAGGAGTTGGTGCGGCGGCTGGGACTGAGCGAGCACGAGATCGAGCGGCTG 1505
              | |||||||||||| || |||||||| || || |||||||| |||||||||| ||||||
Db       1291 TTGCGCTGGAAGGAATTCGTGCGGCGCCTAGGGCTGAGCGACCACGAGATCGATCGGCTG 1350

Qy       1506 GAGCTGGAGAACGGGCGCCACCTGCGCGAGGCGCAGTACAGCATGCTGGCGGCCTGGCGG 1565
              |||||| ||||||||||  |||||||||||||| |||||||||||||| ||||| ||
Db       1351 GAGCTGCAGAACGGGCGCTGCCTGCGCGAGGCGCAATACAGCATGCTGGCGACCTGGAGG 1410

Qy       1566 CGGCGCACGCCGCGCCGCGAGGCCACGCTGGAGCTGCTGGGCCGCGTGCTCAGGGACATG 1625
              |||||||||||||| ||||||||||||||||||||||||||||| ||||||| | ||||||
Db       1411 CGGCGCACGCCGCGGCGCGAGGCCACGCTGGAGCTGCTGGGACGCGTGCTCCGCGACATG 1470

Qy       1626 GACCTGCTGGGTTGCCTGGAAAACATAGAGGAGGCGCTGGGTGGCGCCGCCCGCCTCGCG 1685
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Db       1471 GACCTGCTGGGCTGCCTGGAGGACATCGAGGAGGCGCTTTGCGGCCCCGCCGCCCTCCCG 1530

Qy       1686 TCCGAGCCCCGCCTTCTCTGGTGAAGCCCCGCCCCTCCG 1724
                ||| |||| | |||||| | ||| ||  |||||||
Db       1531 CCCGCGCCCAGTCTTCTCAGATGAGGCTGCGCCCCTGCG 1569
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RESULT 10
ABN95862
ID ABN95862 standard; DNA; 2111 BP.
XX
AC ABN95862;
XX
DT 13-AUG-2002 (first entry)
XX
DE Gene #2360 used to diagnose liver cancer.
XX
KW Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic;
KW metastatic liver tumour; cytostatic; expression profile; disease state;
KW disease progression; drug toxicity; drug efficacy; drug metabolism.
XX
OS Homo sapiens.
XX
PN WO200229103-A2.
XX
PD 11-APR-2002.
XX
PF 02-OCT-2001; 2001WO-US30589.
XX
PR 02-OCT-2000; 2000US-237054P.
XX
PA (GENE-) GENE LOGIC INC.
XX
PI Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;
XX
DR WPI; 2002-426119/45.
XX
PT Diagnosing and detecting the progression of liver cancer,
PT hepatocellular carcinoma or metastatic liver tumor in a patient,
PT involves detecting the level of expression of two or more genes in a
PT liver tissue sample -
XX
PS Claim 1; SEQ ID NO 2360; 298pp; English.
XX
CC The invention relates to a novel method for diagnosing and detecting the
CC progression of liver cancer, hepatocellular carcinoma or metastatic liver
CC tumour in a patient, and differentiating metastatic liver cancer from
CC hepatocellular carcinoma in a patient, involving detecting the level of
CC expression of two or more genes represented in ABN93503-ABN97455 in a
CC tissue sample. The method of the invention has hepatotropic, and
CC cytostatic activity. The method is useful for diagnosing and detecting
CC the progression of liver cancer, hepatocellular carcinoma and metastatic
CC liver carcinoma in a patient. The method is useful for identifying
CC expression profiles which serve as useful diagnostic markers as well as
CC markers that can be used to monitor disease states, disease progression,
CC drug toxicity, drug efficacy and drug metabolism.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 2111 BP; 445 A; 629 C; 587 G; 450 T; 0 other;

Query Match 29.7%; Score 725.8; DB 24; Length 2111;
Best Local Similarity 70.0%; Pred. No. 5e-139;
Matches 1120; Conservative 0; Mismatches 387; Indels 92; Gaps 7;

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Qy        148 TGTCCCCGCCCCAGTCTCAACCCTCCACTCCCCGACCCGAGGCCCGGGCTCCACTGGGCA 207
              | ||   |||| |||||||||||||| |||  |   ||   |  |  ||  |  |  ||
Db         41 TCTCTATGCCCGAGTCTCAACCCTCAACTGTCACCCCAAGGCACTTGGGACGTCCTGGAC 100

Qy        208 TACGCGAGGACCGTGTTGCTGTCACTGTCGCGGGCCGCCACTGCCC-CAGCCCTGATGGG 266
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Db        101 AGACCGAGTCCCGGGAAGCCCCAGCACTGCCGCTGCCACACTGCCCTGAGCCCAAATGGG 160

Qy        267 GGATTGAGAGGCCACAGCTGGCCGGACATGGGCCTCCCCACCGTGCCTGGCCTGCTGCTG 326
              |||  |||||||||| ||||| | || |||||||||  |||||||||| ||||||||||
Db        161 GGAGTGAGAGGCCATAGCTGTCTGG-CATGGGCCTCTCCACCGTGCCTGACCTGCTGCTG 219

Qy        327 CCACTGGTGCTTCCAGCTCTGTTGGCAGATGTGTACCCCGCAGGGGTTCAGGGGCTGGTC 386
              || |||||||| |  | |||||||  |   | ||||| ||||||||   || ||||||
Db        220 CCGCTGGTGCTCCTGGAGCTGTTGGTGGGAATATACCCCTCAGGGGTTATTGGACTGGTC 279

Qy        387 CCTCACCCCGGGGACCTGGAGAAGAGAGAGAGTCCCTGTCCCCAAGGAAAATATAACCAC 446
              |||||||  ||||||  |||||||||||| |||  ||||||||||||||||||| ||||
Db        280 CCTCACCTAGGGGACAGGGAGAAGAGAGATAGTGTGTGTCCCCAAGGAAAATATATCCAC 339

Qy        447 CCGCAAAATAGCACCATTTGCTGCACCAAGTGCCACAAAGGTACCTATCTGTACAATGAC 506
              || |||||||   | |||||||| ||||||||||||||||| |||||  ||||||||||
Db        340 CCTCAAAATAATTCGATTTGCTGTACCAAGTGCCACAAAGGAACCTACTTGTACAATGAC 399

Qy        507 TGTCCGGGTCCAGGGCGAGACACGGACTGCAGGGTGTGTGCCCCTGGCACCTACACTGCC 566
              ||||| || || ||||  || |||||||||||||| |||||      ||| ||| ||| ||
Db        400 TGTCCAGGCCCGGGGCAGGATACGGACTGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCT 459

Qy        567 TTGGAGAACCATCTCAGACGATGCCTGAGCTGCTCCAGGTGCCGGGACGAAATGTTCCAG 626
              |  || ||||| |||||||  |||| |||||||||  |||||  | ||||||   |||
Db        460 TCAGAAAACCACCTCAGACACTGCCTCAGCTGCTCCAAATGCCGAAAGGAAATGGGTCAG 519

Qy        627 GTGGAGATTTCGCCTTGTGTAGTGGACCGGGACACTGTGTGCGGCTGCAGGAAGAACCAG 686
              |||||||| ||  ||||  |||||||||||||||| |||||  |||||||||||||||||
Db        520 GTGGAGATCTCTTCTTGCACAGTGGACCGGGACACCGTGTGTGGCTGCAGGAAGAACCAG 579

Qy        687 TACCGGGAATACTGGGGTGAAACTGGCTTCCGGTGTCTGAACTGCAGCCTCTGTCCCAAT 746
              ||||||  | || ||| ||||||      |||| |||  | || ||||||||||| | ||||
Db        580 TACCGGCATTATTGGAGTGAAAACCTTTTCCAGTGCTTCAATTGCAGCCTCTGCCTCAAT 639

Qy        747 GGCACAGTGAATATCCCCTGCCAGGAGAGACAGGACACCATCTGCCACTGCCATATGGGC 806
              || || ||| |  || |||||||||||| |||| ||||| | |||  |||||||   ||
Db        640 GGGACCGTGCACCTCTCCTGCCAGGAGAAACAGAACACCGTGTGCACCTGCCATGCAGGT 699

Qy        807 TTCTTTCTTAAAGGCGCCAAGTGCATCTCCTGTCATGATTGTAAGAA---CAAGGAGTGC 863
              |||||||  | ||    | ||||  ||||||||  | | ||||||||   |  |||||||
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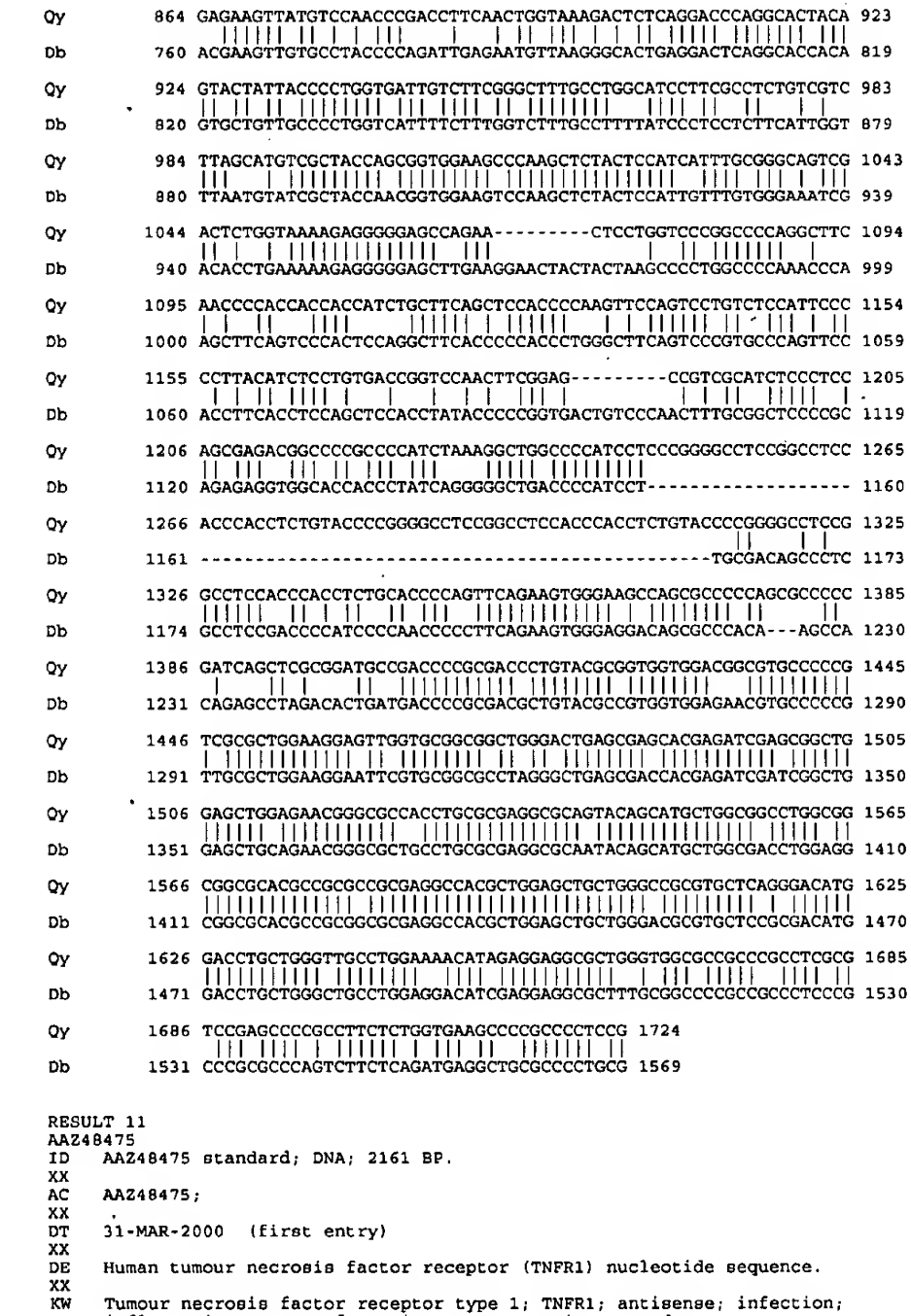
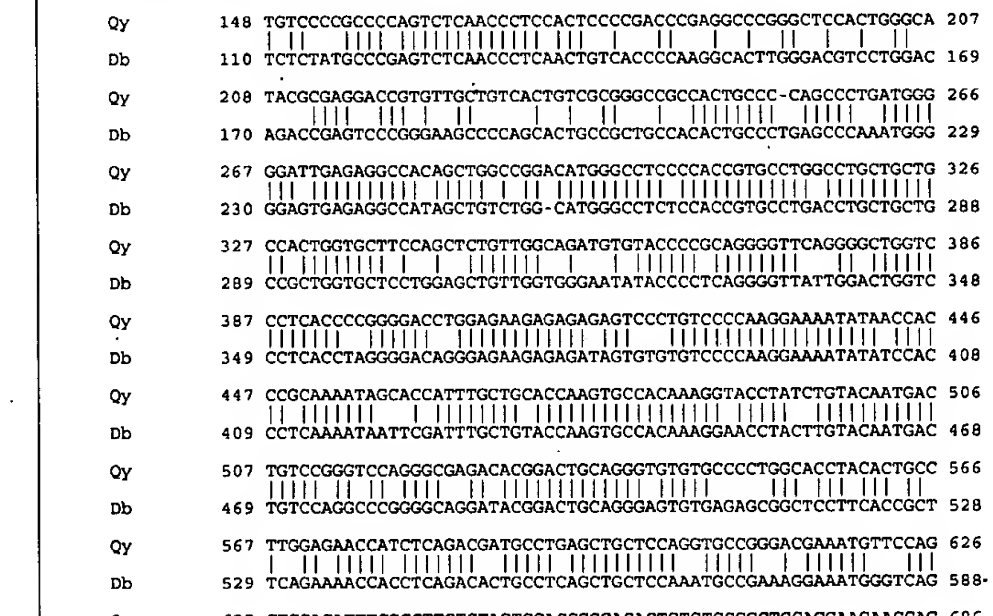


RESULT 11
AAZ48475
ID AAZ48475 standard; DNA; 2161 BP.
XX
AC AAZ48475;
XX
DT 31-MAR-2000 (first entry)
XX
DE Human tumour necrosis factor receptor (TNFR1) nucleotide sequence.
XX
KW Tumour necrosis factor receptor type 1; TNFR1; antisense; infection;
KW inflammation; tumour formation; TNFR1; anticancer; ds.

XX
OS Homo sapiens.
XX
PN US6007995-A.
XX
PD 28-DEC-1999.
XX
PF 26-JUN-1998; 98US-0106038.
XX
PR 26-JUN-1998; 98US-0106038.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Baker BF, Cowsert LM;
XX
DR WPI; 2000-105333/09.
XX
PT Antisense inhibition of tumor necrosis factor type 1 expression for
PT diagnosis, treatment and prevention of disease, particularly tumors -
XX
PS Example 10; Columns 33-36; 34pp; English.
XX
CC The invention provides antisense compounds targeted to human tumour
CC necrosis factor receptor type 1 (TNFR1) RNA. These antisense compounds
CC can be used in a method of inhibiting the expression of TNFR1 human cells
CC or tissues. The antisense compounds specifically hybridize with one or
CC more nucleic acids encoding TNFR1 modulating the function of nucleic
CC acid molecules encoding TNFR1, ultimately modulating the amount of TNFR1
CC produced. The antisense compounds and method are useful as research
CC reagents and diagnostics, and in the treatment and prophylaxis of
CC infection, inflammation or tumour formation. The present sequence
CC represents the nucleotide sequence of human TNFR1 (GenBank Accn No:
CC X55313).
XX
SQ Sequence 2161 BP; 459 A; 642 C; 604 G; 456 T; 0 other;

Query Match 29.7%; Score 725.8; DB 21; Length 2161;
Best Local Similarity 70.0%; Pred. No. 5e-139;
Matches 1120; Conservative 0; Mismatches 387; Indels 92; Gaps 7;



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Db        589 GTGGAGATCTCTTCTTGCACAGTGGACCGGGACACCGTGTGTGGCTGCAGGAAGAACCAG 648

Qy        687 TACCGGGAATACTGGGGTGAAACTGGCTTCCGGTGTCTGAACTGCAGCCTCTGTCCCAAT 746

Db        649 TACCGGCATTATTGGAGTGAAAACCTTTTCCAGTGCTTCAATTGCAGCCTCTGCCTCAAT 708

Qy        747 GGCACAGTGAATATCCCCTGCCAGGAGAGACAGGACACCATCTGCCACTGCCATATGGGC 806

Db        709 GGGACCGTGCACCTCTCCTGCCAGGAGAAACAGAACACCGTGTGCACCTGCCATGCAGGT 768

Qy        807 TTCTTTCTTAAAGGCGCCAAGTGCATCTCCTGTCATGATTGTAAGAA---CAAGGAGTGC 863

Db        769 TTCTTTCTAAGAGAAAACGAGTGTGTCTCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGC 828

Qy        864 GAGAAGTTATGTCCAACCCGACCTTCAACTGGTAAAGACTCTCAGGACCCAGGCACTACA 923

Db        829 ACGAAGTTGTGCCTACCCCAGATTGAGAATGTTAAGGGCACTGAGGACTCAGGCACCACA 888

Qy        924 GTACTATTACCCCTGGTGATTGTCTTCGGGCTTTGCCTGGCATCCTTCGCCTCTGTCGTC 983

Db        889 GTGCTGTTGCCCCTGGTCATTTTCTTTGGTCTTTGCCTTTTATCCCTCCTCTTCATTGGT 948

Qy        984 TTAGCATGTCGCTACCAGCGGTGGAAGCCCAAGCTCTACTCCATCATTTGCGGGCAGTCG 1043

Db        949 TTAATGTATCGCTACCAACGGTGGAAGTCCAAGCTCTACTCCATTGTTTGTGGGAAATCG 1008

Qy       1044 ACTCTGGTAAAAGAGGGGGAGCCAGAA---------CTCCTGGTCCCGGCCCCAGGCTTC 1094

Db       1009 ACACCTGAAAAAGAGGGGGAGCTTGAAGGAACTACTACTAAGCCCCTGGCCCCAAACCCA 1068

Qy       1095 AACCCCACCACCACCATCTGCTTCAGCTCCACCCCAAGTTCCAGTCCTGTCTCCATTCCC 1154

Db       1069 AGCTTCAGTCCCACTCCAGGCTTCACCCCCACCCTGGGCTTCAGTCCCGTGCCCAGTTCC 1128

Qy       1155 CCTTACATCTCCTGTGACCGGTCCAACTTCGGAG---------CCGTCGCATCTCCCTCC 1205

Db       1129 ACCTTCACCTCCAGCTCCACCTATACCCCCGGTGACTGTCCCAACTTTGCGGCTCCCCGC 1188

Qy       1206 AGCGAGACGGCCCCGCCCCATCTAAAGGCTGGCCCCATCCTCCCGGGGCCTCCGGCCTCC 1265

Db       1189 AGAGAGGTGGCACCACCCTATCAGGGGGCTGACCCCATCCT---------- 1229

Qy       1266 ACCCACCTCTGTACCCCGGGGCCTCCGGCCTCCACCCACCTCTGTACCCCGGGGCCTCCG 1325

Db       1230 ----------------------------------------------TGCGACAGCCCTC 1242

Qy       1326 GCCTCCACCCACCTCTGCACCCCAGTTCAGAAGTGGGAAGCCAGCGCCCCCAGCGCCCCC 1385

Db       1243 GCCTCCGACCCCATCCCCAACCCCCTTCAGAAGTGGGAGGACAGCGCCCACA---AGCCA 1299

Qy       1386 GATCAGCTCGCGGATGCCGACCCCGCGACCCTGTACGCGGTGGTGGACGGCGTGCCCCCG 1445

Db       1300 CAGAGCCTAGACACTGATGACCCCGCGACGCTGTACGCCGTGGTGGAGAACGTGCCCCCG 1359

Qy       1446 TCGCGCTGGAAGGAGTTGGTGCGGCGGCTGGGACTGAGCGAGCACGAGATCGAGCGGCTG 1505

Db       1360 TTGCGCTGGAAGGAATTCGTGCGGCGCCTAGGGCTGAGCGACCACGAGATCGATCGGCTG 1419

Qy       1506 GAGCTGGAGAACGGGCGCCACCTGCGCGAGGCGCAGTACAGCATGCTGGCGGCCTGGCGG 1565

Db       1420 GAGCTGCAGAACGGGCGCTGCCTGCGCGAGGCGCAATACAGCATGCTGGCGACCTGGAGG 1479

Qy       1566 CGGCGCACGCCGCGCCGCGAGGCCACGCTGGAGCTGCTGGGCCGCGTGCTCAGGGACATG 1625

Db       1480 CGGCGCACGCCGCGGCGCGAGGCCACGCTGGAGCTGCTGGGACGCGTGCTCCGCGACATG 1539

Qy       1626 GACCTGCTGGGTTGCCTGGAAAACATAGAGGAGGCGCTGGGTGGCGCCGCCCGCCTCGCG 1685

Db       1540 GACCTGCTGGGCTGCCTGGAGGACATCGAGGAGGCGCTTTGCGGCCCCGCCGCCCTCCCG 1599

Qy       1686 TCCGAGCCCCGCCTTCTCTGGTGAAGCCCCGCCCCTCCG 1724

Db       1600 CCCGCGCCCAGTCTTCTCAGATGAGGCTGCGCCCCTGCG 1638
```

RESULT 12
ABT04971
ID ABT04971 standard; DNA; 2161 BP.
XX
AC ABT04971;
XX
DT 11-OCT-2002 (first entry)
XX
DE Cytokine tumour necrosis factor (TNF) polynucleotide SEQ ID No 1.
XX
KW Antisense compound; tumour necrosis factor receptor 1; liver disease;
KW TNFR1; hepatitis; liver injury; hyperproliferative disorder; cancer;
KW human; ds.
XX
OS Homo sapiens.
XX
PN WO200248168-A1.
XX
PD 20-JUN-2002.
XX
PF 22-OCT-2001; 2001WO-US51224.
XX
PR 24-OCT-2000; 2000US-0695451.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Baker BF, Cowsert LM, Zhang H, Dean NM;
XX
DR WPI; 2002-583481/62.
DR P-PSDB; AAO22286.
XX
PT Novel antisense compound targeted to nucleic acid molecule encoding
PT tumor necrosis factor receptor 1 (TNFR1), useful for treating humans
PT having disease associated with TNFR1 e.g. hepatitis, liver injury,
PT liver cancer -
XX
PS Example 10; Page 69-71; 121pp; English.
XX
CC The invention relates to an antisense compound 8 to 30 nucleotides in
CC length targeted to nucleic acid molecule encoding tumour necrosis factor
CC receptor 1 (TNFR1), where the antisense compound inhibits expression of
CC TNFR1. The antisense compound is useful for inhibiting the expression of
CC TNFR1 in cells or tissues. The antisense compound is also useful for
CC treating an animal (preferably human) having a disease or condition
CC associated with TNFR1, e.g. a liver disease (such as hepatitis, or liver
CC injury) or a hyperproliferative disorder such as cancer, by inhibiting
CC the expression of TNFR1. The antisense compound is useful for
CC diagnostics, therapeutics, prophylaxis and as research reagents and kits.
CC This polynucleotide sequence represents a human nucleic acid sequence
CC relating to the TNFR1 of the invention.
XX
SQ Sequence 2161 BP; 459 A; 642 C; 604 G; 456 T; 0 other;

Query Match 29.7%; Score 725.8; DB 24; Length 2161;
Best Local Similarity 70.0%; Pred. No. 5e-139;
Matches 1120; Conservative 0; Mismatches 387; Indels 92; Gaps 7;

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Qy        148 TGTCCCCGCCCCAGTCTCAACCCTCCACTCCCCGACCCGAGGCCCGGGCTCCACTGGGCA 207

Db        110 TCTCTATGCCCGAGTCTCAACCCTCAACTGTCACCCCAAGGCACTTGGGACGTCCTGGAC 169

Qy        208 TACGCGAGGACCGTGTTGCTGTCACTGTCGCGGGCCGCCACTGCCC-CAGCCCTGATGGG 266

Db        170 AGACCGAGTCCCGGGAAGCCCCAGCACTGCCGCTGCCACACTGCCCTGAGCCCAAATGGG 229

Qy        267 GGATTGAGAGGCCACAGCTGGCCGGACATGGGCCTCCCCACCGTGCCTGGCCTGCTGCTG 326

Db        230 GGAGTGAGAGGCCATAGCTGTCTGG-CATGGGCCTCTCCACCGTGCCTGACCTGCTGCTG 288

Qy        327 CCACTGGTGCTTCCAGCTCTGTTGGCAGATGTGTACCCCGCAGGGGTTCAGGGGCTGGTC 386
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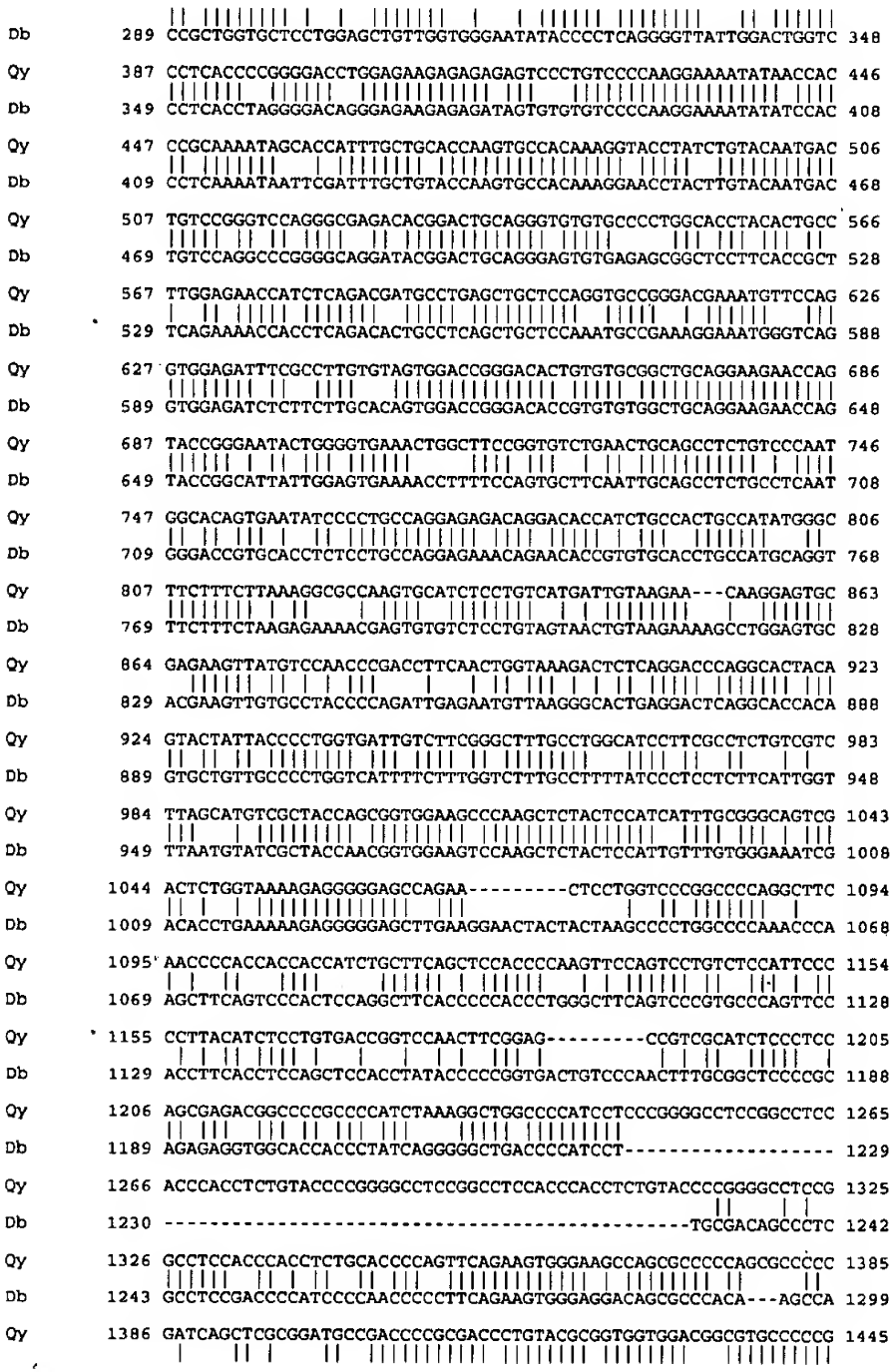

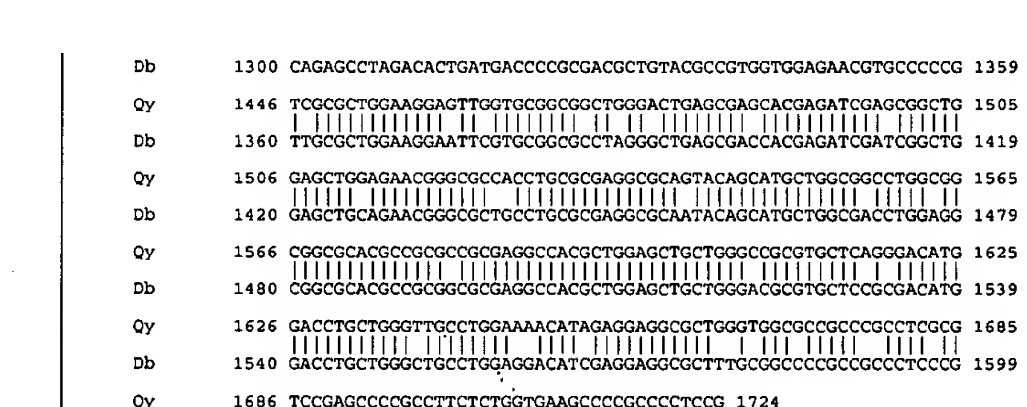

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RESULT 13
ABK13194
ID   ABK13194 standard; DNA; 2161 BP.
XX
AC   ABK13194;
XX
DT   23-APR-2002  (first entry)
XX
DE   Human tumour necrosis factor alpha (TNF alpha) receptor DNA.
XX
KW   TNF alpha; apoptosis; ds; tumour; death domain receptor ligand;
KW   diterpenoid triepoxide; cytostatic activity; c-IAP2; c-IAP1;
KW   carcinoma; mammary adenocarcinoma; non-small cell lung carcinoma;
KW   neurological malignancy; haematological malignancy; lichen planus;
KW   non-Hodgkin's lymphoma; chronic lymphocytic leukaemia; anti-angiogenic;
KW   malignant cutaneous T-cell; lymphomatoid papulosis; anti-metastatic;
KW   non-MF cutaneous T-cell lymphoma; mycosis fungoides; anti-tumour;
KW   T-cell rich cutaneous lymphoid hyperplasia; bullous pemphigoid;
KW   discoid lupus erythematosus; human; gene; receptor; TNF-R1.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             256..1623
FT                   /*tag= a
FT                   /product= "TNF alpha protein"
XX
PN   US6329148-B1.
XX
PD   11-DEC-2001.
XX
PF   15-FEB-2000; 2000US-0505250.
XX
PR   16-FEB-1999;   99US-120313P.
PR   20-AUG-1999;   99US-149989P.
XX
PA   (STRD ) UNIV LELAND STANFORD.
XX
PI   Rosen GD,  Kao P;
XX
DR   WPI; 2002-121125/16.
DR   P-PSDB; AAU75064.
XX
PT   Use of a synergistic combination of death domain receptor ligands and
PT   diterpenoid triepoxides for killing of tumour cells -
XX
PS   Disclosure; Column 23-28; 20pp; English.
XX
CC   This invention relates to a novel method for enhanced killing of tumour
CC   cells comprising contacting a tumour cell with a synergistic
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CC   combination of a death domain receptor ligand and a diterpenoid
CC   triepoxide. This method has cytostatic activity and works by blocking
CC   TNF-alpha mediated induction of c-IAP2 and c-IAP1. The method of the
CC   invention may be used for treating tumours, particularly solid tumours,
CC   e.g. carcinoma, mammary adenocarcinoma and non-small cell lung carcinoma
CC   also neurological malignancies, haematological malignancies, e.g.
CC   non-Hodgkin's lymphoma, chronic lymphocytic leukaemia, malignant
CC   cutaneous T-cells, mycosis fungoides, non-MF cutaneous T-cell lymphoma,
CC   lymphomatoid papulosis, T-cell rich cutaneous lymphoid hyperplasia,
CC   bullous pemphigoid, discoid lupus erythematosus, lichen planus. The
CC   combination may be administered with other active agents, e.g. anti-
CC   metastatic, anti-tumour or anti-angiogenic agents. The potent synergy
CC   between the diterpenoids and the death domain ligands allows increased
CC   killing at equivalent or lower doses, and can sensitise otherwise
CC   resistant cells. This sequence represents the human tumour necrosis
CC   factor alpha receptor (TNF-R1) DNA. TNF-R1 is a death domain receptor
CC   used in the used method of the invention in combination with diterpenoid
CC   triepoxides to kill tumours by inducing apoptosis.
XX
SQ   Sequence 2161 BP; 459 A; 642 C; 604 G; 456 T; 0 other;

  Query Match             29.7%;  Score 725.8;  DB 24;  Length 2161;
  Best Local Similarity   70.0%;  Pred. No. 5e-139;
  Matches 1120;  Conservative    0;  Mismatches  387;  Indels   92;  Gaps    7;

Qy        148 TGTCCCCGCCCCAGTCTCAACCCTCCACTCCCCGACCCGAGGCCCGGGCTCCACTGGGCA 207
Db        110 TCTCTATGCCCGAGTCTCAACCCTCAACTGTCACCCCAAGGCACTTGGGACGTCCTGGAC 169

Qy        208 TACGCGAGGACCGTGTTGCTGTCACTGTCGCGGGCCGCCACTGCCC-CAGCCCTGATGGG 266
Db        170 AGACCGAGTCCCGGGAAGCCCCAGCACTGCCGCTGCCACACTGCCCTGAGCCCAAATGGG 229

Qy        267 GGATTGAGAGGCCACAGCTGGCCGGACATGGGCCTCCCCACCGTGCCTGGCCTGCTGCTG 326
Db        230 GGAGTGAGAGGCCATAGCTGTCTGG-CATGGGCCTCTCCACCGTGCCTGACCTGCTGCTG 288

Qy        327 CCACTGGTGCTTCCAGCTCTGTTGGCAGATGTGTACCCCGCAGGGGTTCAGGGGCTGGTC 386
Db        289 CCGCTGGTGCTCCTGGAGCTGTTGGTGGGAATATACCCCTCAGGGGTTATTGGACTGGTC 348

Qy        387 CCTCACCCCGGGGACCTGGAGAAGAGAGAGAGTCCCTGTCCCCAAGGAAAATATAACCAC 446
Db        349 CCTCACCTAGGGGACAGGGAGAAGAGAGATAGTGTGTGTCCCCAAGGAAAATATATCCAC 408

Qy        447 CCGCAAAATAGCACCATTTGCTGCACCAAGTGCCACAAAGGTACCTATCTGTACAATGAC 506
Db        409 CCTCAAAATAATTCGATTTGCTGTACCAAGTGCCACAAAGGAACCTACTTGTACAATGAC 468

Qy        507 TGTCCGGGTCCAGGGCGAGACACGGACTGCAGGGTGTGTGCCCCTGGCACCTACACTGCC 566
Db        469 TGTCCAGGCCCGGGGCAGGATACGGACTGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCT 528

Qy        567 TTGGAGAACCATCTCAGACGATGCCTGAGCTGCTCCAGGTGCCGGGACGAAATGTTCCAG 626
Db        529 TCAGAAAACCACCTCAGACACTGCCTCAGCTGCTCCAAATGCCGAAAGGAAATGGGTCAG 588

Qy        627 GTGGAGATTTCGCCTTGTGTAGTGGACCGGGACACTGTGTGCGGCTGCAGGAAGAACCAG 686
Db        589 GTGGAGATCTCTTCTTGCACAGTGGACCGGGACACCGTGTGTGGCTGCAGGAAGAACCAG 648

Qy        687 TACCGGGAATACTGGGGTGAAACTGGCTTCCGGTGTCTGAACTGCAGCCTCTGTCCCAAT 746
Db        649 TACCGGCATTATTGGAGTGAAAACCTTTTCCAGTGCTTCAATTGCAGCCTCTGCCTCAAT 708

Qy        747 GGCACAGTGAATATCCCCTGCCAGGAGAGACAGGACACCATCTGCCACTGCCATATGGGC 806
Db        709 GGGACCGTGCACCTCTCCTGCCAGGAGAAACAGAACACCGTGTGCACCTGCCATGCAGGT 768

Qy        807 TTCTTTCTTAAAGGCGCCAAGTGCATCTCCTGTCATGATTGTAAGAA---CAAGGAGTGC 863
Db        769 TTCTTTCTAAGAGAAAACGAGTGTGTCTCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGC 828

Qy        864 GAGAAGTTATGTCCAACCCGACCTTCAACTGGTAAAGACTCTCAGGACCCAGGCACTACA 923
Db        829 ACGAAGTTGTGCCTACCCCAGATTGAGAATGTTAAGGGCACTGAGGACTCAGGCACCACA 888

Qy        924 GTACTATTACCCCTGGTGATTGTCTTCGGGCTTTGCCTGGCATCCTTCGCCTCTGTCGTC 983
Db        889 GTGCTGTTGCCCCTGGTCATTTTCTTTGGTCTTTGCCTTTTATCCCTCCTCTTCATTGGT 948

Qy        984 TTAGCATGTCGCTACCAGCGGTGGAAGCCCAAGCTCTACTCCATCATTTGCGGGCAGTCG 1043
Db        949 TTAATGTATCGCTACCAACGGTGGAAGTCCAAGCTCTACTCCATTGTTTGTGGGAAATCG 1008

Qy       1044 ACTCTGGTAAAAGAGGGGGAGCCAGAA---------CTCCTGGTCCCGGCCCCAGGCTTC 1094
Db       1009 ACACCTGAAAAAGAGGGGGAGCTTGAAGGAACTACTACTAAGCCCCTGGCCCCAAACCCA 1068

Qy       1095 AACCCCACCACCACCATCTGCTTCAGCTCCACCCCAAGTTCCAGTCCTGTCTCCATTCCC 1154
Db       1069 AGCTTCAGTCCCACTCCAGGCTTCACCCCCACCCTGGGCTTCAGTCCCGTGCCCAGTTCC 1128

Qy       1155 CCTTACATCTCCTGTGACCGGTCCAACTTCGGAG---------CCGTCGCATCTCCCTCC 1205
Db       1129 ACCTTCACCTCCAGCTCCACCTATACCCCCGGTGACTGTCCCAACTTTGCGGCTCCCCGC 1188

Qy       1206 AGCGAGACGGCCCCGCCCCATCTAAAGGCTGGCCCCATCCTCCCGGGGCCTCCGGCCTCC 1265
Db       1189 AGAGAGGTGGCACCACCCTATCAGGGGGCTGACCCCATCCT------------------- 1229

Qy       1266 ACCCACCTCTGTACCCCGGGGCCTCCGGCCTCCACCCACCTCTGTACCCCGGGGCCTCCG 1325
Db       1230 ----------------------------------------TGCGACAGCCCTC 1242

Qy       1326 GCCTCCACCCACCTCTGCACCCCAGTTCAGAAGTGGGAAGCCAGCGCCCCCAGCGCCCCC 1385
Db       1243 GCCTCCGACCCCATCCCCAACCCCCTTCAGAAGTGGGAGGACAGCGCCCACA---AGCCA 1299

Qy       1386 GATCAGCTCGCGGATGCCGACCCCGCGACCCTGTACGCGGTGGTGGACGGCGTGCCCCCG 1445
Db       1300 CAGAGCCTAGACACTGATGACCCCGCGACGCTGTACGCCGTGGTGGAGAACGTGCCCCCG 1359

Qy       1446 TCGCGCTGGAAGGAGTTGGTGCGGCGGCTGGGACTGAGCGAGCACGAGATCGAGCGGCTG 1505
Db       1360 TTGCGCTGGAAGGAATTCGTGCGGCGCCTAGGGCTGAGCGACCACGAGATCGATCGGCTG 1419

Qy       1506 GAGCTGGAGAACGGGCGCCACCTGCGCGAGGCGCAGTACAGCATGCTGGCGGCCTGGCGG 1565
Db       1420 GAGCTGCAGAACGGGCGCTGCCTGCGCGAGGCGCAATACAGCATGCTGGCGACCTGGAGG 1479

Qy       1566 CGGCGCACGCCGCGCCGCGAGGCCACGCTGGAGCTGCTGGGCCGCGTGCTCAGGGACATG 1625
Db       1480 CGGCGCACGCCGCGGCGCGAGGCCACGCTGGAGCTGCTGGGACGCGTGCTCCGCGACATG 1539

Qy       1626 GACCTGCTGGGTTGCCTGGAAAACATAGAGGAGGCGCTGGGTGGCGCCGCCCGCCTCGCG 1685
Db       1540 GACCTGCTGGGCTGCCTGGAGGACATCGAGGAGGCGCTTTGCGGCCCCGCCGCCCTCCCG 1599

Qy       1686 TCCGAGCCCCGCCTTCTCTGGTGAAGCCCCGCCCCTCCG 1724
Db       1600 CCCGCGCCCAGTCTTCTCAGATGAGGCTGCGCCCCTGCG 1638


RESULT 14
AAQ90513
ID   AAQ90513 standard; DNA; 2175 BP.
XX
AC   AAQ90513;
XX
DT   19-JAN-1996  (first entry)
XX
DE   p55 TNF-R gene.
XX
KW   p55; tumour necrosis factor receptor; TNF-R; human; murine; chimera;
KW   epidermal growth factor receptor; EGP-R; protease; inhibitor;
```

```
KW   phorbol myristate acetate; PMA; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
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FT                   /*tag= a
FT                   /product= p55 TNF-R
FT   misc_signal     2143..2149
FT                   /*tag= b
FT                   /note= "possible poly-A signal"
XX
PN   AU9475742-A.
XX
PD   04-MAY-1995.
XX
PF   11-OCT-1994;   94AU-0075742.
XX
PR   12-OCT-1993;   93IL-0107268.
XX
PA   (YEDA ) YEDA RES & DEV CO LTD.
XX
PI   Batkin M,  Brakebusch C,  Varfolomeev E,  Wallach D;
XX
DR   WPI; 1995-194342/26.
DR   P-PSDB; AAR75084.
XX
PT   New protease capable of cleaving soluble tumour necrosis factor
PT   (TNF) receptor  - from cell-bound TNF- receptor, useful for
PT   antagonising deleterious effects of TNF.
XX
PS   Disclosure; Fig 1; 40pp; English.
XX
CC   This sequence represents human p55 tumour necrosis factor (TNF-R) DNA.
CC   Expression of this receptor is regulated by shedding of the
CC   extracellular receptor fragment.  The p55 TNF-R can be shed in response
CC   to different inducing agents, e.g. phorbol myristate acetate (PMA),
CC   depending on cell type.  The only region of the receptor whose structure
CC   affects the shedding response is the spacer region (see AAR75012) in the
CC   extracellular domain.  This region is located close to a site of cleavage
CC   of the molecule, and links the Cys rich module to the transmembrane
CC   domain.  The spacer region of the encoded protein was used to create the
CC   chimeras between human p55 TNF-R and murine epidermal growth factor
CC   receptor (EGF-R) that are represented by AAR75007-11.  This spacer region
CC   was subjected to deletion mutations (AAR75013-25) and substitutions
CC   (AAR75026-47).  Of the spacer region, the most important residues are
CC   Asn 172, Val 173, Lys 174 and Gly 175, with Val 173 being the most
CC   important of these.  The shedding of the receptor is independent of the
CC   side chain identity of these residues, with the exception of a limited
CC   dependence on the identity of Val 173.  Mutations which alter the
CC   conformation of the protein adversely effect the shedding process.  The
CC   mutations shown in AAR75013-47 were introduced in order to create an
CC   inhibitor of a protease that is capable of cleaving the soluble TNF-R
CC   from the cell bound TNF-R.  Fragments of these inhibitors can be seen in
CC   AAR75017-9, AAR75025, AAR75033-5 and AAR75042-3.  These protease
CC   inhibitors can  be used for enhancing TNF function.
XX
SQ   Sequence 2175 BP; 474 A; 642 C; 603 G; 456 T; 0 other;

  Query Match           29.7%;  Score 725.4;  DB 16;  Length 2175;
  Best Local Similarity  69.6%;  Pred. No. 6e-139;
  Matches 1128;  Conservative    0;  Mismatches  401;  Indels   92;  Gaps    7;

Qy       148 TGTCCCCGCCCCAGTCTCAACCCTCCACTCCCCGACCCGAGGCCCGGGCTCCACTGGGCA 207
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Qy       208 TACGCGAGGACCGTGTTGCTGTCACTGTCGCGGGCCGCCACTGCCC-CAGCCCTGATGGG 266
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Qy       267 GGATTGAGAGGCCACAGCTGGCCGGACATGGGCCTCCCCACCGTGCCTGGCCTGCTGCTG 326
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Qy       327 CCACTGGTGCTTCCAGCTCTGTTGGCAGATGTGTACCCCGCAGGGGTTCAGGGGCTGGTC 386
Db       289 CCGCTGGTGCTCCTGGAGCTGTTGGTGGGAATATACCCCTCAGGGGTTATTGGACTGGTC 348

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Qy       447 CCGCAAAATAGCACCATTTGCTGCACCAAGTGCCACAAAGGTACCTATCTGTACAATGAC 506
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Qy       507 TGTCCGGGTCCAGGGCGAGACACGGACTGCAGGGTGTGTGCCCCTGGCACCTACACTGCC 566
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Qy       687 TACCGGGAATACTGGGGTGAAACTGGCTTCCGGTGTCTGAACTGCAGCCTCTGTCCCAAT 746
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Qy       747 GGCACAGTGAATATCCCCTGCCAGGAGAGACAGGACACCATCTGCCACTGCCATATGGGC 806
Db       709 GGGACCGTGCACCTCTCCTGCCAGGAGAAACAGAACACCGTGTGCACCTGCCATGCAGGT 768

Qy       807 TTCTTTCTTAAAGGCGCCAAGTGCATCTCCTGTCATGATTGTAAGAA---CAAGGAGTGC 863
Db       769 TTCTTTCTAAGAGAAAACGAGTGTGTCTCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGC 828

Qy       864 GAGAAGTTATGTCCAACCCGACCTTCAACTGGTAAAGACTCTCAGGACCCAGGCACTACA 923
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Db       889 GTGCTGTTGCCCCTGGTCATTTTCTTTGGTCTTTGCCTTTTATCCCTCCTCTTCATTGGT 948

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Db      1243 GCCTCCGACCCCATCCCCAACCCCCTTCAGAAGTGGGAGGACAGCGCCCACA---AGCCA 1299
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Qy       1626 GACCTGCTGGGTTGCCTGGAAAACATAGAGGAGGCGCTGGGTGGCGCCGCCCGCCTCGCG 1685
Db       1540 GACCTGCTGGGCTGCCTGGAGGACATCGAGGAGGCGCTTTGCGGCCCCGCCGCCCTCCCG 1599

Qy       1686 TCCGAGCCCCGCCTTCTCTGGTGAAGCCCCGCCCCTCCGACTGCGGGCCTCCCCGCCCTG 1745
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Qy       1746 C 1746
Db       1660 C 1660
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RESULT 15
AAQ10955
ID AAQ10955 standard; cDNA; 2111 BP.
XX
AC AAQ10955;
XX
DT 09-JAN-2003 (updated)
DT 24-MAY-1991 (first entry)
XX
DE Encodes human 55kD TNF-binding protein.
XX
KW Tumour Necrosis Factor; binding proteins; septic shock;
KW autoimmune glomerulonephritis; lymphokine; cytokine.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT sig_peptide   187..273
PT   /*tag= a
FT mat_peptide   274..1551
FT   /*tag= b
FT   /product= 55kD TNF-BP
XX
PN EP417563-A.
XX
PD 20-MAR-1991.
XX
PF 31-AUG-1990; 90EP-0116707.
XX
PR 20-APR-1990; 90CH-0001347.
PR 12-SEP-1989; 89CH-0003319.
PR 08-MAR-1990; 90CH-0000746.
XX
PA (HOFF) HOFFMANN-LA ROCHE AG.
XX
PI Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Lotscher H;
PI Schlaeger EJ;
XX
DR WPI; 1991-081851/12.
DR P-PSDB; AAR11082.
XX
PT Insoluble tumour necrosis factor binding proteins - and DNA
PT encoding them, useful in pharmaceutical prods. and for antibody
PT prodn.
XX
PS Claim 4; Fig 1; 26pp; German.
XX
CC Partial amino acid sequences were determined for the 55 and 75kD
CC TNF-BPs (see AAR11072-R11081) and oligonucleotide primers were
CC synthesised based on these partial sequences. The primers were used
CC to produce a cDNA fragment for use as aprobe to screen a human
CC placental cDNA bank constructed in lambda gt11. Positive clones were
CC identifed and sequenced. DNA constructs comprising the TNF-BP coding
CC sequence may also contain a fragment encoding a human Ig domain.
CC Recombinant constructs are used to transform cells to confer
CC improved TNF-binding properties.
CC See also AAQ10956.
CC (Updated on 09-JAN-2003 to add missing OS field.)
XX
SQ Sequence 2111 BP; 445 A; 628 C; 588 G; 450 T; 0 other;

  Query Match   29.7%; Score 724.2; DB 12; Length 2111;
  Best Local Similarity 70.0%; Pred. No. 1.1e-138;
  Matches 1119; Conservative   0; Mismatches 388; Indels   92; Gaps   7;

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Qy        148 TGTCCCCGCCCCAGTCTCAACCCTCCACTCCCCGACCCGAGGCCCGGGCTCCACTGGGCA 207
Db         41 TCTCTATGCCCGAGTCTCAACCCTCAACTGTCACCCCAAGGCACTTGGGACGTCCTGGAC 100

Qy        208 TACGCGAGGACCGTGTTGCTGTCACTGTCGCGGGCCGCCACTGCCC-CAGCCCTGATGGG 266
Db        101 AGACCGAGTCCCGGGAAGCCCCAGCACTGCCGCTGCCACACTGCCCTGAGCCCAAATGGG 160

Qy        267 GGATTGAGAGGCCACAGCTGGCCGGACATGGGCCTCCCCACCGTGCCTGGCCTGCTGCTG 326
Db        161 GGAGTGAGAGGCCATAGCTGTCTGG-CATGGGCCTCTCCACCGTGCCTGACCTGCTGCTG 219

Qy        327 CCACTGGTGCTTCCAGCTCTGTTGGCAGATGTGTACCCCGCAGGGGTTCAGGGGCTGGTC 386
Db        220 CCGCTGGTGCTCCTGGAGCTGTTGGTGGGAATATACCCCTCAGGGGTTATTGGACTGGTC 279

Qy        387 CCTCACCCCGGGGACCTGGAGAAGAGAGAGAGTCCCTGTCCCCAAGGAAAATATAACCAC 446
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Qy        447 CCGCAAAATAGCACCATTTGCTGCACCAAGTGCCACAAAGGTACCTATCTGTACAATGAC 506
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Qy        507 TGTCCGGGTCCAGGGCGAGACACGGACTGCAGGGTGTGTGCCCCTGGCACCTACACTGCC 566
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Qy        687 TACCGGGAATACTGGGGTGAAACTGGCTTCCGGTGTCTGAACTGCAGCCTCTGTCCCAAT 746
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Qy        747 GGCACAGTGAATATCCCCTGCCAGGAGAGACAGGACACCATCTGCCACTGCCATATGGGC 806
Db        640 GGGACCGTGCACCTCTCCTGCCAGGAGAAACAGAACACCGTGTGCACCTGCCATGCAGGT 699

Qy        807 TTCTTTCTTAAAGGCGCCAAGTGCATCTCCTGTCATGATTGTAAGAA---CAAGGAGTGC 863
Db        700 TTCTTTCTAAGAGAAAACGAGTGTGTCTCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGC 759

Qy        864 GAGAAGTTATGTCCAACCCGACCTTCAACTGGTAAAGACTCTCAGGACCCAGGCACTACA 923
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Qy      1206 AGCGAGACGGCCCCGCCCCATCTAAAGGCTGGCCCCATCCTCCCGGGGCCTCCGGCCTCC 1265
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Search completed: September 15, 2003, 05:11:31
Job time : 483 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 15, 2003, 04:49:18 ; Search time 125 Seconds
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Title: US-09-970-532-1
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Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2440	100.0	2440	4	US-09-513-007-1	Sequence 1, Appli
2	727	29.8	2175	1	US-08-321-668-1	Sequence 1, Appli
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6	725.8	29.7	2161	3	US-09-106-038A-1	Sequence 1, Appli
7	725.8	29.7	2161	4	US-09-505-250-3	Sequence 3, Appli
8	718.6	29.5	2062	1	US-08-050-319B-24	Sequence 24, Appl
9	718.6	29.5	2062	2	US-08-465-982-24	Sequence 24, Appl
10	683.8	28.0	1368	4	US-08-406-824A-3	Sequence 3, Appli
11	554	22.7	1956	2	US-08-762-308-10	Sequence 10, Appl
12	543	22.3	543	4	US-09-513-007-3	Sequence 3, Appli
13	389.8	16.0	6889	1	US-08-286-740-2	Sequence 2, Appli
14	389.8	16.0	6889	5	PCT-US95-09576-2	Sequence 2, Appli
15	388.6	15.9	6896	2	US-08-627-151A-6	Sequence 6, Appli
16	366.4	15.0	600	1	US-08-050-319B-47	Sequence 47, Appl
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18	336.6	13.8	504	1	US-08-050-319B-56	Sequence 56, Appl
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22	307.2	12.6	1478	3	US-09-149-922-6	Sequence 6, Appli
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24	304.4	12.5	1301	3	US-08-910-991-7	Sequence 7, Appli
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33	256.2	10.5	477	2	US-08-465-982-53	Sequence 53, Appl
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35	249	10.2	372	1	US-08-050-319B-3	Sequence 3, Appli
36	249	10.2	372	2	US-08-465-982-3	Sequence 3, Appli
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38	198.2	8.1	474	2	US-08-465-982-49	Sequence 49, Appl
39	177.2	7.3	462	1	US-08-050-319B-51	Sequence 51, Appl
40	177.2	7.3	462	2	US-08-465-982-51	Sequence 51, Appl
41	101	4.1	1239	4	US-08-600-203-1	Sequence 1, Appli
42	75.8	3.1	1634	4	US-08-928-069-11	Sequence 11, Appl
43	75.8	3.1	1634	4	US-08-828-683A-9	Sequence 9, Appli
44	75.8	3.1	1783	3	US-08-815-469-1	Sequence 1, Appli
45	74.2	3.0	1254	3	US-08-815-469-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-513-007-1
; Sequence 1, Application US/09513007
; Patent No. 6406907
; GENERAL INFORMATION:
; APPLICANT: Taylor, J. Michael
; APPLICANT: Kehrli, Jr., Marcus
; APPLICANT: Lee, Eun-Kyung
; APPLICANT: Mwangi, Simon
; TITLE OF INVENTION: BOVINE TUMOR NECROSIS FACTOR RECEPTOR-1
; TITLE OF INVENTION: AND METHODS OF USE
; FILE REFERENCE: 08411-018001
; CURRENT APPLICATION NUMBER: US/09/513,007
; CURRENT FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 60/122,156
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2440
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (294)...(1706)
US-09-513-007-1

Query Match 100.0%; Score 2440; DB 4; Length 2440;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2440; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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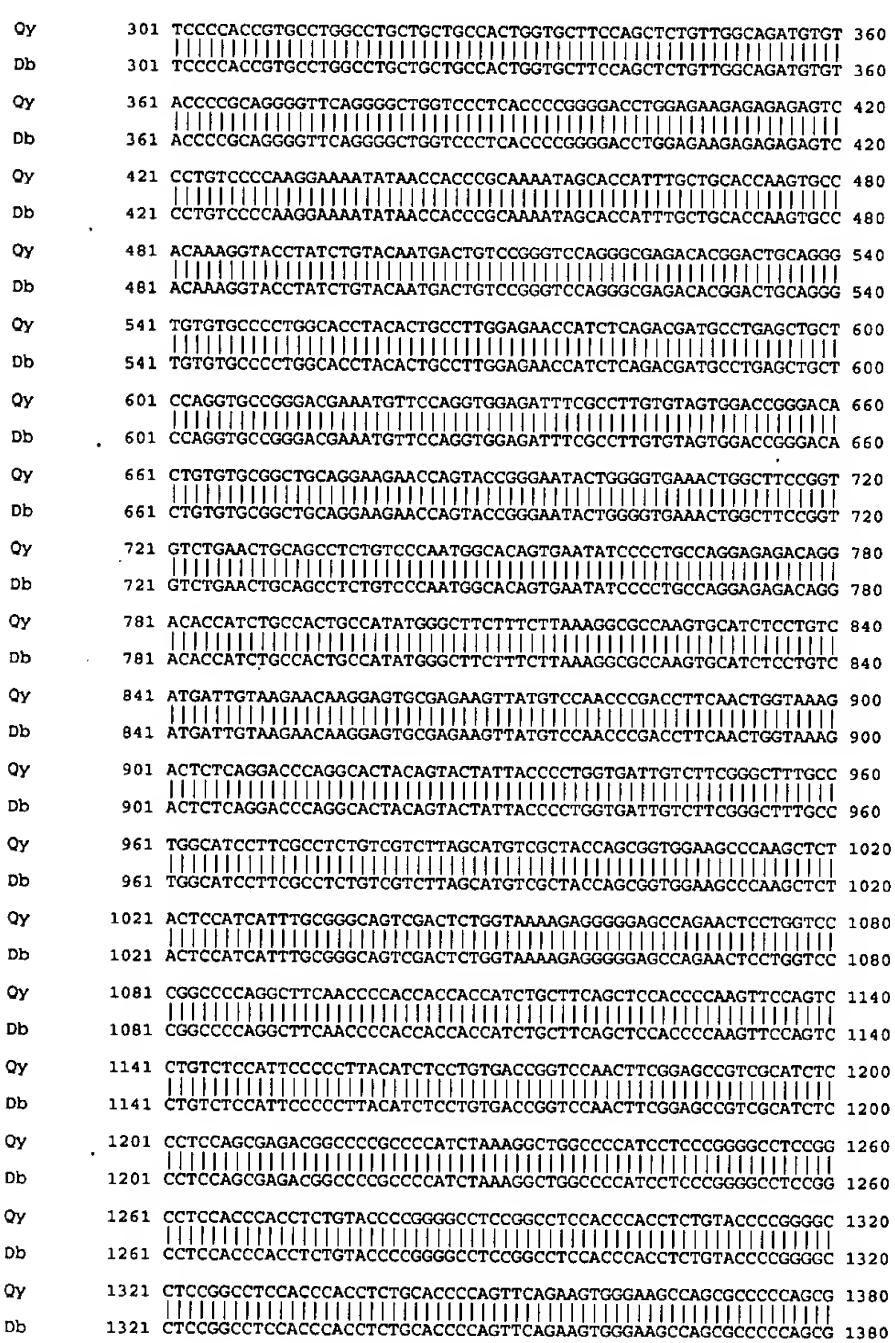
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Db 541 TGTGTGCCCCTGGCACCTACACTGCCTTGGAGAACCATCTCAGACGATGCCTGAGCTGCT 600
Qy 601 CCAGGTGCCGGGACGAAATGTTCCAGGTGGAGATTTCGCCTTGTGTAGTGGACCGGGACA 660
Db 601 CCAGGTGCCGGGACGAAATGTTCCAGGTGGAGATTTCGCCTTGTGTAGTGGACCGGGACA 660
Qy 661 CTGTGTGCGGCTGCAGGAAGAACCAGTACCGGGAATACTGGGGTGAAACTGGCTTCCGGT 720
Db 661 CTGTGTGCGGCTGCAGGAAGAACCAGTACCGGGAATACTGGGGTGAAACTGGCTTCCGGT 720
Qy 721 GTCTGAACTGCAGCCTCTGTCCCAATGGCACAGTGAATATCCCCTGCCAGGAGAGACAGG 780
Db 721 GTCTGAACTGCAGCCTCTGTCCCAATGGCACAGTGAATATCCCCTGCCAGGAGAGACAGG 780
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Qy 841 ATGATTGTAAGAACAAGGAGTGCGAGAAGTTATGTCCAACCCGACCTTCAACTGGTAAAG 900
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Db 901 ACTCTCAGGACCCAGGCACTACAGTACTATTACCCCTGGTGATTGTCTTCGGGCTTTGCC 960
Qy 961 TGGCATCCTTCGCCTCTGTCGTCTTAGCATGTCGCTACCAGCGGTGGAAGCCCAAGCTCT 1020
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Qy 1021 ACTCCATCATTTGCGGGCAGTCGACTCTGGTAAAAGAGGGGGAGCCAGAACTCCTGGTCC 1080
Db 1021 ACTCCATCATTTGCGGGCAGTCGACTCTGGTAAAAGAGGGGGAGCCAGAACTCCTGGTCC 1080
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Db 1081 CGGCCCCAGGCTTCAACCCCACCACCACCATCTGCTTCAGCTCCACCCCAAGTTCCAGTC 1140
Qy 1141 CTGTCTCCATTCCCCCTTACATCTCCTGTGACCGGTCCAACTTCGGAGCCGTCGCATCTC 1200
Db 1141 CTGTCTCCATTCCCCCTTACATCTCCTGTGACCGGTCCAACTTCGGAGCCGTCGCATCTC 1200
Qy 1201 CCTCCAGCGAGACGGCCCCGCCCCATCTAAAGGCTGGCCCCATCCTCCCGGGGCCTCCGG 1260
Db 1201 CCTCCAGCGAGACGGCCCCGCCCCATCTAAAGGCTGGCCCCATCCTCCCGGGGCCTCCGG 1260
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Qy 1321 CTCCGGCCTCCACCCACCTCTGCACCCCAGTTCAGAAGTGGGAAGCCAGCGCCCCCAGCG 1380
Db 1321 CTCCGGCCTCCACCCACCTCTGCACCCCAGTTCAGAAGTGGGAAGCCAGCGCCCCCAGCG 1380
Qy 1381 CCCCCGATCAGCTCGCGGATGCCGACCCCGCGACCCTGTACGCGGTGGTGGACGGCGTGC 1440
Db 1381 CCCCCGATCAGCTCGCGGATGCCGACCCCGCGACCCTGTACGCGGTGGTGGACGGCGTGC 1440
Qy 1441 CCCCGTCGCGCTGGAAGGAGTTGGTGCGGCGGCTGGGACTGAGCGAGCACGAGATCGAGC 1500
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Qy 1501 GGCTGGAGCTGGAGAACGGGCGCCACCTGCGCGAGGCGCAGTACAGCATGCTGGCGGCCT 1560
Db 1501 GGCTGGAGCTGGAGAACGGGCGCCACCTGCGCGAGGCGCAGTACAGCATGCTGGCGGCCT 1560
Qy 1561 GGCGGCGGCGCACGCCGCGCCGCGAGGCCACGCTGGAGCTGCTGGGCCGCGTGCTCAGGG 1620
Db 1561 GGCGGCGGCGCACGCCGCGCCGCGAGGCCACGCTGGAGCTGCTGGGCCGCGTGCTCAGGG 1620
Qy 1621 ACATGGACCTGCTGGGTTGCCTGGAAAACATAGAGGAGGCGCTGGGTGGCGCCGCCCGCC 1680
Db 1621 ACATGGACCTGCTGGGTTGCCTGGAAAACATAGAGGAGGCGCTGGGTGGCGCCGCCCGCC 1680
Qy 1681 TCGCGTCCGAGCCCCGCCTTCTCTGGTGAAGCCCCGCCCCTCCGACTGCGGGCCTCCCCG 1740
Db 1681 TCGCGTCCGAGCCCCGCCTTCTCTGGTGAAGCCCCGCCCCTCCGACTGCGGGCCTCCCCG 1740
Qy 1741 CCCTGCAGACGGCTGCTTCCTTCCTGTGCCAGGCAGCCCGGAAGGATCTGCGAGATGCCC 1800
Db 1741 CCCTGCAGACGGCTGCTTCCTTCCTGTGCCAGGCAGCCCGGAAGGATCTGCGAGATGCCC 1800
Qy 1801 TGTGGACCTCCTGTTTTGTTTTGTTTTTTTCTGGAGAGGAAGTCTTGGAGGAGCAGGCAC 1860
Db 1801 TGTGGACCTCCTGTTTTGTTTTGTTTTTTTCTGGAGAGGAAGTCTTGGAGGAGCAGGCAC 1860
Qy 1861 GATCTGGCAGCCACTGACCTGGTGCTACTCACTCAGTGTACATAGCTTTTCTCAGCTGCC 1920
Db 1861 GATCTGGCAGCCACTGACCTGGTGCTACTCACTCAGTGTACATAGCTTTTCTCAGCTGCC 1920
Qy 1921 TGAGTGTGTGTCTGTGTGTAGTGTGTGTCTGCGTGCAGTGCGTGTGTTTGTGTCTCTGTA 1980
Db 1921 TGAGTGTGTGTCTGTGTGTAGTGTGTGTCTGCGTGCAGTGCGTGTGTTTGTGTCTCTGTA 1980
Qy 1981 TGTGCGTCTGTGTGATGTGGAGTGTGTGTACTCGTGAGAGAGGCCGAGTGTGCCCGGAGC 2040
Db 1981 TGTGCGTCTGTGTGATGTGGAGTGTGTGTACTCGTGAGAGAGGCCGAGTGTGCCCGGAGC 2040
Qy 2041 CCAAGGCAGTGGTTGCGAAGATGAGGGGCGCCCTGCCTTATTGCCTGTTTTTTGGGCTTG 2100
Db 2041 CCAAGGCAGTGGTTGCGAAGATGAGGGGCGCCCTGCCTTATTGCCTGTTTTTTGGGCTTG 2100
Qy 2101 GAGAACTCAGCAAGGCGACTTGGGGAACCTACGTCGGTCCCTGAGCCGGTTTCGCAGTAG 2160
Db 2101 GAGAACTCAGCAAGGCGACTTGGGGAACCTACGTCGGTCCCTGAGCCGGTTTCGCAGTAG 2160
Qy 2161 ATAAGCCATCTTTGTATCCACTCTGCACATCCACTCATCCACTCTGTACACTAATAGAAA 2220
Db 2161 ATAAGCCATCTTTGTATCCACTCTGCACATCCACTCATCCACTCTGTACACTAATAGAAA 2220
Qy 2221 CTTTGTTGCCCTGCCTGGACCAGCTGAACTGTCCCCAGGCAGCGGGGGAGCACAGAAAAA 2280
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Qy 2281 TGGGGCCTCCCAAGGGAGCTAGCTGTTCAGTTCAGTTCAGTCGCTCAGTCGTGTCCGACT 2340
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Qy 2341 CTTTGCGACCCTGTGAATCGCAGGGACTTCTGTAAATACACTAAAATCTTCCAATTAAAG 2400
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Db 2401 CTCTGCCCTGGAGGGACTGGTTAAAAAAAAAAAAAAAAAA 2440

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RESULT 2
US-08-321-668-1
; Sequence 1, Application US/08321668
; Patent No. 5665859
;  GENERAL INFORMATION:
;    APPLICANT:  WALLACH, David
;    APPLICANT:  BRAKEBUSCH, Cord
;    APPLICANT:  VARFOLOMEEV, Eugene
;    APPLICANT:  BATKIN, Michael
;    TITLE OF INVENTION:  MOLECULES INFLUENCING THE SHEDDING OF
;    TITLE OF INVENTION:  THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE
;    NUMBER OF SEQUENCES:  42
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/321,668
;      FILING DATE:  12-OCT-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  IL 107268
;      FILING DATE:  12-OCT-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  WALLACH=13
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;      TELEX:  248633
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2175 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  256..1620
US-08-321-668-1

  Query Match             29.8%;  Score 727;  DB 1;  Length 2175;
  Best Local Similarity   69.6%;  Pred. No. 5.4e-150;
  Matches 1129;  Conservative    0;  Mismatches  400;  Indels   92;  Gaps    7;

Qy        148 TGTCCCCGCCCCAGTCTCAACCCTCCACTCCCCGACCCGAGGCCCGGGCTCCACTGGGCA 207
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Db        110 TCTCTATGCCCGAGTCTCAACCCTCAACTGTCACCCCAAGGCACTTGGGACGTCCTGGAC 169

Qy        208 TACGCGAGGACCGTGTTGCTGTCACTGTCGCGGGCCGCCACTGCCC-CAGCCCTGATGGG 266
                  ||||  ||| |  ||     |  |  ||   |  |||||||  |||||  |||||
Db        170 AGACCGAGTCCCGGGAAGCCCCAGCACTGCCGCTGCCACACTGCCCTGAGCCCAAATGGG 229

Qy        267 GGATTGAGAGGCCACAGCTGGCCGGACATGGGCCTCCCCACCGTGCCTGGCCTGCTGCTG 326
              ||| |||||||||| ||||| | || |||||||||| ||||||||||| ||||||||||
Db        230 GGAGTGAGAGGCCATAGCTGTCTGG-CATGGGCCTCTCCACCGTGCCTGACCTGCTGCTG 288

Qy        327 CCACTGGTGCTTCCAGCTCTGTTGGCAGATGTGTACCCCGCAGGGGTTCAGGGGCTGGTC 386
              || |||||||| |  |  |||||||  |   | ||||| ||||||||   || ||||||
Db        289 CCGCTGGTGCTCCTGGAGCTGTTGGTGGGAATATACCCCTCAGGGGTTATTGGACTGGTC 348

Qy        387 CCTCACCCCGGGGACCTGGAGAAGAGAGAGAGTCCCTGTCCCCAAGGAAAATATAACCAC 446
              |||||||  ||||||  |||||||||||| |||   ||||||||||||||||||| ||||

Db        349 CCTCACCTAGGGGACAGGGAGAAGAGAGATAGTGTGTGTCCCCAAGGAAAATATATCCAC 408

Qy        447 CCGCAAAATAGCACCATTTGCTGCACCAAGTGCCACAAAGGTACCTATCTGTACAATGAC 506
              || |||||||   | |||||||| |||||||||||||||| |||||  ||||||||||
Db        409 CCTCAAAATAATTCGATTTGCTGTACCAAGTGCCACAAAGGAACCTACTTGTACAATGAC 468

Qy        507 TGTCCGGGTCCAGGGCGAGACACGGACTGCAGGGTGTGTGCCCCTGGCACCTACACTGCC 566
              ||||| || || |||| || ||||||||||||| |||||     ||| ||| ||| ||
Db        469 TGTCCAGGCCCGGGGCAGGATACGGACTGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCT 528

Qy        567 TTGGAGAACCATCTCAGACGATGCCTGAGCTGCTCCAGGTGCCGGGACGAAATGTTCCAG 626
              |  || |||||·|||||||  |||||  ||||||||||  |||||  | ||||||   |||
Db        529 TCAGAAAACCACCTCAGACACTGCCTCAGCTGCTCCAAATGCCGAAAGGAAATGGGTCAG 588

Qy        627 GTGGAGATTTCGCCTTGTGTAGTGGACCGGGACACTGTGTGCGGCTGCAGGAAGAACCAG 686
              |||||||| ||  ||||  |||||||||||||||| |||||  |||||||||||||||||
Db        589 GTGGAGATCTCTTCTTGCACAGTGGACCGGGACACCGTGTGTGGCTGCAGGAAGAACCAG 648

Qy        687 TACCGGGAATACTGGGGTGAAACTGGCTTCCGGTGTCTGAACTGCAGCCTCTGTCCCAAT 746
              |||||| | || ||| ||||||     |||| |||  | || ||||||||||| | ||||
Db        649 TACCGGCATTATTGGAGTGAAAACCTTTTCCAGTGCTTCAATTGCAGCCTCTGCCTCAAT 708

Qy        747 GGCACAGTGAATATCCCCTGCCAGGAGAGACAGGACACCATCTGCCACTGCCATATGGGC 806
              || || ||| |  || |||||||||||| |||| |||||  | |||  |||||||   ||
Db        709 GGGACCGTGCACCTCTCCTGCCAGGAGAAACAGAACACCGTGTGCACCTGCCATGCAGGT 768

Qy        807 TTCTTTCTTAAAGGCGCCAAGTGCATCTCCTGTCATGATTGTAAGAA---CAAGGAGTGC 863
              |||||||| | ||    | ||||  ||||||||  | | ||||||||    | |||||||
Db        769 TTCTTTCTAAGAGAAAACGAGTGTGTCTCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGC 828

Qy        864 GAGAAGTTATGTCCAACCCGACCTTCAACTGGTAAAGACTCTCAGGACCCAGGCACTACA 923
              ||||||  || | | |||    |  | || ||| | | || ||||| |||||| |||
Db        829 ACGAAGTTGTGCCTACCCCAGATTGAGAATGTTAAGGGCACTGAGGACTCAGGCACCACA 888

Qy        924 GTACTATTACCCCTGGTGATTGTCTTCGGGCTTTGCCTGGCATCCTTCGCCTCTGTCGTC 983
              || || || |||||||| ||| |||| || ||||||||   |||| ||  ||   | |
Db        889 GTGCTGTTGCCCCTGGTCATTTTCTTTGGTCTTTGCCTTTTATCCCTCCTCTTCATTGGT 948

Qy        984 TTAGCATGTCGCTACCAGCGGTGGAAGCCCAAGCTCTACTCCATCATTTGCGGGCAGTCG 1043
              |||  | |||||||| |||||||||||||||| |||| ||| | |||
Db        949 TTAATGTATCGCTACCAACGGTGGAAGTCCAAGCTCTACTCCATTGTTTGTGGGAAATCG 1008

Qy       1044 ACTCTGGTAAAAGAGGGGGAGCCAGAA---------CTCCTGGTCCCGGCCCCAGGCTTC 1094
              || |  | |||||||||||||| |||          | || |||||||  |
Db       1009 ACACCTGAAAAAGAGGGGGAGCTTGAAGGAACTACTACTAAGCCCCTGGCCCCAAACCCA 1068

Qy       1095 AACCCCACCACCACCATCTGCTTCAGCTCCACCCCAAGTTCCAGTCCTGTCTCCATTCCC 1154
              | |  ||  ||||     |||||| | ||||||   | | |||||| ||  ||| | ||
Db       1069 AGCTTCAGTCCCACTCCAGGCTTCACCCCCACCCTGGGCTTCAGTCCCGTGCCCAGTTCC 1128

Qy       1155 CCTTACATCTCCTGTGACCGGTCCAACTTCGGAG---------CCGTCGCATCTCCCTCC 1205
              | | || |||| |  |  | | | ||| |          | | ||  |||||  |
Db       1129 ACCTTCACCTCCAGCTCCACCTATACCCCCGGTGACTGTCCCAACTTTGCGGCTCCCCGC 1188

Qy       1206 AGCGAGACGGCCCCGCCCCATCTAAAGGCTGGCCCCATCCTCCCGGGGCCTCCGGCCTCC 1265
              || ||| ||| || ||| |||  ||||| ||||||||
Db       1189 AGAGAGGTGGCACCACCCTATCAGGGGGCTGACCCCATCCT------------------- 1229

Qy       1266 ACCCACCTCTGTACCCCGGGGCCTCCGGCCTCCACCCACCTCTGTACCCCGGGGCCTCCG 1325
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Db       1230 ----------------------------------------------TGCGACAGCCCTC 1242

Qy       1326 GCCTCCACCCACCTCTGCACCCCAGTTCAGAAGTGGGAAGCCAGCGCCCCCAGCGCCCCC 1385
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Db       1243 GCCTCCGACCCCATCCCCAACCCCCTTCAGAAGTGGGAGGACAGCGCCCACA---AGCCA 1299

Qy       1386 GATCAGCTCGCGGATGCCGACCCCGCGACCCTGTACGCGGTGGTGGACGGCGTGCCCCCG 1445
              |   || |   ||  |||||||| |||||||| |||||||| |||||||||||||||||
Db       1300 CAGAGCCTAGACACTGATGACCCCGCGACGCTGTACGCCGTGGTGGAGAACGTGCCCCCG 1359

Qy       1446 TCGCGCTGGAAGGAGTTGGTGCGGCGGCTGGGACTGAGCGAGCACGAGATCGAGCGGCTG 1505
              | |||||||||||| || |||||||| || || |||||||| |||||||||| ||||||
Db       1360 TTGCGCTGGAAGGAATTCGTGCGGCGCCTAGGGCTGAGCGACCACGAGATCGATCGGCTG 1419
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Qy       1506 GAGCTGGAGAACGGGCGCCACCTGCGCGAGGCGCAGTACAGCATGCTGGCGGCCTGGCGG 1565
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Db       1420 GAGCTGCAGAACGGGCGCTGCCTGCGCGAGGCGCAATACAGCATGCTGGCGACCTGGAGG 1479

Qy       1566 CGGCGCACGCCGCGCCGCGAGGCCACGCTGGAGCTGCTGGGCCGCGTGCTCAGGGACATG 1625
             |||||||||||||| |||||||||||||||||||||||||| ||||||||| | ||||||
Db       1480 CGGCGCACGCCGCGGCGCGAGGCCACGCTGGAGCTGCTGGGACGCGTGCTCCGCGACATG 1539

Qy       1626 GACCTGCTGGGTTGCCTGGAAAACATAGAGGAGGCGCTGGGTGGCGCCGCCCGCCTCGCG 1685
             |||||||||| |||||||| |||| |||||||||||  | ||| |||||  |||| ||
Db       1540 GACCTGCTGGGCTGCCTGGAGGACATCGAGGAGGCGCTTTGCGGCCCCGCCGCCCTCCCG 1599

Qy       1686 TCCGAGCCCCGCCTTCTCTGGTGAAGCCCCGCCCCTCCGACTGCGGGCCTCCCCGCCCTG 1745
              ||| |||| | |||||| | ||| ||  |||||  | | | ||         ||| ||||
Db       1600 CCCGCGCCCAGTCTTCTCAGATGAGGCTGCGCCCTGCGGGCAGCTCTAAGGACCGTCCTG 1659

Qy       1746 C 1746
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RESULT 3
US-08-837-941-1
; Sequence 1, Application US/08837941
; Patent No. 5766917
;  GENERAL INFORMATION:
;    APPLICANT:  WALLACH, David
;    APPLICANT:  BRAKEBUSCH, Cord
;    APPLICANT:  VARFOLOMEEV, Eugene
;    APPLICANT:  BATKIN, Michael
;    TITLE OF INVENTION:  MOLECULES INFLUENCING THE SHEDDING OF
;    TITLE OF INVENTION:  THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE
;    NUMBER OF SEQUENCES:  42
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:.
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/837,941
;      FILING DATE:  28-APR-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/321,668
;      FILING DATE:  12-OCT-1994
;      APPLICATION NUMBER:  IL 107268
;      FILING DATE:  12-OCT-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  WALLACH=13
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;      TELEX:  248633
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2175 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  256..1620
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US-08-837-941-1

Query Match 29.8%; Score 727; DB 1; Length 2175;
Best Local Similarity 69.6%; Pred. No. 5.4e-150;
Matches 1129; Conservative 0; Mismatches 400; Indels 92; Gaps 7;

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Db        110 TCTCTATGCCCGAGTCTCAACCCTCAACTGTCACCCCAAGGCACTTGGGACGTCCTGGAC 169

Qy        208 TACGCGAGGACCGTGTTGCTGTCACTGTCGCGGGCCGCCACTGCCC-CAGCCCTGATGGG 266
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Db        170 AGACCGAGTCCCGGGAAGCCCCAGCACTGCCGCTGCCACACTGCCCTGAGCCCAAATGGG 229

Qy        267 GGATTGAGAGGCCACAGCTGGCCGGACATGGGCCTCCCCACCGTGCCTGGCCTGCTGCTG 326
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Db        230 GGAGTGAGAGGCCATAGCTGTCTGG-CATGGGCCTCTCCACCGTGCCTGACCTGCTGCTG 288

Qy        327 CCACTGGTGCTTCCAGCTCTGTTGGCAGATGTGTACCCCGCAGGGGTTCAGGGGCTGGTC 386
              || ||||||||  |  |  |||||||  |    | ||||||  ||||||||     || ||||||
Db        289 CCGCTGGTGCTCCTGGAGCTGTTGGTGGGAATATACCCCTCAGGGGTTATTGGACTGGTC 348

Qy        387 CCTCACCCCGGGGACCTGGAGAAGAGAGAGAGTCCCTGTCCCCAAGGAAAATATAACCAC 446
              |||||||  ||||||  ||||||||||||  |||   ||||||||||||||||||| ||||
Db        349 CCTCACCTAGGGGACAGGGAGAAGAGAGATAGTGTGTGTCCCCAAGGAAAATATATCCAC 408

Qy        447 CCGCAAAATAGCACCATTTGCTGCACCAAGTGCCACAAAGGTACCTATCTGTACAATGAC 506
              || |||||||   | ||||||||  ||||||||||||||||  |||||  ||||||||||
Db        409 CCTCAAAATAATTCGATTTGCTGTACCAAGTGCCACAAAGGAACCTACTTGTACAATGAC 468

Qy        507 TGTCCGGGTCCAGGGCGAGACACGGACTGCAGGGTGTGTGCCCCTGGCACCTACACTGCC 566
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Db        469 TGTCCAGGCCCGGGGCAGGATACGGACTGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCT 528

Qy        567 TTGGAGAACCATCTCAGACGATGCCTGAGCTGCTCCAGGTGCCGGGACGAAATGTTCCAG 626
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Db        529 TCAGAAAACCACCTCAGACACTGCCTCAGCTGCTCCAAATGCCGAAAGGAAATGGGTCAG 588

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Qy        687 TACCGGGAATACTGGGGTGAAACTGGCTTCCGGTGTCTGAACTGCAGCCTCTGTCCCAAT 746
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Db        649 TACCGGCATTATTGGAGTGAAAACCTTTTCCAGTGCTTCAATTGCAGCCTCTGCCTCAAT 708

Qy        747 GGCACAGTGAATATCCCCTGCCAGGAGAGACAGGACACCATCTGCCACTGCCATATGGGC 806
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Db        709 GGGACCGTGCACCTCTCCTGCCAGGAGAAACAGAACACCGTGTGCACCTGCCATGCAGGT 768

Qy        807 TTCTTTCTTAAAGGCGCCAAGTGCATCTCCTGTCATGATTGTAAGAA---CAAGGAGTGC 863
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Db        769 TTCTTTCTAAGAGAAAACGAGTGTGTCTCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGC 828

Qy        864 GAGAAGTTATGTCCAACCCGACCTTCAACTGGTAAAGACTCTCAGGACCCAGGCACTACA 923
              ||||||  ||  |  |  |||      |  ||  |||  |  |  ||  |||||  |||||||  |||
Db        829 ACGAAGTTGTGCCTACCCCAGATTGAGAATGTTAAGGGCACTGAGGACTCAGGCACCACA 888

Qy        924 GTACTATTACCCCTGGTGATTGTCTTCGGGCTTTGCCTGGCATCCTTCGCCTCTGTCGTC 983
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Db        889 GTGCTGTTGCCCCTGGTCATTTTCTTTGGTCTTTGCCTTTTATCCCTCCTCTTCATTGGT 948

Qy        984 TTAGCATGTCGCTACCAGCGGTGGAAGCCCAAGCTCTACTCCATCATTTGCGGGCAGTCG 1043
              |||   | |||||||||  |||||||||  ||||||||||||||||   ||||  |||  | |||
Db        949 TTAATGTATCGCTACCAACGGTGGAAGTCCAAGCTCTACTCCATTGTTTGTGGGAAATCG 1008

Qy       1044 ACTCTGGTAAAAGAGGGGGAGCCAGAA---------CTCCTGGTCCCGGCCCCAGGCTTC 1094
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Db       1009 ACACCTGAAAAAGAGGGGGAGCTTGAAGGAACTACTACTAAGCCCCTGGCCCCAAACCCA 1068

Qy       1095 AACCCCACCACCACCATCTGCTTCAGCTCCACCCCAAGTTCCAGTCCTGTCTCCATTCCC 1154
              | |  ||   ||||      ||||||  | ||||||   | |  ||||||  ||  |||  | ||
Db       1069 AGCTTCAGTCCCACTCCAGGCTTCACCCCCACCCTGGGCTTCAGTCCCGTGCCCAGTTCC 1128
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Qy       1155 CCTTACATCTCCTGTGACCGGTCCAACTTCGGAG---------CCGTCGCATCTCCCTCC 1205
Db       1129 ACCTTCACCTCCAGCTCCACCTATACCCCCGGTGACTGTCCCAACTTTGCGGCTCCCCGC 1188

Qy       1206 AGCGAGACGGCCCCGCCCCATCTAAAGGCTGGCCCCATCCTCCCGGGGCCTCCGGCCTCC 1265
Db       1189 AGAGAGGTGGCACCACCCTATCAGGGGGCTGACCCCATCCT------------------- 1229

Qy       1266 ACCCACCTCTGTACCCCGGGGCCTCCGGCCTCCACCCACCTCTGTACCCCGGGGCCTCCG 1325
Db       1230 ----------------------------------------------TGCGACAGCCCTC 1242

Qy       1326 GCCTCCACCCACCTCTGCACCCCAGTTCAGAAGTGGGAAGCCAGCGCCCCCAGCGCCCCC 1385
Db       1243 GCCTCCGACCCCATCCCCAACCCCCTTCAGAAGTGGGAGGACAGCGCCCACA---AGCCA 1299

Qy       1386 GATCAGCTCGCGGATGCCGACCCCGCGACCCTGTACGCGGTGGTGGACGGCGTGCCCCCG 1445
Db       1300 CAGAGCCTAGACACTGATGACCCCGCGACGCTGTACGCCGTGGTGGAGAACGTGCCCCCG 1359

Qy       1446 TCGCGCTGGAAGGAGTTGGTGCGGCGGCTGGGACTGAGCGAGCACGAGATCGAGCGGCTG 1505
Db       1360 TTGCGCTGGAAGGAATTCGTGCGGCGCCTAGGGCTGAGCGACCACGAGATCGATCGGCTG 1419

Qy       1506 GAGCTGGAGAACGGGCGCCACCTGCGCGAGGCGCAGTACAGCATGCTGGCGGCCTGGCGG 1565
Db       1420 GAGCTGCAGAACGGGCGCTGCCTGCGCGAGGCGCAATACAGCATGCTGGCGACCTGGAGG 1479

Qy       1566 CGGCGCACGCCGCGCCGCGAGGCCACGCTGGAGCTGCTGGGCCGCGTGCTCAGGGACATG 1625
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Qy       1626 GACCTGCTGGGTTGCCTGGAAAACATAGAGGAGGCGCTGGGTGGCGCCGCCCGCCTCGCG 1685
Db       1540 GACCTGCTGGGCTGCCTGGAGGACATCGAGGAGGCGCTTTGCGGCCCCGCCGCCCTCCCG 1599

Qy       1686 TCCGAGCCCCGCCTTCTCTGGTGAAGCCCCGCCCCTCCGACTGCGGGCCTCCCCGCCCTG 1745
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Qy       1746 C 1746
Db       1660 C 1660
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US-08-126-016-1
; Sequence 1, Application US/08126016
; Patent No. 5811261
;  GENERAL INFORMATION:
;    APPLICANT:  WALLACH, DAVID
;    APPLICANT:  NOPHAR, YARON
;    APPLICANT:  KEMPER, OLIVER
;    APPLICANT:  ENGELMANN, HARTMUT
;    APPLICANT:  BRAKEBUSCH, CORD
;    APPLICANT:  ADERKA, DAN
;    TITLE OF INVENTION:  EXPRESSION OF THE RECOMBINANT TUMOR
;    TITLE OF INVENTION:  NECROSIS FACTOR BINDING PROTEIN I (TBP-I)
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Browdy and Neimark
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/126,016
;      FILING DATE:  24-SEP-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/625668
;      FILING DATE:  13-DEC-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, ROGER L
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  WALLACH4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;      TELEX:  248633
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2175 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  256..1620
;    FEATURE:
;      NAME/KEY:  mat_peptide
;      LOCATION:  319..1620
US-08-126-016-1

  Query Match             29.8%;  Score 727;  DB 1;  Length 2175;
  Best Local Similarity   69.6%;  Pred. No. 5.4e-150;
  Matches 1129;  Conservative    0;  Mismatches  400;  Indels   92;  Gaps    7;
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Db        110 TCTCTATGCCCGAGTCTCAACCCTCAACTGTCACCCCAAGGCACTTGGGACGTCCTGGAC 169

Qy        208 TACGCGAGGACCGTGTTGCTGTCACTGTCGCGGGCCGCCACTGCCC-CAGCCCTGATGGG 266
Db        170 AGACCGAGTCCCGGGAAGCCCCAGCACTGCCGCTGCCACACTGCCCTGAGCCCAAATGGG 229

Qy        267 GGATTGAGAGGCCACAGCTGGCCGGACATGGGCCTCCCCACCGTGCCTGGCCTGCTGCTG 326
Db        230 GGAGTGAGAGGCCATAGCTGTCTGG-CATGGGCCTCTCCACCGTGCCTGACCTGCTGCTG 288

Qy        327 CCACTGGTGCTTCCAGCTCTGTTGGCAGATGTGTACCCCGCAGGGGTTCAGGGGCTGGTC 386
Db        289 CCGCTGGTGCTCCTGGAGCTGTTGGTGGGAATATACCCCTCAGGGGTTATTGGACTGGTC 348

Qy        387 CCTCACCCCGGGGACCTGGAGAAGAGAGAGAGTCCCTGTCCCCAAGGAAAATATAACCAC 446
Db        349 CCTCACCTAGGGGACAGGGAGAAGAGAGATAGTGTGTGTCCCCAAGGAAAATATATCCAC 408

Qy        447 CCGCAAAATAGCACCATTTGCTGCACCAAGTGCCACAAAGGTACCTATCTGTACAATGAC 506
Db        409 CCTCAAAATAATTCGATTTGCTGTACCAAGTGCCACAAAGGAACCTACTTGTACAATGAC 468

Qy        507 TGTCCGGGTCCAGGGCGAGACACGGACTGCAGGGTGTGTGCCCCTGGCACCTACACTGCC 566
Db        469 TGTCCAGGCCCGGGGCAGGATACGGACTGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCT 528

Qy        567 TTGGAGAACCATCTCAGACGATGCCTGAGCTGCTCCAGGTGCCGGGACGAAATGTTCCAG 626
Db        529 TCAGAAAACCACCTCAGACACTGCCTCAGCTGCTCCAAATGCCGAAAGGAAATGGGTCAG 588

Qy        627 GTGGAGATTTCGCCTTGTGTAGTGGACCGGGACACTGTGTGCGGCTGCAGGAAGAACCAG 686
Db        589 GTGGAGATCTCTTCTTGCACAGTGGACCGGGACACCGTGTGTGGCTGCAGGAAGAACCAG 648

Qy        687 TACCGGGAATACTGGGGTGAAACTGGCTTCCGGTGTCTGAACTGCAGCCTCTGTCCCAAT 746
Db        649 TACCGGCATTATTGGAGTGAAAACCTTTTCCAGTGCTTCAATTGCAGCCTCTGCCTCAAT 708
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Qy       807 TTCTTTCTTAAAGGCGCCAAGTGCATCTCCTGTCATGATTGTAAGAA---CAAGGAGTGC 863
Db       769 TTCTTTCTAAGAGAAAACGAGTGTGTCTCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGC 828

Qy       864 GAGAAGTTATGTCCAACCCGACCTTCAACTGGTAAAGACTCTCAGGACCCAGGCACTACA 923
Db       829 ACGAAGTTGTGCCTACCCCAGATTGAGAATGTTAAGGGCACTGAGGACTCAGGCACCACA 888

Qy       924 GTACTATTACCCCTGGTGATTGTCTTCGGGCTTTGCCTGGCATCCTTCGCCTCTGTCGTC 983
Db       889 GTGCTGTTGCCCCTGGTCATTTTCTTTGGTCTTTGCCTTTTATCCCTCCTCTTCATTGGT 948

Qy       984 TTAGCATGTCGCTACCAGCGGTGGAAGCCCAAGCTCTACTCCATCATTTGCGGGCAGTCG 1043
Db       949 TTAATGTATCGCTACCAACGGTGGAAGTCCAAGCTCTACTCCATTGTTTGTGGGAAATCG 1008

Qy      1044 ACTCTGGTAAAAGAGGGGGAGCCAGAA---------CTCCTGGTCCCGGCCCCAGGCTTC 1094
Db      1009 ACACCTGAAAAAGAGGGGGAGCTTGAAGGAACTACTACTAAGCCCCTGGCCCCAAACCCA 1068

Qy      1095 AACCCCACCACCACCATCTGCTTCAGCTCCACCCCAAGTTCCAGTCCTGTCTCCATTCCC 1154
Db      1069 AGCTTCAGTCCCACTCCAGGCTTCACCCCCACCCTGGGCTTCAGTCCCGTGCCCAGTTCC 1128

Qy      1155 CCTTACATCTCCTGTGACCGGTCCAACTTCGGAG---------CCGTCGCATCTCCCTCC 1205
Db      1129 ACCTTCACCTCCAGCTCCACCTATACCCCCGGTGACTGTCCCAACTTTGCGGCTCCCCGC 1188

Qy      1206 AGCGAGACGGCCCCGCCCCATCTAAAGGCTGGCCCCATCCTCCCGGGGGCCTCCGGCCTCC 1265
Db      1189 AGAGAGGTGGCACCACCCTATCAGGGGGCTGACCCCATCCT------------------- 1229

Qy      1266 ACCCACCTCTGTACCCCGGGGCCTCCGGCCTCCACCCACCTCTGTACCCCGGGGCCTCCG 1325
Db      1230 ----------------------------------------------TGCGACAGCCCTC 1242

Qy      1326 GCCTCCACCCACCTCTGCACCCCAGTTCAGAAGTGGGAAGCCAGCGCCCCCAGCGCCCCC 1385
Db      1243 GCCTCCGACCCCATCCCCAACCCCCTTCAGAAGTGGGAGGACAGCGCCCACA---AGCCA 1299

Qy      1386 GATCAGCTCGCGGATGCCGACCCCGCGACCCTGTACGCGGTGGTGGACGGCGTGCCCCCG 1445
Db      1300 CAGAGCCTAGACACTGATGACCCCGCGACGCTGTACGCCGTGGTGGAGAACGTGCCCCCG 1359

Qy      1446 TCGCGCTGGAAGGAGTTGGTGCGGCGGCTGGGACTGAGCGAGCACGAGATCGAGCGGCTG 1505
Db      1360 TTGCGCTGGAAGGAATTCGTGCGGCGCCTAGGGCTGAGCGACCACGAGATCGATCGGCTG 1419

Qy      1506 GAGCTGGAGAACGGGCGCCACCTGCGCGAGGCGCAGTACAGCATGCTGGCGGCCTGGCGG 1565
Db      1420 GAGCTGCAGAACGGGCGCTGCCTGCGCGAGGCGCAATACAGCATGCTGGCGACCTGGAGG 1479

Qy      1566 CGGCGCACGCCGCGCCGCGAGGCCACGCTGGAGCTGCTGGGCCGCGTGCTCAGGGACATG 1625
Db      1480 CGGCGCACGCCGCGGCGCGAGGCCACGCTGGAGCTGCTGGGACGCGTGCTCCGCGACATG 1539

Qy      1626 GACCTGCTGGGTTGCCTGGAAAACATAGAGGAGGCGCTGGGTGGCGCCGCCCGCCTCGCG 1685
Db      1540 GACCTGCTGGGCTGCCTGGAGGACATCGAGGAGGCGCTTTGCGGCCCCGCCGCCCTCCCG 1599

Qy      1686 TCCGAGCCCCGCCTTCTCTGGTGAAGCCCCGCCCCTCCGACTGCGGGCCTCCCCGCCCTG 1745
Db      1600 CCCGCGCCCAGTCTTCTCAGATGAGGCTGCGCCCTGCGGGCAGCTCTAAGGACCGTCCTG 1659

Qy      1746 C 1746
Db      1660 C 1660
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RESULT 5
US-08-054-970-1
; Sequence 1, Application US/08054970
; Patent No. 6395267
;  GENERAL INFORMATION:
;    APPLICANT:  WALLACH, David
;    APPLICANT:  BRAKEBUSCH, Cord
;    TITLE OF INVENTION:  TNF RECEPTOR ACTION MODULATION
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/054,970
;      FILING DATE:  03-MAY-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Townsend, Kevin G.
;      REGISTRATION NUMBER:  34,033
;      REFERENCE/DOCKET NUMBER:  WALLACH=9
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;      TELEX:  248633
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2175 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  256..1620
US-08-054-970-1

  Query Match             29.8%;  Score 727;  DB 4;  Length 2175;
  Best Local Similarity   69.6%;  Pred. No. 5.4e-150;
  Matches 1129;  Conservative    0;  Mismatches  400;  Indels   92;  Gaps    7;

Qy       148 TGTCCCCGCCCCAGTCTCAACCCTCCACTCCCCGACCCGAGGCCCGGGCTCCACTGGGCA 207
Db       110 TCTCTATGCCCGAGTCTCAACCCTCAACTGTCACCCCAAGGCACTTGGGACGTCCTGGAC 169

Qy       208 TACGCGAGGACCGTGTTGCTGTCACTGTCGCGGGCCGCCACTGCCC-CAGCCCTGATGGG 266
Db       170 AGACCGAGTCCCGGGAAGCCCCAGCACTGCCGCTGCCACACTGCCCTGAGCCCAAATGGG 229

Qy       267 GGATTGAGAGGCCACAGCTGGCCGGACATGGGCCTCCCCACCGTGCCTGGCCTGCTGCTG 326
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Qy       327 CCACTGGTGCTTCCAGCTGTGTTGGCAGATGTGTACCCCGCAGGGGTTCAGGGGCTGGTC 386
Db       289 CCGCTGGTGCTCCTGGAGCTGTTGGTGGGAATATACCCCTCAGGGGTTATTGGACTGGTC 348

Qy       387 CCTCACCCCGGGGACCTGGAGAAGAGAGAGAGTCCCTGTCCCCAAGGAAAATATAACCAC 446
Db       349 CCTCACCTAGGGGACAGGGAGAAGAGAGATAGTGTGTGTCCCCAAGGAAAATATATCCAC 408

Qy       447 CCGCAAAATAGCACCATTTGCTGCACCAAGTGCCACAAAGGTACCTATCTGTACAATGAC 506
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Qy       507 TGTCCGGGTCCAGGGCGAGACACGGACTGCAGGGTGTGTGCCCCTGGCACCTACACTGCC 566
Db       469 TGTCCAGGCCCGGGGCAGGATACGGACTGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCT 528

Qy       567 TTGGAGAACCATCTCAGACGATGCCTGAGCTGCTCCAGGTGCCGGGACGAAATGTTCCAG 626
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Qy       747 GGCACAGTGAATATCCCCTGCCAGGAGAGACAGGACACCATCTGCCACTGCCATATGGGC 806
Db       709 GGGACCGTGCACCTCTCCTGCCAGGAGAAACAGAACACCGTGTGCACCTGCCATGCAGGT 768

Qy       807 TTCTTTCTTAAAGGCGCCAAGTGCATCTCCTGTCATGATTGTAAGAA---CAAGGAGTGC 863
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Qy       864 GAGAAGTTATGTCCAACCCGACCTTCAACTGGTAAAGACTCTCAGGACCCAGGCACTACA 923
Db       829 ACGAAGTTGTGCCTACCCCAGATTGAGAATGTTAAGGGCACTGAGGACTCAGGCACCACA 888

Qy       924 GTACTATTACCCCTGGTGATTGTCTTCGGGCTTTGCCTGGCATCCTTCGCCTCTGTCGTC 983
Db       889 GTGCTGTTGCCCCTGGTCATTTTCTTTGGTCTTTGCCTTTTATCCCTCCTCTTCATTGGT 948

Qy       984 TTAGCATGTCGCTACCAGCGGTGGAAGCCCAAGCTCTACTCCATCATTTGCGGGCAGTCG 1043
Db       949 TTAATGTATCGCTACCAACGGTGGAAGTCCAAGCTCTACTCCATTGTTTGTGGGAAATCG 1008

Qy      1044 ACTCTGGTAAAAGAGGGGGAGCCAGAA---------CTCCTGGTCCCGGCCCCAGGCTTC 1094
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Db      1069 AGCTTCAGTCCCACTCCAGGCTTCACCCCCACCCTGGGCTTCAGTCCCGTGCCCAGTTCC 1128

Qy      1155 CCTTACATCTCCTGTGACCGGTCCAACTTCGGAG---------CCGTCGCATCTCCCTCC 1205
Db      1129 ACCTTCACCTCCAGCTCCACCTATACCCCCGGTGACTGTCCCAACTTTGCGGCTCCCCGC 1188

Qy      1206 AGCGAGACGGCCCCGCCCCATCTAAAGGCTGGCCCCATCCTCCCGGGGCCTCCGGCCTCC 1265
Db      1189 AGAGAGGTGGCACCACCCTATCAGGGGGCTGACCCCATCCT------------------- 1229

Qy      1266 ACCCACCTCTGTACCCCGGGGCCTCCGGCCTCCACCCACCTCTGTACCCCGGGGCCTCCG 1325
Db      1230 ----------------------------------------------TGCGACAGCCCTC 1242

Qy      1326 GCCTCCACCCACCTCTGCACCCCAGTTCAGAAGTGGGAAGCCAGCGCCCCCAGCGCCCCC 1385
Db      1243 GCCTCCGACCCCATCCCCAACCCCCTTCAGAAGTGGGAGGACAGCGCCCACA---AGCCA 1299

Qy      1386 GATCAGCTCGCGGATGCCGACCCCGCGACCCTGTACGCGGTGGTGGACGGCGTGCCCCCG 1445
Db      1300 CAGAGCCTAGACACTGATGACCCCGCGACGCTGTACGCCGTGGTGGAGAACGTGCCCCCG 1359

Qy      1446 TCGCGCTGGAAGGAGTTGGTGCGGCGGCTGGGACTGAGCGAGCACGAGATCGAGCGGCTG 1505
Db      1360 TTGCGCTGGAAGGAATTCGTGCGGCGCCTAGGGCTGAGCGACCACGAGATCGATCGGCTG 1419

Qy      1506 GAGCTGGAGAACGGGCGCCACCTGCGCGAGGCGCAGTACAGCATGCTGGCGGCCTGGCGG 1565
Db      1420 GAGCTGCAGAACGGGCGCTGCCTGCGCGAGGCGCAATACAGCATGCTGGCGACCTGGAGG 1479

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Db      1480 CGGCGCACGCCGCGGCGCGAGGCCACGCTGGAGCTGCTGGGACGCGTGCTCCGCGACATG 1539

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Db      1540 GACCTGCTGGGCTGCCTGGAGGACATCGAGGAGGCGCTTTGCGGCCCCGCCGCCCTCCCG 1599

Qy      1686 TCCGAGCCCCGCCTTCTCTGGTGAAGCCCCGCCCCTCCGACTGCGGGCCTCCCCGCCCTG 1745
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Qy      1746 C 1746
Db      1660 C 1660
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RESULT 6
US-09-106-038A-1
; Sequence 1, Application US/09106038A
; Patent No. 6007995
; GENERAL INFORMATION:
; APPLICANT: Brenda F. Baker and Lex M. Cowsert
; TITLE OF INVENTION: ANTISENSE MODULATION OF TNFR1
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Isis Pharmaceuticals, Inc.
; STREET: 2292 Faraday Avenue
; CITY: Carlsbad
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92008
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows NT
; SOFTWARE: Microsoft Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/106,038A
; FILING DATE: June 26, 1998
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Laurel Spear Bernstein
; REGISTRATION NUMBER: 37,280
; REFERENCE/DOCKET NUMBER: RTS-0004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (760) 931-9200
; TELEFAX: (760) 603-3820
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2161
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-106-038A-1

Query Match 29.7%; Score 725.8; DB 3; Length 2161;
Best Local Similarity 70.0%; Pred. No. 9.9e-150;
Matches 1120; Conservative 0; Mismatches 387; Indels 92; Gaps 7;

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Qy       208 TACGCGAGGACCGTGTTGCTGTCACTGTCGCGGGCCGCCACTGCCC-CAGCCCTGATGGG 266
Db       170 AGACCGAGTCCCGGGAAGCCCCAGCACTGCCGCTGCCACACTGCCCTGAGCCCAAATGGG 229

Qy       267 GGATTGAGAGGCCACAGCTGGCCGGACATGGGCCTCCCCACCGTGCCTGGCCTGCTGCTG 326
Db       230 GGAGTGAGAGGCCATAGCTGTCTGG-CATGGGCCTCTCCACCGTGCCTGACCTGCTGCTG 288

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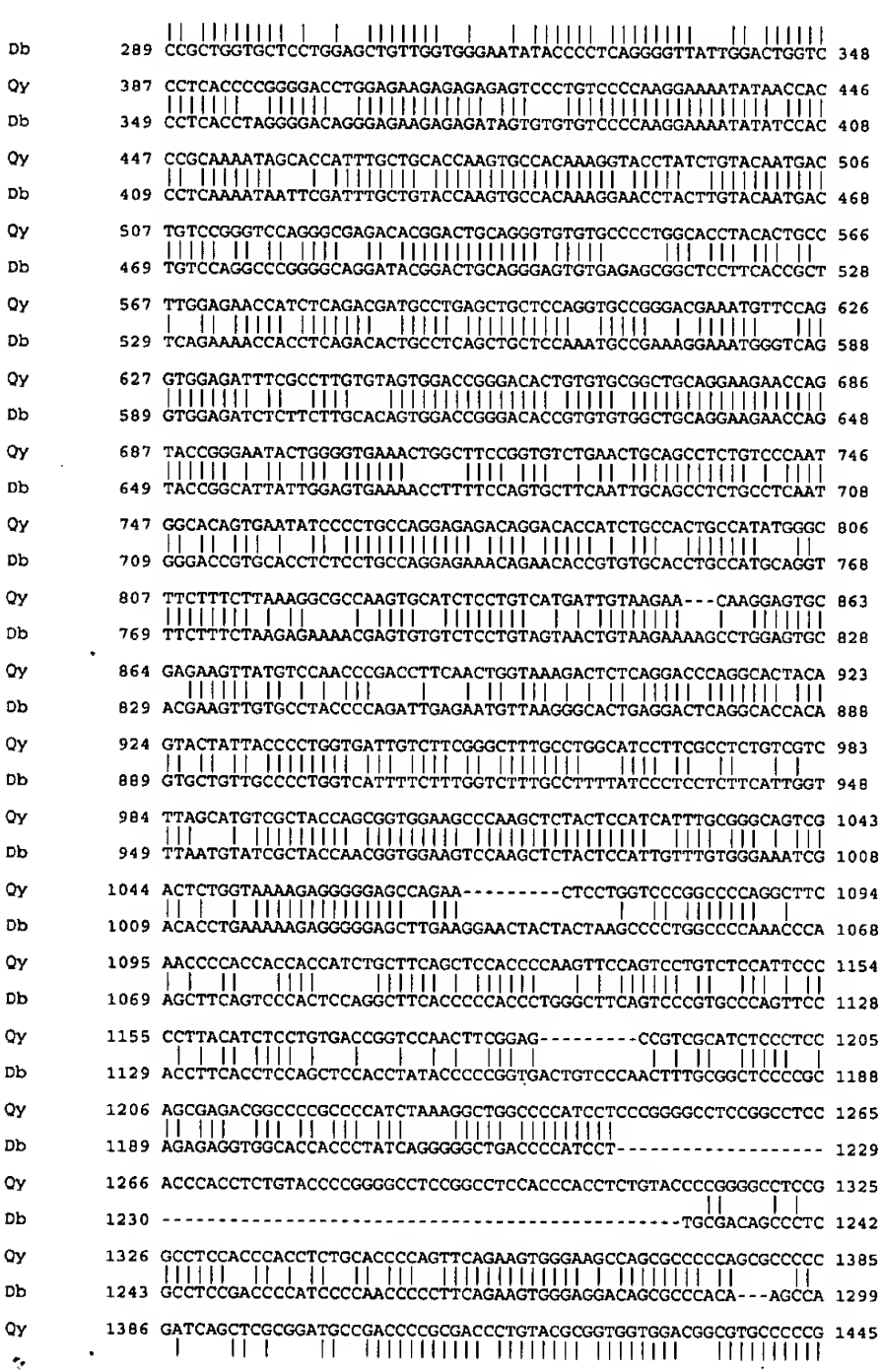

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Qy        387 CCTCACCCCGGGGACCTGGAGAAGAGAGAGAGTCCCTGTCCCCAAGGAAAATATAACCAC 446
Db        349 CCTCACCTAGGGGACAGGGAGAAGAGAGATAGTGTGTGTCCCCAAGGAAAATATATCCAC 408
Qy        447 CCGCAAAATAGCACCATTTGCTGCACCAAGTGCCACAAAGGTACCTATCTGTACAATGAC 506
Db        409 CCTCAAAATAATTCGATTTGCTGTACCAAGTGCCACAAAGGAACCTACTTGTACAATGAC 468
Qy        507 TGTCCGGGTCCAGGGCGAGACACGGACTGCAGGGTGTGTGCCCCTGGCACCTACACTGCC 566
Db        469 TGTCCAGGCCCGGGGCAGGATACGGACTGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCT 528
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Db        529 TCAGAAAACCACCTCAGACACTGCCTCAGCTGCTCCAAATGCCGAAAGGAAATGGGTCAG 588
Qy        627 GTGGAGATTTCGCCTTGTGTAGTGGACCGGGACACTGTGTGCGGCTGCAGGAAGAACCAG 686
Db        589 GTGGAGATCTCTTCTTGCACAGTGGACCGGGACACCGTGTGTGGCTGCAGGAAGAACCAG 648
Qy        687 TACCGGGAATACTGGGGTGAAACTGGCTTCCGGTGTCTGAACTGCAGCCTCTGTCCCAAT 746
Db        649 TACCGGCATTATTGGAGTGAAAACCTTTTCCAGTGCTTCAATTGCAGCCTCTGCCTCAAT 708
Qy        747 GGCACAGTGAATATCCCCTGCCAGGAGAGACAGGACACCATCTGCCACTGCCATATGGGC 806
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Qy        807 TTCTTTCTTAAAGGCGCCAAGTGCATCTCCTGTCATGATTGTAAGAA---CAAGGAGTGC 863
Db        769 TTCTTTCTAAGAGAAAACGAGTGTGTCTCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGC 828
Qy        864 GAGAAGTTATGTCCAACCCGACCTTCAACTGGTAAAGACTCTCAGGACCCAGGCACTACA 923
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Qy        924 GTACTATTACCCCTGGTGATTGTCTTCGGGCTTTGCCTGGCATCCTTCGCCTCTGTCGTC 983
Db        889 GTGCTGTTGCCCCTGGTCATTTTCTTTGGTCTTTGCCTTTTATCCCTCCTCTTCATTGGT 948
Qy        984 TTAGCATGTCGCTACCAGCGGTGGAAGCCCAAGCTCTACTCCATCATTTGCGGGCAGTCG 1043
Db        949 TTAATGTATCGCTACCAACGGTGGAAGTCCAAGCTCTACTCCATTGTTTGTGGGAAATCG 1008
Qy       1044 ACTCTGGTAAAAGAGGGGGAGCCAGAA---------CTCCTGGTCCCGGCCCCAGGCTTC 1094
Db       1009 ACACCTGAAAAAGAGGGGGAGCTTGAAGGAACTACTACTAAGCCCCTGGCCCCAAACCCA 1068
Qy       1095 AACCCCACCACCACCATCTGCTTCAGCTCCACCCCAAGTTCCAGTCCTGTCTCCATTCCC 1154
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Qy       1155 CCTTACATCTCCTGTGACCGGTCCAACTTCGGAG---------CCGTCGCATCTCCCTCC 1205
Db       1129 ACCTTCACCTCCAGCTCCACCTATACCCCCGGTGACTGTCCCAACTTTGCGGCTCCCCGC 1188
Qy       1206 AGCGAGACGGCCCCGCCCCATCTAAAGGCTGGCCCCATCCTCCCGGGGGCCTCCGGCCTCC 1265
Db       1189 AGAGAGGTGGCACCACCCTATCAGGGGGCTGACCCCATCCT------------------- 1229
Qy       1266 ACCCACCTCTGTACCCCGGGGCCTCCGGCCTCCACCCACCTCTGTACCCCGGGGCCTCCG 1325
Db       1230 ----------------------------------------------TGCGACAGCCCTC 1242
Qy       1326 GCCTCCACCCACCTCTGCACCCCAGTTCAGAAGTGGGAAGCCAGCGCCCCCAGCGCCCCC 1385
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Qy       1386 GATCAGCTCGCGGATGCCGACCCCGCGACCCTGTACGCGGTGGTGGACGGCGTGCCCCCG 1445
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Db       1300 CAGAGCCTAGACACTGATGACCCCGCGACGCTGTACGCCGTGGTGGAGAACGTGCCCCCG 1359
Qy       1446 TCGCGCTGGAAGGAGTTGGTGCGGCGGCTGGGACTGAGCGAGCACGAGATCGAGCGGCTG 1505
Db       1360 TTGCGCTGGAAGGAATTCGTGCGGCGCCTAGGGCTGAGCGACCACGAGATCGATCGGCTG 1419
Qy       1506 GAGCTGGAGAACGGGCGCCACCTGCGCGAGGCGCAGTACAGCATGCTGGCGGCCTGGCGG 1565
Db       1420 GAGCTGCAGAACGGGCGCTGCCTGCGCGAGGCGCAATACAGCATGCTGGCGACCTGGAGG 1479
Qy       1566 CGGCGCACGCCGCGCCGCGAGGCCACGCTGGAGCTGCTGGGCCGCGTGCTCAGGGACATG 1625
Db       1480 CGGCGCACGCCGCGGCGCGAGGCCACGCTGGAGCTGCTGGGACGCGTGCTCCGCGACATG 1539
Qy       1626 GACCTGCTGGGTTGCCTGGAAAACATAGAGGAGGCGCTGGGTGGCGCCGCCCGCCTCGCG 1685
Db       1540 GACCTGCTGGGCTGCCTGGAGGACATCGAGGAGGCGCTTTGCGGCCCCGCCGCCCTCCCG 1599
Qy       1686 TCCGAGCCCCGCCTTCTCTGGTGAAGCCCCGCCCCTCCG 1724
Db       1600 CCCGCGCCCAGTCTTCTCAGATGAGGCTGCGCCCCTGCG 1638
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RESULT 7
US-09-505-250-3
; Sequence 3, Application US/09505250A
; Patent No. 6329148
; GENERAL INFORMATION:
; APPLICANT: Rosen, Glenn
; APPLICANT: Kao, Peter
; TITLE OF INVENTION: Synergistic Anti-Cancer Therapy with
; TITLE OF INVENTION: Triptolides and Death Domain Ligands
; FILE REFERENCE: SUN-109PRV2
; CURRENT APPLICATION NUMBER: US/09/505,250A
; CURRENT FILING DATE: 2000-02-15
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: .FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 2161
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (256)...(1623)
US-09-505-250-3

Query Match 29.7%; Score 725.8; DB 4; Length 2161;
Best Local Similarity 70.0%; Pred. No. 9.9e-150;
Matches 1120; Conservative 0; Mismatches 387; Indels 92; Gaps 7;

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Qy        148 TGTCCCCGCCCCAGTCTCAACCCTCCACTCCCCGACCCGAGGCCCGGGCTCCACTGGGCA 207
Db        110 TCTCTATGCCCGAGTCTCAACCCTCAACTGTCACCCCAAGGCACTTGGGACGTCCTGGAC 169
Qy        208 TACGCGAGGACCGTGTTGCTGTCACTGTCGCGGGCCGCCACTGCCC-CAGCCCTGATGGG 266
Db        170 AGACCGAGTCCCGGGAAGCCCCAGCACTGCCGCTGCCACACTGCCCTGAGCCCAAATGGG 229
Qy        267 GGATTGAGAGGCCACAGCTGGCCGGACATGGGCCTCCCCACCGTGCCTGGCCTGCTGCTG 326
Db        230 GGAGTGAGAGGCCATAGCTGTCTGG-CATGGGCCTCTCCACCGTGCCTGACCTGCTGCTG 288
Qy        327 CCACTGGTGCTTCCAGCTCTGTTGGCAGATGTGTACCCCGCAGGGGTTCAGGGGCTGGTC 386
Db        289 CCGCTGGTGCTCCTGGAGCTGTTGGTGGGAATATACCCCTCAGGGGTTATTGGACTGGTC 348
Qy        387 CCTCACCCCGGGGACCTGGAGAAGAGAGAGAGTCCCTGTCCCCAAGGAAAATATAACCAC 446
Db        349 CCTCACCTAGGGGACAGGGAGAAGAGAGATAGTGTGTGTCCCCAAGGAAAATATATCCAC 408
Qy        447 CCGCAAAATAGCACCATTTGCTGCACCAAGTGCCACAAAGGTACCTATCTGTACAATGAC 506
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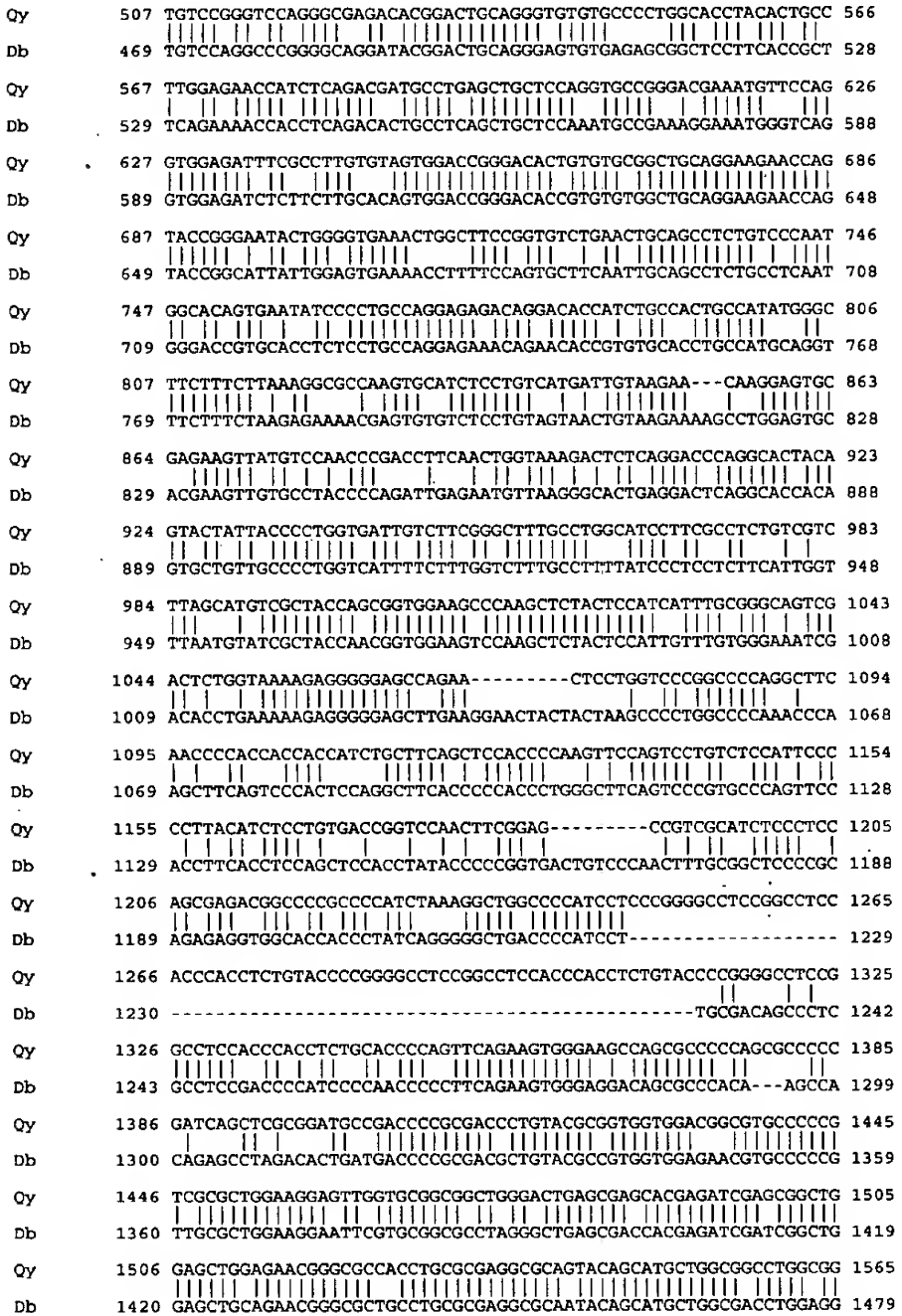
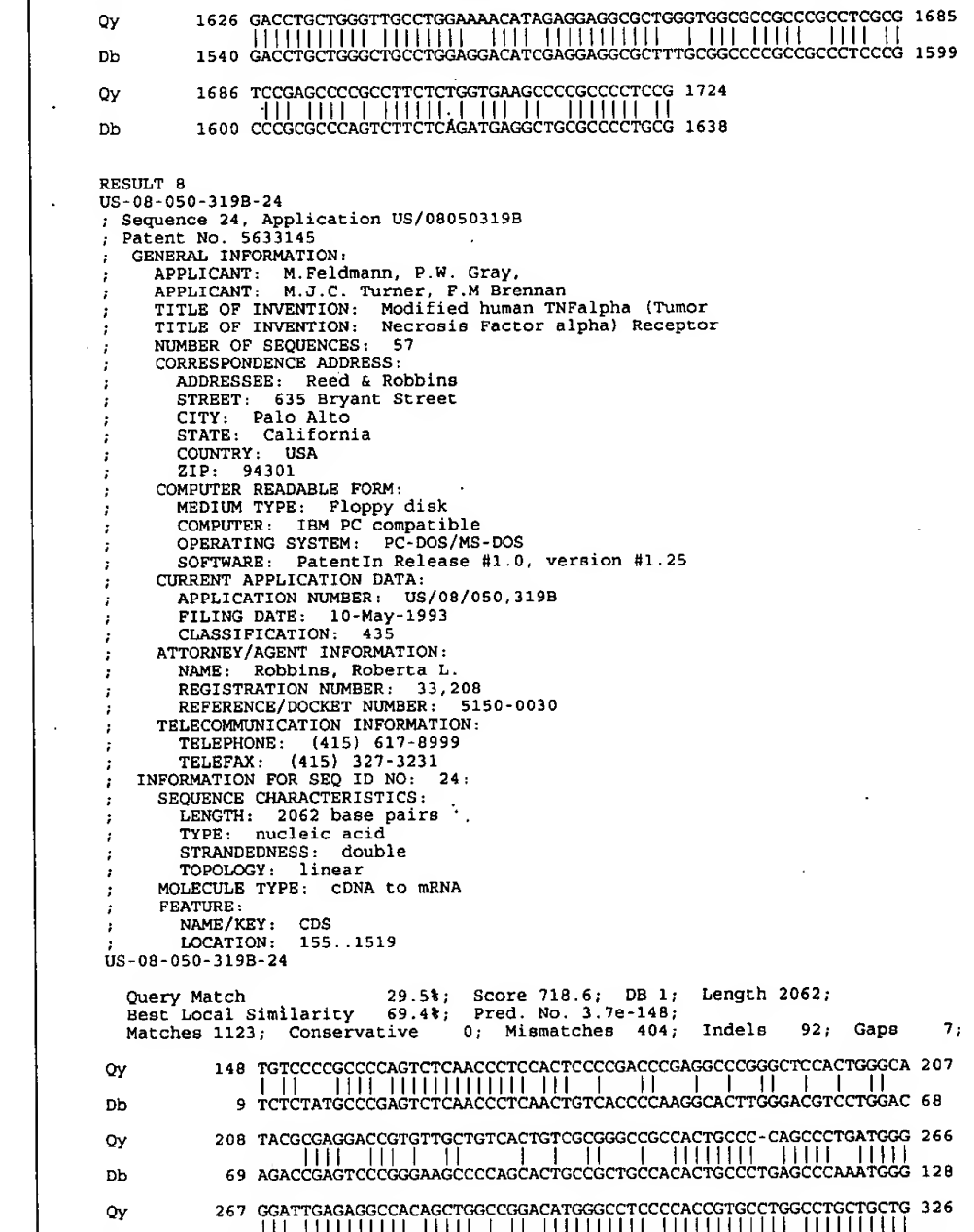
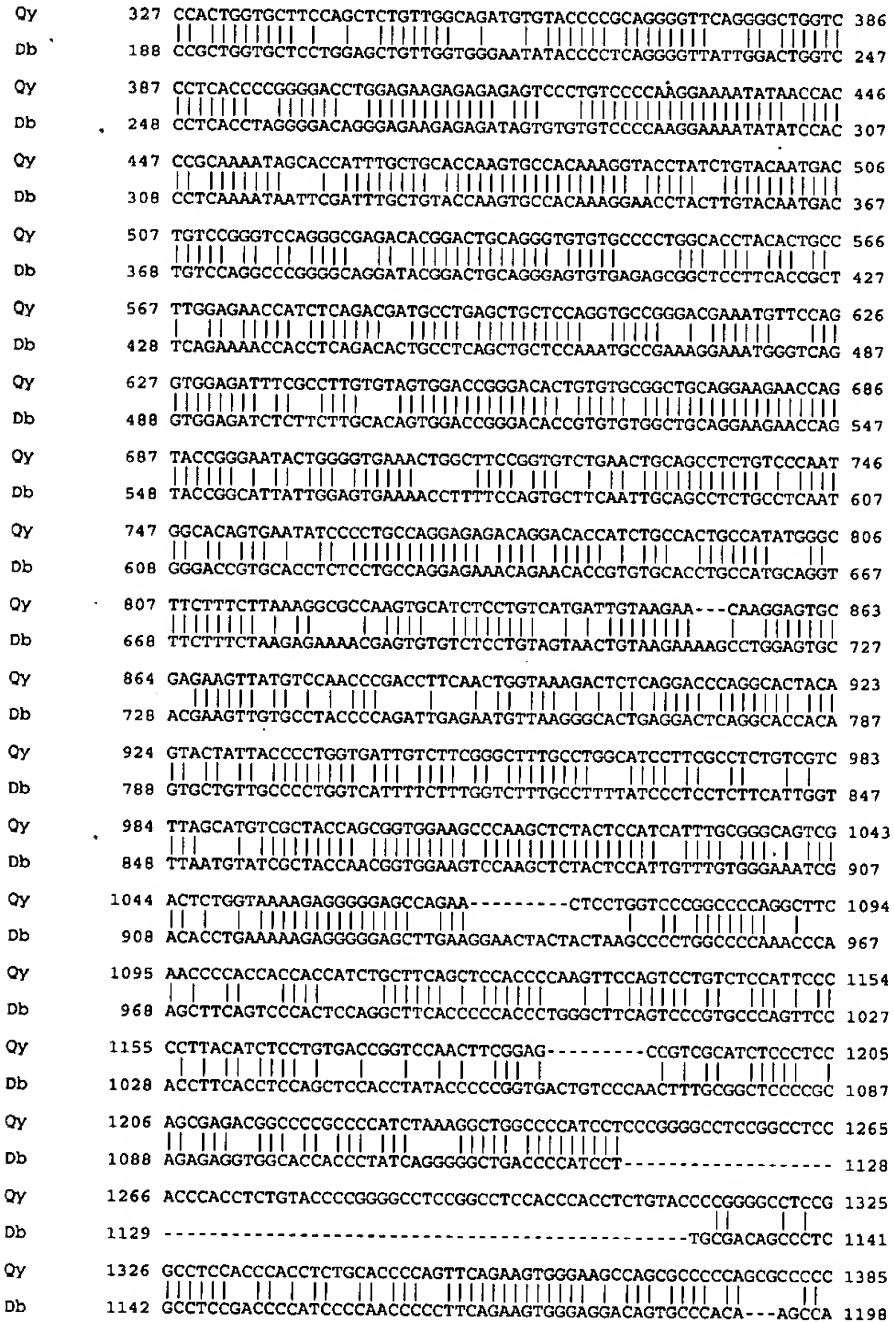
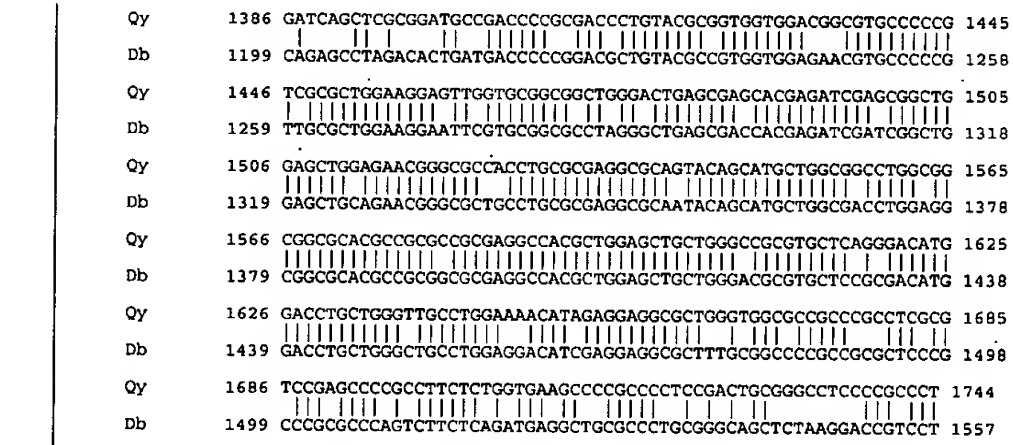




RESULT 8
US-08-050-319B-24
; Sequence 24, Application US/08050319B
; Patent No. 5633145
; GENERAL INFORMATION:
; APPLICANT: M.Feldmann, P.W. Gray,
; APPLICANT: M.J.C. Turner, F.M Brennan
; TITLE OF INVENTION: Modified human TNFalpha (Tumor
; TITLE OF INVENTION: Necrosis Factor alpha) Receptor
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reed & Robbins
; STREET: 635 Bryant Street
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/050,319B
; FILING DATE: 10-May-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Robbins, Roberta L.
; REGISTRATION NUMBER: 33,208
; REFERENCE/DOCKET NUMBER: 5150-0030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 617-8999
; TELEFAX: (415) 327-3231
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2062 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 155..1519
US-08-050-319B-24

Query Match 29.5%; Score 718.6; DB 1; Length 2062;
Best Local Similarity 69.4%; Pred. No. 3.7e-148;
Matches 1123; Conservative 0; Mismatches 404; Indels 92; Gaps 7;





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RESULT 9
US-08-465-982-24
; Sequence 24, Application US/08465982
; Patent No. 5863786
;  GENERAL INFORMATION:
;    APPLICANT:  M.Feldmann, P.W. Gray,
;    APPLICANT:  M.J.C. Turner, F.M Brennan
;    TITLE OF INVENTION:  Modified human TNFalpha (Tumor
;    TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
;    NUMBER OF SEQUENCES:  57
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Reed & Robbins
;      STREET:  635 Bryant Street
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94301
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/465,982
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/050,319
;      FILING DATE:  10-May-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Robbins, Roberta L.
;      REGISTRATION NUMBER:  33,208
;      REFERENCE/DOCKET NUMBER:  5150-0030
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 617-8999
;      TELEFAX:  (415) 327-3231
;  INFORMATION FOR SEQ ID NO:  24:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2062 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  155..1519
US-08-465-982-24
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  Query Match           29.5%;  Score 718.6;  DB 2;  Length 2062;
  Best Local Similarity  69.4%;  Pred. No. 3.7e-148;
  Matches 1123;  Conservative    0;  Mismatches  404;  Indels   92;  Gaps    7;

Qy       148 TGTCCCCGCCCCAGTCTCAACCCTCCACTCCCCGACCCGAGGCCCGGGCTCCACTGGGCA 207
Db         9 TCTCTATGCCCGAGTCTCAACCCTCAACTGTCACCCCAAGGCACTTGGGACGTCCTGGAC 68

Qy       208 TACGCGAGGACCGTGTTGCTGTCACTGTCGCGGGCCGCCACTGCCC-CAGCCCTGATGGG 266
Db        69 AGACCGAGTCCCGGGAAGCCCCAGCACTGCCGCTGCCACACTGCCCTGAGCCCAAATGGG 128

Qy       267 GGATTGAGAGGCCACAGCTGGCCGGACATGGGCCTCCCCACCGTGCCTGGCCTGCTGCTG 326
Db       129 GGAGTGAGAGGCCATAGCTGTCTGG-CATGGGCCTCTCCACCGTGCCTGACCTGCTGCTG 187

Qy       327 CCACTGGTGCTTCCAGCTCTGTTGGCAGATGTGTACCCCGCAGGGGTTCAGGGGCTGGTC 386
Db       188 CCGCTGGTGCTCCTGGAGCTGTTGGTGGGAATATACCCCTCAGGGGTTATTGGACTGGTC 247

Qy       387 CCTCACCCCGGGGACCTGGAGAAGAGAGAGAGTCCCTGTCCCCAAGGAAAATATAACCAC 446
Db       248 CCTCACCTAGGGGACAGGGAGAAGAGAGATAGTGTGTGTCCCCAAGGAAAATATATCCAC 307

Qy       447 CCGCAAAATAGCACCATTTGCTGCACCAAGTGCCACAAAGGTACCTATCTGTACAATGAC 506
Db       308 CCTCAAAATAATTCGATTTGCTGTACCAAGTGCCACAAAGGAACCTACTTGTACAATGAC 367

Qy       507 TGTCCGGGTCCAGGGCGAGACACGGACTGCAGGGTGTGTGCCCCTGGCACCTACACTGCC 566
Db       368 TGTCCAGGCCCGGGGCAGGATACGGACTGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCT 427

Qy       567 TTGGAGAACCATCTCAGACGATGCCTGAGCTGCTCCAGGTGCCGGGACGAAATGTTCCAG 626
Db       428 TCAGAAAACCACCTCAGACACTGCCTCAGCTGCTCCAAATGCCGAAAGGAAATGGGTCAG 487

Qy       627 GTGGAGATTTCGCCTTGTGTAGTGGACCGGGACACTGTGTGCGGCTGCAGGAAGAACCAG 686
Db       488 GTGGAGATCTCTTCTTGCACAGTGGACCGGGACACCGTGTGTGGCTGCAGGAAGAACCAG 547

Qy       687 TACCGGGAATACTGGGGTGAAACTGGCTTCCGGTGTCTGAACTGCAGCCTCTGTCCCAAT 746
Db       548 TACCGGCATTATTGGAGTGAAAACCTTTTCCAGTGCTTCAATTGCAGCCTCTGCCTCAAT 607

Qy       747 GGCACAGTGAATATCCCCTGCCAGGAGAGACAGGACACCATCTGCCACTGCCATATGGGC 806
Db       608 GGGACCGTGCACCTCTCCTGCCAGGAGAAACAGAACACCGTGTGCACCTGCCATGCAGGT 667

Qy       807 TTCTTTCTTAAAGGCGCCAAGTGCATCTCCTGTCATGATTGTAAGAA---CAAGGAGTGC 863
Db       668 TTCTTTCTAAGAGAAAACGAGTGTGTCTCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGC 727

Qy       864 GAGAAGTTATGTCCAACCCGACCTTCAACTGGTAAAGACTCTCAGGACCCAGGCACTACA 923
Db       728 ACGAAGTTGTGCCTACCCCAGATTGAGAATGTTAAGGGCACTGAGGACTCAGGCACCACA 787

Qy       924 GTACTATTACCCCTGGTGATTGTCTTCGGGCTTTGCCTGGCATCCTTCGCCTCTGTCGTC 983
Db       788 GTGCTGTTGCCCCTGGTCATTTTCTTTGGTCTTTGCCTTTTATCCCTCCTCTTCATTGGT 847

Qy       984 TTAGCATGTCGCTACCAGCGGTGGAAGCCCAAGCTCTACTCCATCATTTGCGGGCAGTCG 1043
Db       848 TTAATGTATCGCTACCAACGGTGGAAGTCCAAGCTCTACTCCATTGTTTGTGGGAAATCG 907

Qy      1044 ACTCTGGTAAAAGAGGGGGAGCCAGAA---------CTCCTGGTCCCGGCCCCAGGCTTC 1094
Db       908 ACACCTGAAAAAGAGGGGGAGCTTGAAGGAACTACTACTAAGCCCCTGGCCCCAAACCCA 967

Qy      1095 AACCCCACCACCACCATCTGCTTCAGCTCCACCCCAAGTTCCAGTCCTGTCTCCATTCCC 1154
Db       968 AGCTTCAGTCCCACTCCAGGCTTCACCCCCACCCTGGGCTTCAGTCCCGTGCCCAGTTCC 1027

Qy      1155 CCTTACATCTCCTGTGACCGGTCCAACTTCGGAG---------CCGTCGCATCTCCCTCC 1205

Db      1028 ACCTTCACCTCCAGCTCCACCTATACCCCCGGTGACTGTCCCAACTTTGCGGCTCCCCGC 1087

Qy      1206 AGCGAGACGGCCCCGCCCCATCTAAAGGCTGGCCCCATCCTCCCGGGGCCTCCGGCCTCC 1265
Db      1088 AGAGAGGTGGCACCACCCTATCAGGGGGCTGACCCCATCCT------------------- 1128

Qy      1266 ACCCACCTCTGTACCCCGGGGCCTCCGGCCTCCACCCACCTCTGTACCCCGGGGCCTCCG 1325
Db      1129 ----------------------------------------------TGCGACAGCCCTC 1141

Qy      1326 GCCTCCACCCACCTCTGCACCCCAGTTCAGAAGTGGGAAGCCAGCGCCCCCAGCGCCCCC 1385
Db      1142 GCCTCCGACCCCATCCCCAACCCCCTTCAGAAGTGGGAGGACAGTGCCCACA---AGCCA 1198

Qy      1386 GATCAGCTCGCGGATGCCGACCCCGCGACCCTGTACGCGGTGGTGGACGGCGTGCCCCCG 1445
Db      1199 CAGAGCCTAGACACTGATGACCCCCGGACGCTGTACGCCGTGGTGGAGAACGTGCCCCCG 1258

Qy      1446 TCGCGCTGGAAGGAGTTGGTGCGGCGGCTGGGACTGAGCGAGCACGAGATCGAGCGGCTG 1505
Db      1259 TTGCGCTGGAAGGAATTCGTGCGGCGCCTAGGGCTGAGCGACCACGAGATCGATCGGCTG 1318

Qy      1506 GAGCTGGAGAACGGGCGCCACCTGCGCGAGGCGCAGTACAGCATGCTGGCGGCCTGGCGG 1565
Db      1319 GAGCTGCAGAACGGGCGCTGCCTGCGCGAGGCGCAATACAGCATGCTGGCGACCTGGAGG 1378

Qy      1566 CGGCGCACGCCGCGCCGCCGAGGCCACGCTGGAGCTGCTGGGCCGCGTGCTCAGGGACATG 1625
Db      1379 CGGCGCACGCCGCGGCGCGAGGCCACGCTGGAGCTGCTGGGACGCGTGCTCCGCGACATG 1438

Qy      1626 GACCTGCTGGGTTGCCTGGAAAACATAGAGGAGGCGCTGGGTGGCGCCGCCCGCCTCGCG 1685
Db      1439 GACCTGCTGGGCTGCCTGGAGGACATCGAGGAGGCGCTTTGCGGCCCCGCCGCGCTCCCG 1498

Qy      1686 TCCGAGCCCCGCCTTCTCTGGTGAAGCCCCGCCCCTCCGACTGCGGGCCTCCCCGCCCT 1744
Db      1499 CCCGCGCCCAGTCTTCTCAGATGAGGCTGCGCCCTGCGGGCAGCTCTAAGGACCGTCCT 1557
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RESULT 10
US-08-406-824A-3
; Sequence 3, Application US/08406824A
; Patent No. 6541610
; GENERAL INFORMATION:
;  APPLICANT: SMITH, Craig A.
;  TITLE OF INVENTION: TUMOR NECROSIS FACTOR-ALPHA AND BETA-RECEPTORS
;  FILE REFERENCE: A-71592
;  CURRENT APPLICATION NUMBER: US/08/406,824A
;  CURRENT FILING DATE:  1995-03-20
;  PRIOR APPLICATION NUMBER: US 08/255,849
;  PRIOR FILING DATE: 1994-06-08
;  PRIOR APPLICATION NUMBER: US 07/860,710
;  PRIOR FILING DATE: 1992-03-30
;  PRIOR APPLICATION NUMBER: US  07/523,635
;  PRIOR FILING DATE: 1990-05-10
;  PRIOR APPLICATION NUMBER: US 07/421,417
;  PRIOR FILING DATE: 1989-10-13
;  PRIOR APPLICATION NUMBER: US 07/405,370
;  PRIOR FILING DATE: 1989-09-11
;  PRIOR APPLICATION NUMBER: US 07/403,241
;  PRIOR FILING DATE: 1989-09-05
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 1368
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1365)
;   OTHER INFORMATION:
;   FEATURE:
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;   NAME/KEY: mat_peptide
;   LOCATION: (121)..()
;   OTHER INFORMATION:
;   FEATURE:
;   NAME/KEY: sig_peptide
;   LOCATION: (1)..(120)
;   OTHER INFORMATION:
US-08-406-824A-3

  Query Match           28.0%;  Score 683.8;  DB 4;  Length 1368;
  Best Local Similarity  71.0%;  Pred. No. 1.3e-140;
  Matches 1020;  Conservative    0;  Mismatches  327;  Indels   90;  Gaps    5;

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            ||||||||| |||||||||||| |||||||||||| |||||||| | | |||||||
Db         1 ATGGGCCTCTCCACCGTGCCTGACCTGCTGCTGCCGCTGGTGCTCCTGGAGCTGTTGGTG 60

Qy       354 GATGTGTACCCCGCAGGGGTTCAGGGGCTGGTCCCTCACCCCGGGGACCTGGAGAAGAGA 413
             | | |||||| ||||||||   || ||||||||||||  |||||| ||||||||||
Db        61 GGAATATACCCCTCAGGGGTTATTGGACTGGTCCCTCACCTAGGGGACAGGGAGAAGAGA 120

Qy       414 GAGAGTCCCTGTCCCCAAGGAAAATATAACCACCCGCAAAATAGCACCATTTGCTGCACC 473
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Db       121 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 180

Qy       474 AAGTGCCACAAAGGTACCTATCTGTACAATGACTGTCCGGGTCCAGGGCGAGACACGGAC 533
             |||||||||||||| |||||  |||||||||||||||| || || ||||  || ||||||
Db       181 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 240

Qy       534 TGCAGGGTGTGTGCCCCTGGCACCTACACTGCCTTGGAGAACCATCTCAGACGATGCCTG 593
             |||||||  |||||      ||| ||| ||| || |  || ||||| |||||||  |||||
Db       241 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 300

Qy       594 AGCTGCTCCAGGTGCCGGGACGAAATGTTCCAGGTGGAGATTTCGCCTTGTGTAGTGGAC 653
             ||||||||||  |||||  | ||||||   ||||||||||| || ||||  |||||||||
Db       301 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 360

Qy       654 CGGGACACTGTGTGTGCGGCTGCAGGAAGAACCAGTACCGGGAATACTGGGGTGAAACTGGC 713
             |||||||| ||||| |||||||||||||||||||||||||| | || ||| ||||||
Db       361 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 420

Qy       714 TTCCGGTGTCTGAACTGCAGCCTCTGTCCCAATGGCACAGTGAATATCCCCTGCCAGGAG 773
             |||| |||  | || |||||||||||| | |||||| || ||| |  || ||||||||||
Db       421 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 480

Qy       774 AGACAGGACACCATCTGCCACTGCCATATGGGCTTCTTTCTTAAAGGCGCCAAGTGCATC 833
             | |||| |||||  | |||  |||||||   || |||||||| | ||    | ||||  ||
Db       481 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 540

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Db       541 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 600

Qy       891 ACTGGTAAAGACTCTCAGGACCCAGGCACTACAGTACTATTACCCCTGGTGATTGTCTTC 950
             | || ||| | | || ||||| ||||||| ||||| || || |||||||| ||| ||||
Db       601 AATGTTAAGGGCACTGAGGACTCAGGCACCACAGTGCTGTTGCCCCTGGTCATTTTCTTT 660

Qy       951 GGGCTTTGCCTGGCATCCTTCGCCTCTGTCGTCTTAGCATGTCGCTACCAGCGGTGGAAG 1010
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Db       661 GGTCTTTGCCTTTTATCCCTCCTCTTCATTGGTTTAAGTTATCGCTACCAACGGTGGAAG 720

Qy      1011 CCCAAGCTCTACTCCATCATTTGCGGGCAGTCGACTCTGGTAAAAGAGGGGGAGCCAGAA 1070
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Db       721 TCCAAGCTCTACTCCATTGTTTGTGGGAAATCGACACCTGAAAAAGAGGGGGAGCTTGAA 780

Qy      1071 ---------CTCCTGGTCCCGGCCCCAGGCTTCAACCCCACCACCACCATCTGCTTCAGC 1121
                     | || |||||||  |   | | ||  ||||    |||||| |
Db       781 GGAACTACTACTAAGCCCCTGGCCCCAAACCCAAGCTTCAGTCCCACTCCAGGCTTCACC 840

Qy      1122 TCCACCCCAAGTTCCAGTCCTGTCTCCATTCCCCCTTACATCTCCTGTGACCGGTCCAAC 1181
             ||||||   | | |||||| ||  ||| | || | | || |||| |   |  | | |
Db       841 CCCACCCTGGGCTTCAGTCCCGTGCCCAGTTCCACCTTCACCTCCAGCTCCACCTATACC 900

Qy      1182 TTCGGAG---------CCGTCGCATCTCCCTCCAGCGAGACGGCCCCGCCCCATCTAAAG 1232
                ||| |           | | ||  |||||  ||| |||  ||| || ||| |||    |
Db        901 CCCGGTGACTGTCCCAACTTTGCGGCTCCCCGCAGAGAGGTGGCACCACCCTATCAGGGG 960

Qy      1233 GCTGGCCCCATCCTCCCGGGGCCTCCGGCCTCCACCCACCTCTGTACCCCGGGGCCTCCG 1292
             |||| ||||||||||  ||    | |  ||||||  || | ||
Db        961 GCTGACCCCATCCTTGCGACAGCCCTCGCCTCCGACCCCATCCC---------------- 1004

Qy      1293 GCCTCCACCCACCTCTGTACCCCGGGGCCTCCGGCCTCCACCCACCTCTGCACCCCAGTT 1352
                                                                || |||  ||
Db      1005 ----------------------------------------------------CAACCCCCTT 1014

Qy      1353 CAGAAGTGGGAAGCCAGCGCCCCCAGCGCCCCCGATCAGCTCGCGGATGCCGACCCCGCG 1412
             |||||||||| | |||||||| ||      ||  |    || |    ||  |||||||||
Db      1015 CAGAAGTGGGAGGACAGCGCCCACA---AGCCACAGAGCCTAGACACTGATGACCCCGCG 1071

Qy      1413 ACCCTGTACGCGGTGGTGGACGGCGTGCCCCCGTCGCGCTGGAAGGAGTTGGTGCGGCGG 1472
             || |||||||| ||||||||  |||||||||| |||||||||| || |||||||||
Db      1072 ACGCTGTACGCCGTGGTGGAGAACGTGCCCCCGTTGCGCTGGAAGGAATTCGTGCGGCGC 1131

Qy      1473 CTGGGACTGAGCGAGCACGAGATCGAGCGGCTGGAGCTGGAGAACGGGCGCCACCTGCGC 1532
             || || |||||||| |||||||||| |||||||||||| ||||||||||  |||||||
Db      1132 CTAGGGCTGAGCGACCACGAGATCGATCGGCTGGAGCTGCAGAACGGGCGCTGCCTGCGC 1191

Qy      1533 GAGGCGCAGTACAGCATGCTGGCGGCCTGGCGGCGGCGCACGCCGCGCCGCGAGGCCACG 1592
             |||||||| |||||||||||||||| ||||| ||||||||||||| ||||||||||
Db      1192 GAGGCGCAATACAGCATGCTGGCGACCTGGAGGCGGCGCACGCCGCGGCGCGAGGCCACG 1251

Qy      1593 CTGGAGCTGCTGGGCCGCGTGCTCAGGGACATGGACCTGCTGGGTTGCCTGGAAAACATA 1652
             |||||||||||||| |||||||| | |||||||||||||||| |||||||  ||||
Db      1252 CTGGAGCTGCTGGGACGCGTGCTCCGCGACATGGACCTGCTGGGCTGCCTGGAGGACATC 1311

Qy      1653 GAGGAGGCGCTGGGTGGCGCCGCCCGCCTCGCGTCCGAGCCCCGCCTTCTCTGGTGA 1709
             |||||||||||  | ||| |||||  |||| || ||| |||| | |||||| | |||
Db      1312 GAGGAGGCGCTTTGCGGCCCCGCCGCCCTCCCGCCCGCGCCCAGTCTTCTCAGATGA 1368

RESULT 11
US-08-762-308-10
; Sequence 10, Application US/08762308
; Patent No. 5925548
;  GENERAL INFORMATION:
;    APPLICANT:  Beutler, Bruce A.
;    APPLICANT:  Bazzoni, Flavia M.
;    TITLE OF INVENTION:  MODIFIED RECEPTORS THAT CONTINUOUSLY
;    TITLE OF INVENTION:  SIGNAL
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold, White & Durkee
;      STREET:  P.O. Box 4433
;      CITY:  Houston
;      STATE:  TX
;      COUNTRY:  USA
;      ZIP:  77210-4433
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/762,308
;      FILING DATE:  09-DEC-1996
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/224,593
;      PILING DATE:  05-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kitchell, Barbara S.
;      REGISTRATION NUMBER:  33,928
;      REFERENCE/DOCKET NUMBER:  UTSD:335--1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  418-3000
;      TELEFAX:  474-7577
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;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1956 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-762-308-10

  Query Match             22.7%;  Score 554;  DB 2;  Length 1956;
  Best Local Similarity   64.3%;  Pred. No. 3.5e-112;
  Matches  962;  Conservative    0;  Mismatches  465;  Indels   69;  Gaps    6;

Qy        233 TGTCGCGGGCCGCCACTGCCCCAGCCCTGATGGGGGATTGAGAGGCCACAGCTGGCCGGA 292
Db         35 TGTCAATTGCTGCCCTGTCCCCAGCCCCAATGGGGGAGTGAGAGGCCACTGCCGGCCGGA 94

Qy        293 CATGGGCCTCCCCACCGTGCCTGGCCTGCTGCTGCCACTGGTGCTTCCAGCTCTGTTGGC 352
Db         95 CATGGGTCTCCCCACCGTGCCTGGCCTGCTGCTGTCACTGGTGCTCCTGGCTCTGCTGAT 154

Qy        353 AGATGTGTACCCCGCAGGGGTTCAGGGGCTGGTCCCTCACCCCGGGGACCTGGAGAAGAG 412
Db        155 GGGGATACATCCATCAGGGGTCACTGGACTAGTCCCTTCTCTTGGTGACCGGGAGAAGAG 214

Qy        413 AGAGAGTCCCTGTCCCCAAGGAAAATATAACCACCCGCAAAATAGCACCATTTGCTGCAC 472
Db        215 GGATAGCTTGTGTCCCCAAGGAAAGTATGTCCATTCTAAGAACAATTCCATCTGCTGCAC 274

Qy        473 CAAGTGCCACAAAGGTACCTATCTGTACAATGACTGTCCGGGTCCAGGGCGAGACACGGA 532
Db        275 CAAGTGCCACAAAGGAACCTACTTGGTGAGTGACTGTCCGAGCCCAGGGCGGGATACAGT 334

Qy        533 CTGCAGGGTGTGTGCCCCTGGCACCTACACTGCCTTGGAGAACCATCTCAGACGATGCCT 592
Db        335 CTGCAGGGAGTGTGAAAAGGGCACCTTTACGGCTTCCCAGAATTACCTCAGGCAGTGTCT 394

Qy        593 GAGCTGCTCCAGGTGCCGGGACGAAATGTTCCAGGTGGAGATTTCGCCTTGTGTAGTGGA 652
Db        395 CAGTTGCAAGACATGTCGGAAAGAAATGTCCCAGGTGGAGATCTCTCCTTGCCAAGCTGA 454

Qy        653 CCGGGACACTGTGTGCGGCTGCAGGAAGAACCAGTACCGGGAATACTGGGGTGAAACTGG 712
Db        455 CAAGGACACGGTGTGTGGCTGTAAGGAGAACCAGTTCCAACGCTACCTGAGTGAGACACA 514

Qy        713 CTTCCGGTGTCTGAACTGCAGCCTCTGTCCCAATGGCACAGTGAATATCCCCTGCCAGGA 772
Db        515 CTTCCAGTGCGTGGACTGCAGCCCCTGCTTCAACGGCACCGTGACAATCCCCTGTAAGGA 574

Qy        773 GAGACAGGACACCATCTGCCACTGCCATATGGGCTTCTTTCTTAAAGGCGCCAAGTGCAT 832
Db        575 GACTCAGAACACCGTGTGTAACTGCCATGCAGGGTTCTTTCTGAGAGAAAGTGAGTGCGT 634

Qy        833 CTCCTGTCATGATTGTAAGAACA---AGGAGTGCGAGAAGTTATGTCCAACCCGACC--- 886
Db        635 CCCTTGCAGCCACTGCAAGAAAAATGAGGAGTGTATGAAGTTGTGCCTACCTCCTCCGCT 694

Qy        887 TTCAACTGGTAAAGACTCTCAGGACCCAGGCACTACAGTACTATTACCCCTGGTGATTGT 946
Db        695 TGCAAATGTCACAAACCCCCAGGACTCAGGTACTGCGGTGCTGTTGCCCCTGGTTATCTT 754

Qy        947 CTTCGGGCTTTGCCTGGCATCCTTCGCCTCTGTCGTCTTAGCATGTCGCTACCAGCGGTG 1006
Db        755 GCTAGGTCTTTGCCTTCTATCCTTTATCTTCATCAGTTTAATGTGCCGATATCCCCGGTG 814

Qy       1007 GAAGCCCAAGCTCTACTCCATCATTTGCGGGCAGTCGACTCTGGTAAAAGAGGGGGAGCC 1066
Db        815 GAGGCCCGAAGTCTACTCCATCATTTGTAGGGATCCCGTGCCTGTCAAAGAGGAGAAGGC 874

Qy       1067 ---AGAACTCCTGGTCCCGGCCCCAGGCTTCAACCCCACCACCACCATCTGCTTCAGCTC 1123
Db        875 TGGAAAGCCCCTAACTCCAGCCCCCTCCCCAGCCTTCAGCCCCACCTCCGGCTTCAACCC 934

Qy       1124 CACCCCAAGTTCCAGTCCTGTCTCCATTCCCCCTTACATCTCCTGTGACCGGTCCAACTT 1183

Db        935 CACTCTGGGCTTCAGCACCCCAGGCTTTAGTTCTCCTGTCTCCAGTACCCCCATCAGCCC 994

Qy       1184 CGGAGCCGTCGCATCTCCCTCCAGCGAGACGGCCCCGCCCCATCTAAAGGCTGGCCCCAT 1243
Db        995 CATCTTCGGTCCTAGTAACTGGCACTTCATGCCACCTGTCAGTGAGGTAGTCCCAACCCA 1054

Qy       1244 CCTCCCGGGGCCTCCGGCCTCCACCCACCTCTGTACCCCGGGGCCTCCGGCCTCCACCCA 1303
Db        1055 GGGAGCTGACCCTCTGCTCTACGAATCACTCTGCTCCGTGCCAGCCCC------------ 1102

Qy       1304 CCTCTGTACCCCGGGGCCTCCGGCCTCCACCCACCTCTGCACCCCAGTTCAGAAGTGGGA 1363
Db        1103 ------------------------------------CACCTCTGTTCAGAAATGGGA 1123

Qy       1364 AGCCAGCGCCCCCAGCGCCCCCGATCAGCTCGCGGATGCCGACCCCGCGACCCTGTACGC 1423
Db        1124 AGACTCCGCCC------ACCCGCAACGTCCTGACAATGCAGACCTTGCGATTCTGTATGC 1177

Qy       1424 GGTGGTGGACGGCGTGCCCCCGTCGCGCTGGAAGGAGTTGGTGCGGCGGCTGGGACTGAG 1483
Db        1178 TGTGGTGGATGGCGTGCCTCCAGCGCGCTGGAAGGAGTTCATGCGTTTCATGGGGCTGAG 1237

Qy       1484 CGAGCACGAGATCGAGCGGCTGGAGCTGGAGAACGGGCGCCACCTGCGCGAGGCGCAGTA 1543
Db        1238 CGAGCACGAGATCGAGAGGCTGGAGATGCAGAACGGGCGCTGCCTGCGCGAGGCTCAGTA 1297

Qy       1544 CAGCATGCTGGCGGCCTGGCGGCGGCGCACGCCGCGCCGCGAGGCCACGCTGGAGCTGCT 1603
Db        1298 CAGCATGCTGGAAGCCTGGCGGCGCCGCACGCCGCGCCACGAGGACACGCTGGAAGTAGT 1357

Qy       1604 GGGCCGCGTGCTCAGGGACATGGACCTGCTGGGTTGCCTGGAAAACATAGAGGAGGCGCT 1663
Db        1358 GGGCCTCGTGCTTTCCAAGATGAACCTGGCTGGGTGCCTGGAGAATATCCTCGAGGCTCT 1417

Qy       1664 GGGTGGCGCCGCCCGCCTCGCGTCCGAGCCCCGCCTTCTCTGGTGAAGCCCCGCCC 1719
Db        1418 GAGAAATCCCGC---CCCCTCGTCCACGACCCGCCTCCCGCGATAAAGCCACACCC 1470


RESULT 12
US-09-513-007-3
; Sequence 3, Application US/09513007
; Patent No. 6406907
; GENERAL INFORMATION:
;  APPLICANT: Taylor, J. Michael
;  APPLICANT:  Kehrli, Jr., Marcus
;  APPLICANT:  Lee, Eun-Kyung
;  APPLICANT:  Mwangi, Simon
;  TITLE OF INVENTION: BOVINE TUMOR NECROSIS FACTOR RECEPTOR-1
;  TITLE OF INVENTION:  AND METHODS OF USE
;  FILE REFERENCE: 08411-018001
;  CURRENT APPLICATION NUMBER: US/09/513,007
;  CURRENT FILING DATE:  2000-02-25
;  PRIOR APPLICATION NUMBER: 60/122,156
;  PRIOR FILING DATE: 1999-02-26
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;  LENGTH: 543
;  TYPE: DNA
;  ORGANISM: Bos taurus
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (1)...(543)
US-09-513-007-3

  Query Match             22.3%;  Score 543;  DB 4;  Length 543;
  Best Local Similarity   100.0%;  Pred. No. 6.5e-110;
  Matches  543;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        381 CTGGTCCCTCACCCCGGGGACCTGGAGAAGAGAGAGAGTCCCTGTCCCCAAGGAAAATAT 440
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Db          1 CTGGTCCCTCACCCCGGGGACCTGGAGAAGAGAGAGAGTCCCTGTCCCCAAGGAAAATAT 60

Qy        441 AACCACCCGCAAAATAGCACCATTTGCTGCACCAAGTGCCACAAAGGTACCTATCTGTAC 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AACCACCCGCAAAATAGCACCATTTGCTGCACCAAGTGCCACAAAGGTACCTATCTGTAC 120

Qy        501 AATGACTGTCCGGGTCCAGGGCGAGACACGGACTGCAGGGTGTGTGCCCCTGGCACCTAC 560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AATGACTGTCCGGGTCCAGGGCGAGACACGGACTGCAGGGTGTGTGCCCCTGGCACCTAC 180

Qy        561 ACTGCCTTGGAGAACCATCTCAGACGATGCCTGAGCTGCTCCAGGTGCCGGGACGAAATG 620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTGCCTTGGAGAACCATCTCAGACGATGCCTGAGCTGCTCCAGGTGCCGGGACGAAATG 240

Qy        621 TTCCAGGTGGAGATTTCGCCTTGTGTAGTGGACCGGGACACTGTGTGCGGCTGCAGGAAG 680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TTCCAGGTGGAGATTTCGCCTTGTGTAGTGGACCGGGACACTGTGTGCGGCTGCAGGAAG 300

Qy        681 AACCAGTACCGGGGAATACTGGGGTGAAACTGGCTTCCGGTGTCTGAACTGCAGCCTCTGT 740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AACCAGTACCGGGGAATACTGGGGTGAAACTGGCTTCCGGTGTCTGAACTGCAGCCTCTGT 360

Qy        741 CCCAATGGCACAGTGAATATCCCCTGCCAGGAGAGACAGGACACCATCTGCCACTGCCAT 800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CCCAATGGCACAGTGAATATCCCCTGCCAGGAGAGACAGGACACCATCTGCCACTGCCAT 420

Qy        801 ATGGGCTTCTTTCTTAAAGGCGCCAAGTGCATCTCCTGTCATGATTGTAAGAACAAGGAG 860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATGGGCTTCTTTCTTAAAGGCGCCAAGTGCATCTCCTGTCATGATTGTAAGAACAAGGAG 480

Qy        861 TGCGAGAAGTTATGTCCAACCCGACCTTCAACTGGTAAAGACTCTCAGGACCCAGGCACT 920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TGCGAGAAGTTATGTCCAACCCGACCTTCAACTGGTAAAGACTCTCAGGACCCAGGCACT 540

Qy        921 ACA 923
              |||
Db        541 ACA 543


RESULT 13
US-08-286-740-2
; Sequence 2, Application US/08286740
; Patent No. 5561053
;  GENERAL INFORMATION:
;    APPLICANT:  Crowley, Craig W.
;    TITLE OF INVENTION:  METHOD FOR SELECTING HIGH-EXPRESSING
;    TITLE OF INVENTION:  HOST CELLS
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/286,740
;      FILING DATE:  05-AUG-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lee, Wendy M.
;      REGISTRATION NUMBER:
;      REFERENCE/DOCKET NUMBER:  798
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-1994
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6889 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
US-08-286-740-2

  Query Match             16.0%;  Score 389.8;  DB 1;  Length 6889;
  Best Local Similarity   76.6%;  Pred. No. 3.9e-76;
  Matches  491;  Conservative    0;  Mismatches  147;  Indels    3;  Gaps    1;

Qy        287 GCCGGACATGGGCCTCCCCACCGTGCCTGGCCTGCTGCTGCCACTGGTGCTTCCAGCTCT 346
              | | | |||||||||| |||||||||||| |||||||||||| |||||||| | |  ||
Db       1598 GTCTGGCATGGGCCTCTCCACCGTGCCTGACCTGCTGCTGCCGCTGGTGCTCCTGGAGCT 1657

Qy        347 GTTGGCAGATGTGTACCCCGCAGGGGTTCAGGGGCTGGTCCCTCACCCCGGGGACCTGGA 406
              |||||  |   | |||||| ||||||||  || ||||||||||||  ||||||  |||
Db       1658 GTTGGTGGGAATATACCCCTCAGGGGTTATTGGACTGGTCCCTCACCTAGGGGACAGGGA 1717

Qy        407 GAAGAGAGAGAGTCCCTGTCCCCAAGGAAAATATAACCACCCGCAAAATAGCACCATTTG 466
              |||||||| |||  |||||||||||||||||||| |||||| |||||||    | |||||
Db       1718 GAAGAGAGATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTG 1777

Qy        467 CTGCACCAAGTGCCACAAAGGTACCTATCTGTACAATGACTGTCCGGGTCCAGGGCGAGA 526
              ||| |||||||||||||||| |||||  |||||||||||||||| || ||  ||||  ||
Db       1778 CTGTACCAAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGA 1837

Qy        527 CACGGACTGCAGGGTGTGTGCCCCTGGCACCTACACTGCCTTGGAGAACCATCTCAGACG 586
              |||||||||||||| |||||      ||| ||| ||| || |  || |||||  |||||||
Db       1838 TACGGACTGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACA 1897

Qy        587 ATGCCTGAGCTGCTCCAGGTGCCGGGACGAAATGTTCCAGGTGGAGATTTCGCCTTGTGT 646
              |||||  |||||||||  |||||  | ||||||   |||||||||| ||  ||||
Db       1898 CTGCCTCAGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCAC 1957

Qy        647 AGTGGACCGGGACACTGTGTGCGGCTGCAGGAAGAACCAGTACCGGGAATACTGGGGTGA 706
              |||||||||||||||| ||||| |||||||||||||||||||||||| | || ||| ||||
Db       1958 AGTGGACCGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGA 2017

Qy        707 AACTGGCTTCCGGTGTCTGAACTGCAGCCTCTGTCCCAATGGCACAGTGAATATCCCCTG 766
              ||      |||| ||| | || |||||||||||| | |||||| || ||| |  || ||||
Db       2018 AAACCTTTTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTG 2077

Qy        767 CCAGGAGAGACAGGACACCATCTGCCACTGCCATATGGGCTTCTTTCTTCTAAAGGCGCCAA 826
              |||||||| |||| ||||| | |||  |||||||   || |||||||| | ||    | |
Db       2078 CCAGGAGAAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTTAAGAGAAAACGA 2137

Qy        827 GTGCATCTCCTGTCATGATTGTAAGAA---CAAGGAGTGCGAGAAGTTATGTCCAACCCG 883
              |||  |||||||| | | ||||||||   | |||||||  |||||| || | | |||
Db       2138 GTGTGTCTCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCA 2197

Qy        884 ACCTTCAACTGGTAAAGACTCTCAGGACCCAGGCACTACAG 924
                |   | || ||| | | || ||||| |||||||| ||||
Db       2198 GATTGAGAATGTTAAGGGCACTGAGGACTCAGGCACCACAG 2238


RESULT 14
PCT-US95-09576-2
; Sequence 2, Application PC/TUS9509576
;  GENERAL INFORMATION:
;    APPLICANT:  GENENTECH, INC.
;    TITLE OF INVENTION:  METHOD FOR SELECTING HIGH-EXPRESSING
;    TITLE OF INVENTION:  HOST CELLS
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
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;       ZIP:  94080
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  patin (Genentech)
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US95/09576
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/286740
;       FILING DATE:  05-AUG-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Lee, Wendy M.
;       REGISTRATION NUMBER:  00,000
;       REFERENCE/DOCKET NUMBER:  798PCT
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415/225-1994
;       TELEFAX:  415/952-9881
;       TELEX:  910/371-7168
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  6889 bases
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
PCT-US95-09576-2

  Query Match             16.0%;  Score 389.8;  DB 5;  Length 6889;
  Best Local Similarity   76.6%;  Pred. No. 3.9e-76;
  Matches  491;  Conservative    0;  Mismatches  147;  Indels    3;  Gaps    1;

Qy        287 GCCGGACATGGGCCTCCCCACCGTGCCTGGCCTGCTGCTGCCACTGGTGCTTCCAGCTCT 346
Db       1598 GTCTGGCATGGGCCTCTCCACCGTGCCTGACCTGCTGCTGCCGCTGGTGCTCCTGGAGCT 1657

Qy        347 GTTGGCAGATGTGTACCCCGCAGGGGTTCAGGGGCTGGTCCCTCACCCCGGGGACCTGGA 406
Db       1658 GTTGGTGGGAATATACCCCTCAGGGGTTATTGGACTGGTCCCTCACCTAGGGGACAGGGA 1717

Qy        407 GAAGAGAGAGAGTCCCTGTCCCCAAGGAAAATATAACCACCCGCAAAATAGCACCATTTG 466
Db       1718 GAAGAGAGATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTG 1777

Qy        467 CTGCACCAAGTGCCACAAAGGTACCTATCTGTACAATGACTGTCCGGGTCCAGGGCGAGA 526
Db       1778 CTGTACCAAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGA 1837

Qy        527 CACGGACTGCAGGGTGTGTGCCCCTGGCACCTACACTGCCTTGGAGAACCATCTCAGACG 586
Db       1838 TACGGACTGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACA 1897

Qy        587 ATGCCTGAGCTGCTCCAGGTGCCGGGACGAAATGTTCCAGGTGGAGATTTCGCCTTGTGT 646
Db       1898 CTGCCTCAGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCAC 1957

Qy        647 AGTGGACCGGGACACTGTGTGCGGCTGCAGGAAGAACCAGTACCGGGAATACTGGGGTGA 706
Db       1958 AGTGGACCGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGA 2017

Qy        707 AACTGGCTTCCGGTGTCTGAACTGCAGCCTCTGTCCCAATGGCACAGTGAATATCCCCTG 766
Db       2018 AAACCTTTTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTG 2077

Qy        767 CCAGGAGAGACAGGACACCATCTGCCACTGCCATATGGGCTTCTTTCTTAAAGGCGCCAA 826
Db       2078 CCAGGAGAAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGA 2137

Qy        827 GTGCATCTCCTGTCATGATTGTAAGAA---CAAGGAGTGCGAGAAGTTATGTCCAACCCG 883
Db       2138 GTGTGTCTCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCA 2197

Qy        884 ACCTTCAACTGGTAAAGACTCTCAGGACCCAGGCACTACAG 924
Db       2198 GATTGAGAATGTTAAGGGCACTGAGGACTCAGGCACCACAG 2238


RESULT 15
US-08-627-151A-6
; Sequence 6, Application US/08627151A
; Patent No. 5866341
;  GENERAL INFORMATION:
;    APPLICANT:  SPINELLA, Dominic
;    APPLICANT:  BECHERER, Kathleen
;    APPLICANT:  BROWN, Steven
;    TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR
;    TITLE OF INVENTION:  SCREENING DRUG LIBRARIES
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Gen-Probe Incorporated
;      STREET:  10210 Genetic Center Drive
;      CITY:  San Diego
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92121
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/627,151A
;      FILING DATE:  03-APR-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fisher, Carlos A
;      REGISTRATION NUMBER:  36,510
;      REFERENCE/DOCKET NUMBER:  CBI016
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619-410-8926
;      TELEFAX:  619-410-8928
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6896 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-627-151A-6

  Query Match             15.9%;  Score 388.6;  DB 2;  Length 6896;
  Best Local Similarity   76.9%;  Pred. No. 7.1e-76;
  Matches  488;  Conservative    0;  Mismatches  144;  Indels    3;  Gaps    1;

Qy        293 CATGGGCCTCCCCACCGTGCCTGGCCTGCTGCTGCCACTGGTGCTTCCAGCTCTGTTGGC 352
Db        934 CATGGGCCTCTCCACCGTGCCTGACCTGCTGCTGCCGCTGGTGCTCCTGGAGCTGTTGGT 993

Qy        353 AGATGTGTACCCCGCAGGGGTTCAGGGGCTGGTCCCTCACCCCGGGGACCTGGAGAAGAG 412
Db        994 GGGAATATACCCCTCAGGGGTTATTGGACTGGTCCCTCACCTAGGGGACAGGGAGAAGAG 1053

Qy        413 AGAGAGTCCCTGTCCCCAAGGAAAATATAACCACCCGCAAAATAGCACCATTTGCTGCAC 472
Db       1054 AGATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTAC 1113

Qy        473 CAAGTGCCACAAAGGTACCTATCTGTACAATGACTGTCCGGGTCCAGGGCGAGACACGGA 532
Db       1114 CAAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGA 1173

Qy        533 CTGCAGGGTGTGTGCCCCTGGCACCTACACTGCCTTGGAGAACCATCTCAGACGATGCCT 592
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Db       1174 CTGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCT 1233

Qy        593 GAGCTGCTCCAGGTGCCGGGACGAAATGTTCCAGGTGGAGATTTCGCCTTGTGTAGTGGA 652

Db       1234 CAGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGA 1293

Qy        653 CCGGGACACTGTGTGCGGCTGCAGGAAGAACCAGTACCGGGAATACTGGGGTGAAACTGG 712

Db       1294 CCGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCT 1353

Qy        713 CTTCCGGTGTCTGAACTGCAGCCTCTGTCCCAATGGCACAGTGAATATCCCCTGCCAGGA 772

Db       1354 TTTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGA 1413

Qy        773 GAGACAGGACACCATCTGCCACTGCCATATGGGCTTCTTTCTTAAAGGCGCCAAGTGCAT 832

Db       1414 GAAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGT 1473

Qy        833 CTCCTGTCATGATTGTAAGAA---CAAGGAGTGCGAGAAGTTATGTCCAACCCGACCTTC 889

Db       1474 CTCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGA 1533

Qy        890 AACTGGTAAAGACTCTCAGGACCCAGGCACTACAG 924

Db       1534 GAATGTTAAGGGCACTGAGGACTCAGGCACCACAG 1568
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Job time : 139 secs

OM nucleic - nucleic search, using sw model

Run on: September 15, 2003, 06:52:44 ; Search time 441 Seconds
(without alignments)
13432.484 Million cell updates/sec

Title: US-09-970-532-1
Perfect score: 2440
Sequence: 1 ttttttattttttttttctt.....ttaaaaaaaaaaaaaaaaaa 2440

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1632420 seqs, 1213878141 residues

Total number of hits satisfying chosen parameters: 3264840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2440	100.0	2440	9	US-09-970-532-1	Sequence 1, Appli
2	737	30.2	2141	9	US-09-899-422-16	Sequence 16, Appl
3	737	30.2	2141	10	US-09-898-234-16	Sequence 16, Appl
4	737	30.2	2141	10	US-09-899-429A-26	Sequence 26, Appl
5	737	30.2	2141	10	US-09-792-356-16	Sequence 16, Appl
6	727	29.8	2175	13	US-10-120-397-1	Sequence 1, Appli
7	725.8	29.7	2111	10	US-09-880-107-2360	Sequence 2360, Ap
8	685.4	28.1	1368	9	US-09-899-422-1	Sequence 1, Appli
9	685.4	28.1	1368	10	US-09-898-234-1	Sequence 1, Appli
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11	685.4	28.1	1368	10	US-09-792-356-1	Sequence 1, Appli
12	683.8	28.0	1368	14	US-10-252-408-3	Sequence 3, Appli
13	682.2	28.0	1368	12	US-09-945-505-2	Sequence 2, Appli
14	628	25.7	1380	12	US-10-157-305A-18	Sequence 18, Appl
15	628	25.7	1380	12	US-10-157-391-18	Sequence 18, Appl
16	600.6	24.6	1320	12	US-10-157-305A-17	Sequence 17, Appl
17	600.6	24.6	1320	12	US-10-157-391-17	Sequence 17, Appl
18	599.2	24.6	2130	10	US-09-917-800A-1601	Sequence 1601, Ap
19	591.2	24.2	2173	9	US-09-899-422-14	Sequence 14, Appl
20	591.2	24.2	2173	10	US-09-898-234-14	Sequence 14, Appl
21	591.2	24.2	2173	10	US-09-899-429A-24	Sequence 24, Appl
22	591.2	24.2	2173	10	US-09-792-356-14	Sequence 14, Appl
23	551	22.6	1334	9	US-09-899-422-11	Sequence 11, Appl
24	551	22.6	1334	10	US-09-898-234-11	Sequence 11, Appl
25	551	22.6	1334	10	US-09-792-356-11	Sequence 11, Appl
26	547.8	22.5	1334	10	US-09-899-429A-21	Sequence 21, Appl
27	543	22.3	543	9	US-09-970-532-3	Sequence 3, Appli
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29	388.2	15.9	633	10	US-09-899-429A-7	Sequence 7, Appli
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33	314	12.9	519	10	US-09-899-429A-15	Sequence 15, Appl
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45	286.4	11.7	483	11	US-09-882-735-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
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; Sequence 1, Application US/09970532
; Patent No. US20020076765A1
; GENERAL INFORMATION:
; APPLICANT: Taylor, J. Michael
; APPLICANT: Kehrli, Jr., Marcus
; APPLICANT: Lee, Eun-Kyung
; APPLICANT: Mwangi, Simon
; TITLE OF INVENTION: BOVINE TUMOR NECROSIS FACTOR RECEPTOR-1
; TITLE OF INVENTION: AND METHODS OF USE
; FILE REFERENCE: 08411-018001
; CURRENT APPLICATION NUMBER: US/09/970,532
; CURRENT FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 09/513,007
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2440
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (294)...(1706)
US-09-970-532-1

Query Match 100.0%; Score 2440; DB 9; Length 2440;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2440; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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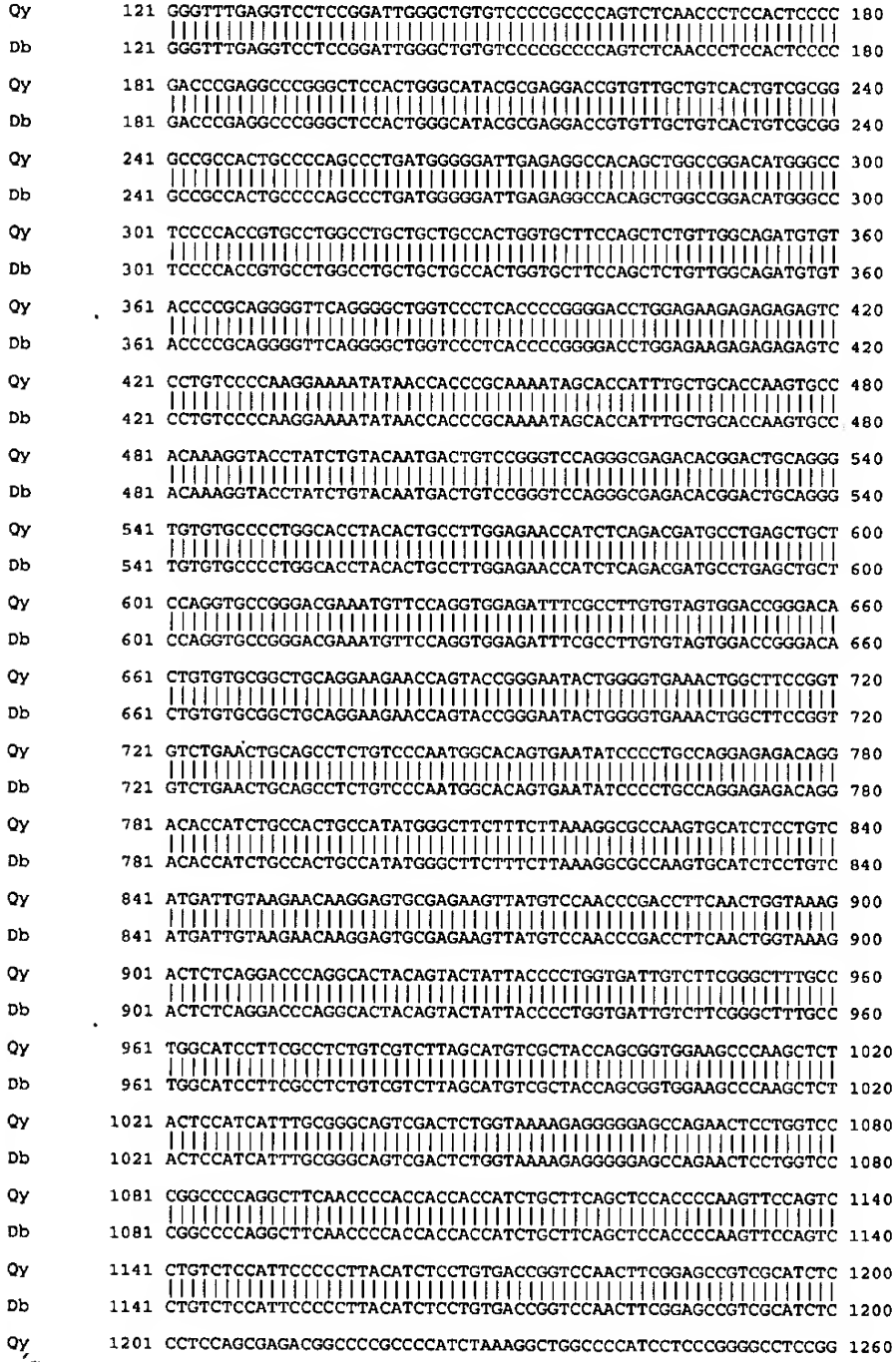
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RESULT 2
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; Sequence 16, Application US/09899422
; Patent No. US20020090676A1
; GENERAL INFORMATION:
;  APPLICANT: Hauptmann, Rudolph
;  APPLICANT:  Himmler, Adolph
;  APPLICANT:  Maurer-Fogy, Ingrid
;  APPLICANT:  Stratowa, Christian
;  TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
;  TITLE OF INVENTION:  Them
;  FILE REFERENCE: 98,385-H
;  CURRENT APPLICATION NUMBER: US/09/899,422
;  CURRENT FILING DATE:  2001-08-21
;  PRIOR APPLICATION NUMBER: 09/525,998
;  PRIOR FILING DATE: 2000-03-15
;  PRIOR APPLICATION NUMBER: 08/383,676
;  PRIOR FILING DATE: 1995-02-01
;  PRIOR APPLICATION NUMBER: 08/153,287
;  PRIOR FILING DATE: 1993-11-17
;  PRIOR APPLICATION NUMBER: 07/821,750
;  PRIOR FILING DATE: 1992-01-02
;  PRIOR APPLICATION NUMBER: 07/511,430
;  PRIOR FILING DATE: 1990-04-20
;  NUMBER OF SEQ ID NOS: 87
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
;   LENGTH: 2141
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (213)..(1580)
;   OTHER INFORMATION: Description of Artificial Sequence: human TNF-R in
;   OTHER INFORMATION: 1TNF-R2
US-09-899-422-16

  Query Match             30.2%;  Score 737;  DB 9;  Length 2141;
  Best Local Similarity   69.9%;  Pred. No. 8.2e-177;
  Matches 1152;  Conservative    1;  Mismatches  401;  Indels   95;  Gaps    8;

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Qy        337 TTCCAGCTCTGTTGGCAGATGTGTACCCCGCAGGGGTTCAGGGGCTGGTCCCTCACCCCG 396
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Qy       1216 CCCCGCCCCATCTAAAGGCTGGCCCCATCCTCCCGGGGCCTCCGGCCTCCACCCACCTCT 1275
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Db       1156 CACCACCCTATCAGGGGGCTGACCCCATCCT---------------------------- 1186

Qy       1276 GTACCCCGGGGCCTCCGGCCTCCACCCACCTCTGTACCCCGGGGCCTCCGGCCTCCACCC 1335
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Qy       1576 CGCGCCGCGAGGCCACGCTGGAGCTGCTGGGCCGCGTGCTCAGGGACATGGACCTGCTGG 1635
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Db       1447 CGCGGCGCGAGGCCACGCTGGAGCTGCTGGGACGCGTGCTCCGCGACATGGACCTGCTGG 1506

Qy       1636 GTTGCCTGGAAAACATAGAGGAGGCGCTGGGTGGCGCCGCCCGCCTCGCGTCCGAGCCCC 1695
              | ||||||||  ||||  ||||||||||||  | ||| |||||  |||| || ||| ||||
Db       1507 GCTGCCTGGAGGACATCGAGGAGGCGCTTTGCGGCCCCGCCGCCCTCCCGCCCGCGCCCA 1566

Qy       1696 GCCTTCTCTGGTGAAGCCCCGCCCCTCCG 1724
              | |||||| | ||| ||  |||||| ||
Db       1567 GTCTTCTCAGATGAGGCTGCGCCCCTGCG 1595


RESULT 3
US-09-898-234-16
; Sequence 16, Application US/09898234
; Patent No. US20020155112A1
; GENERAL INFORMATION:
;  APPLICANT: Hauptmann, Rudolph
;  APPLICANT:  Himmler, Adolph
;  APPLICANT:  Maurer-Fogy, Ingrid
;  APPLICANT:  Stratowa, Christian
;  TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
;  TITLE OF INVENTION:  Them
;  FILE REFERENCE: 98,385-I
;  CURRENT APPLICATION NUMBER: US/09/898,234
;  CURRENT FILING DATE:  2001-07-03
;  PRIOR APPLICATION NUMBER: 09/525,998
;  PRIOR FILING DATE: 2000-03-15
;  PRIOR APPLICATION NUMBER: 08/383,676
;  PRIOR FILING DATE: 1995-02-01
;  PRIOR APPLICATION NUMBER: 08/153,287
;  PRIOR FILING DATE: 1993-11-17
;  PRIOR APPLICATION NUMBER: 07/821,750
;  PRIOR FILING DATE: 1992-01-02
;  PRIOR APPLICATION NUMBER: 07/511,430
;  PRIOR FILING DATE: 1990-04-20
;  NUMBER OF SEQ ID NOS: 87
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
;   LENGTH: 2141
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (213)..(1580)
;   OTHER INFORMATION: Description of Artificial Sequence: human TNF-R in
;   OTHER INFORMATION: lTNF-R2
US-09-898-234-16

  Query Match           30.2%;  Score 737;  DB 10;  Length 2141;
  Best Local Similarity  69.9%;  Pred. No. 8.2e-177;
  Matches 1152;  Conservative    1;  Mismatches  401;  Indels   95;  Gaps    8;

Qy        101 GGCCGCAGGGCTGGCCTTCCGGGTTTGAGGTCCTCCGGATTGGGCTGTG---TCCCCGCC 157
              |||  |||  |||||||| |||||  || ||    |||  ||| |||   ||  |||
Db         17 GGCTCCAGTTCTGGCCTTTGGGGTTCAAGATCACTGGGACCAGGCCGTGATCTCTATGCC 76

Qy        158 CCAGTCTCAACCCTCCACTCCCCGACCCGAGGCCCGGGCTCCACTGGGCATACGCGAGGA 217
              | |||||||||||||| |||  |   ||   |  |  ||  |  |  ||       ||||
Db         77 CGAGTCTCAACCCTCAACTGTCACCCCAAGGCACTTGGGACGTCCTGGACAGACCGAGTC 136

Qy        218 CCGTGTTGCTGTCACTGTCGCGGGCCGCCACTGCCCC-AGCCCTGATGGGGGATTGAGAG 276
              ||| |  ||      |  |  ||   | |||||||| ||||| :|||||||| ||||||
Db        137 CCGGGAAGCCCCAGCACTGCCGCTGCCACACTGCCCTGAGCCCAKATGGGGGAGTGAGAG 196

Qy        277 GCCACAGCTGGCCGGACATGGGCCTCCCCACCGTGCCTGGCCTGCTGCTGCCACTGGTGC 336
              |||| ||||| | || |||||||||| |||||||||||| |||||||||||||||||||
Db        197 GCCATAGCTGTCTGG-CATGGGCCTCTCCACCGTGCCTGACCTGCTGCTGCCACTGGTGC 255

Qy        337 TTCCAGCTCTGTTGGCAGATGTGTACCCCGCAGGGGTTCAGGGGCTGGTCCCTCACCCCG 396
              | |  |  |||||||  |   | |||||| ||||||||   || ||||||||||||  |
Db        256 TCCTGGAGCTGTTGGTGGGAATATACCCCTCAGGGGTTATTGGACTGGTCCCTCACCTAG 315

Qy        397 GGGACCTGGAGAAGAGAGAGAGTCCCTGTCCCCAAGGAAAATATAACCACCCGCAAAATA 456
              |||||  |||||||||||| |||  |||||||||||||||||||| ||||||  |||||||
Db        316 GGGACAGGGAGAAGAGAGATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATA 375

Qy        457 GCACCATTTGCTGCACCAAGTGCCACAAAGGTACCTATCTGTACAATGACTGTCCGGGTC 516
              | |||||||| |||||||||||||||||| |||||  |||||||||||||||||  || |
Db        376 ATTCGATTTGCTGTACCAAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCC 435

Qy        517 CAGGGCGAGACACGGACTGCAGGGTGTGTGCCCCTGGCACCTACACTGCCTTGGAGAACC 576
              | ||||  || |||||||||||||| |||||      ||| ||| ||| || |  ||||
Db        436 CGGGGCAGGATACGGACTGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACC 495

Qy        577 ATCTCAGACGATGCCTGAGCTGCTCCAGGTGCCGGGACGAAATGTTCCAGGTGGAGATTT 636
              | |||||||  |||||  |||||||||  |||||  | ||||||  |||||||||||  |
Db        496 ACCTCAGACACTGCCTCAGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCT 555

Qy        637 CGCCTTGTGTAGTGGACCGGGACACTGTGTGCGGCTGCAGGAAGAACCAGTACCGGGAAT 696
              |  ||||   |||||||||||||||| ||||| |||||||||||||||||||||||| | |
Db        556 CTTCTTGCACAGTGGACCGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATT 615

Qy        697 ACTGGGGTGAAACTGGCTTCCGGTGTCTGAACTGCAGCCTCTGTCCCAATGGCACAGTGA 756
              | |||  ||||||     |||| |||  | || ||||||||||| | ||||||  || |||
Db        616 ATTGGAGTGAAAACCTTTTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGC 675

Qy        757 ATATCCCCTGCCAGGAGAGACAGGACACCATCTGCCACTGCCATATGGGCTTCTTTCTTA 816
              |  || ||||||||||||  |||| |||||  | |||  |||||||   || |||||||  |
Db        676 ACCTCTCCTGCCAGGAGAAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAA 735

Qy        817 AAGGCGCCAAGTGCATCTCCTGTCATGATTGTAAGAA---CAAGGAGTGCGAGAAGTTAT 873
              ||    | ||||  |||||||| | | ||||||||   |  |||||||  ||||||  |
Db        736 GAGAAAACGAGTGTGTCTCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGT 795

Qy        874 GTCCAACCCGACCTTCAACTGGTAAAGACTCTCAGGACCCAGGCACTACAGTACTATTAC 933
              | | | |||    |  | || ||| | | || ||||| |||||||  |||| || || |
Db        796 GCCTACCCCAGATTGAGAATGTTAAGGGCACTGAGGACTCAGGCACCACAGTGCTGTTGC 855

Qy        934 CCCTGGTGATTGTCTTCGGGCTTTGCCTGGCATCCTTCGCCTCTGTCGTCTTAGCATGTC 993
              ||||||| ||| |||| || |||||||    |||| ||  ||   | |  |||   | ||
Db        856 CCCTGGTCATTTTCTTTGGTCTTTGCCTTTTATCCCTCCTCTTCATTGGTTTAATGTATC 915

Qy        994 GCTACCAGCGGTGGAAGCCCAAGCTCTACTCCATCATTTGCGGGCAGTCGACTCTGGTAA 1053
              ||||||| |||||||| |||||||||||||||  |||| ||| | ||||| |  | ||
Db        916 GCTACCAACGGTGGAAGTCCAAGCTCTACTCCATTGTTTGTGGGAAATCGACACCTGAAA 975

Qy       1054 AAGAGGGGGAGCCAGAA---------CTCCTGGTCCCGGCCCCAGGCTTCAACCCCACCA 1104
              ||||||||||||  |||          | || |||||||  |   | |  ||
Db        976 AAGAGGGGGAGCTTGAAGGAACTACTACTAAGCCCCTGGCCCCAAACCCAAGCTTCAGTC 1035

Qy       1105 CCACCATCTGCTTCAGCTCCACCCCAAGTTCCAGTCCTGTCTCCATTCCCCCTTACATCT 1164
              ||||      |||||| | ||||||   | | |||||| ||  ||| | || | | || ||
Db       1036 CCACTCCAGGCTTCACCCCCACCCTGGGCTTCAGTCCCGTGCCCAGTTCCACCTTCACCT 1095

Qy       1165 CCTGTGACCGGTCCAACTTCGGAG---------CCGTCGCATCTCCCTCCAGCGAGACGG 1215
              || |   |  | | | ||| |           | | ||  |||||  ||| |||  ||
Db       1096 CCAGCTCCACCTATACCCCCGGTGACTGTCCCAACTTTGCGGCTCCCCGCAGAGAGGTGG 1155

Qy       1216 CCCCGCCCCATCTAAAGGCTGGCCCCATCCTCCCGGGGGCCTCCGGCCTCCACCCACCTCT 1275
              | || ||| |||   |||| ||||||||||
Db       1156 CACCACCCTATCAGGGGGCTGACCCCATCCT---------------------------- 1186

Qy       1276 GTACCCCGGGGCCTCCGGCCTCCACCCACCTCTGTACCCCGGGGCCTCCGGCCTCCACCC 1335
                                                    ||    | |  |||||  ||
Db       1187 ----------------------------------TGCGACAGCCCTCGCCTCCGACC 1209

Qy       1336 ACCTCTGCACCCCAGTTCAGAAGTGGGAAGCCAGCGCCCCCAGCGCCCCCGATCAGCTCG 1395
              | ||  || |||  |||||||||||||| |||||||||  ||     ||  |   || |
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Db       1210 CCATCCCCAACCCCCTTCAGAAGTGGGAGGACAGCGCCCACA---AGCCACAGAGCCTAG 1266

Qy       1396 CGGATGCCGACCCCGCGACCCTGTACGCGGTGGTGGACGGCGTGCCCCCGTCGCGCTGGA 1455
Db       1267 ACACTGATGACCCCGCGACGCTGTACGCCGTGGTGGAGAACGTGCCCCCGTTGCGCTGGA 1326

Qy       1456 AGGAGTTGGTGCGGCGGCTGGGACTGAGCGAGCACGAGATCGAGCGGCTGGAGCTGGAGA 1515
Db       1327 AGGAATTCGTGCGGCGCCTAGGGCTGAGCGACCACGAGATCGATCGGCTGGAGCTGCAGA 1386

Qy       1516 ACGGGCGCCACCTGCGCGAGGCGCAGTACAGCATGCTGGCGGCCTGGCGGCGGCGCACGC 1575
Db       1387 ACGGGCGCTGCCTGCGCGAGGCGCAATACAGCATGCTGGCGACCTGGAGGCGGCGCACGC 1446

Qy       1576 CGCGCCGCGAGGCCACGCTGGAGCTGCTGGGCCGCGTGCTCAGGGACATGGACCTGCTGG 1635
Db       1447 CGCGGCGCGAGGCCACGCTGGAGCTGCTGGGACGCGTGCTCCGCGACATGGACCTGCTGG 1506

Qy       1636 GTTGCCTGGAAAACATAGAGGAGGCGCTGGGTGGCGCCGCCCGCCTCGCGTCCGAGCCCC 1695
Db       1507 GCTGCCTGGAGGACATCGAGGAGGCGCTTTGCGGCCCCGCCGCCCTCCCGCCCGCGCCCA 1566

Qy       1696 GCCTTCTCTGGTGAAGCCCCGCCCCTCCG 1724
Db       1567 GTCTTCTCAGATGAGGCTGCGCCCCTGCG 1595


RESULT 4
US-09-899-429A-26
; Sequence 26, Application US/09899429A
; Patent No. US20020169118A1
; GENERAL INFORMATION:
;  APPLICANT: Hauptmann, Rudolph
;  APPLICANT:  Himmler, Adolph
;  APPLICANT:  Maurer-Fogy, Ingrid
;  APPLICANT:  Stratowa, Christian
;  TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
;  TITLE OF INVENTION:  Them
;  FILE REFERENCE: 98-385-J
;  CURRENT APPLICATION NUMBER: US/09/899,429A
;  CURRENT FILING DATE:  2001-07-03
;  PRIOR APPLICATION NUMBER: 09/792,356
;  PRIOR FILING DATE: 2000-02-23
;  PRIOR APPLICATION NUMBER: 08/477,639
;  PRIOR FILING DATE: 1955-06-07
;  PRIOR APPLICATION NUMBER: 08/383,676
;  PRIOR FILING DATE: 1995-02-01
;  PRIOR APPLICATION NUMBER: 08/153,287
;  PRIOR FILING DATE: 1993-11-17
;  PRIOR APPLICATION NUMBER: 07/821,750
;  PRIOR FILING DATE: 1992-01-02
;  PRIOR APPLICATION NUMBER: 07/511,430
;  PRIOR FILING DATE: 1990-04-20
;  NUMBER OF SEQ ID NOS: 97
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
;   LENGTH: 2141
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: human TNF-R in
;   OTHER INFORMATION: lTNF-R2
;   NAME/KEY: CDS
;   LOCATION: (213)..(1577)
US-09-899-429A-26

  Query Match           30.2%;  Score 737;  DB 10;  Length 2141;
  Best Local Similarity   69.9%;  Pred. No. 8.2e-177;
  Matches 1152;  Conservative    1;  Mismatches  401;  Indels   95;  Gaps    8;

Qy        101 GGCCGCAGGGCTGGCCTTCCGGGTTTGAGGTCCTCCGGATTGGGCTGTG---TCCCCGCC 157
Db         17 GGCTCCAGTTCTGGCCTTTGGGGTTCAAGATCACTGGGACCAGGCCGTGATCTCTATGCC 76

Qy        158 CCAGTCTCAACCCTCCACTCCCCGACCCGAGGCCCGGGCTCCACTGGGCATACGCGAGGA 217
Db         77 CGAGTCTCAACCCTCAACTGTCACCCCAAGGCACTTGGGACGTCCTGGACAGACCGAGTC 136

Qy        218 CCGTGTTGCTGTCACTGTCGCGGGCCGCCACTGCCCC-AGCCCTGATGGGGGATTGAGAG 276
Db        137 CCGGGAAGCCCCAGCACTGCCGCTGCCACACTGCCCTGAGCCCAKATGGGGGAGTGAGAG 196

Qy        277 GCCACAGCTGGCCGGACATGGGCCTCCCCACCGTGCCTGGCCTGCTGCTGCCACTGGTGC 336
Db        197 GCCATAGCTGTCTGG-CATGGGCCTCTCCACCGTGCCTGACCTGCTGCTGCCACTGGTGC 255

Qy        337 TTCCAGCTCTGTTGGCAGATGTGTACCCCGCAGGGGTTCAGGGGCTGGTCCCTCACCCCG 396
Db        256 TCCTGGAGCTGTTGGTGGGAATATACCCCTCAGGGGTTATTGGACTGGTCCCTCACCTAG 315

Qy        397 GGGACCTGGAGAAGAGAGAGAGTCCCTGTCCCCAAGGAAAATATAACCACCCGCAAAATA 456
Db        316 GGGACAGGGAGAAGAGAGATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATA 375

Qy        457 GCACCATTTGCTGCACCAAGTGCCACAAAGGTACCTATCTGTACAATGACTGTCCGGGTC 516
Db        376 ATTCGATTTGCTGTACCAAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCC 435

Qy        517 CAGGGCGAGACACGGACTGCAGGGTGTGTGCCCCTGGCACCTACACTGCCTTGGAGAACC 576
Db        436 CGGGGCAGGATACGGACTGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACC 495

Qy        577 ATCTCAGACGATGCCTGAGCTGCTCCAGGTGCCGGGACGAAATGTTCCAGGTGGAGATTT 636
Db        496 ACCTCAGACACTGCCTCAGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCT 555

Qy        637 CGCCTTGTGTAGTGGACCGGGACACTGTGTGCGGCTGCAGGAAGAACCAGTACCGGGAAT 696
Db        556 CTTCTTGCACAGTGGACCGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATT 615

Qy        697 ACTGGGGTGAAACTGGCTTCCGGTGTCTGAACTGCAGCCTCTGTCCCAATGGCACAGTGA 756
Db        616 ATTGGAGTGAAAACCTTTTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGC 675

Qy        757 ATATCCCCTGCCAGGAGAGACAGGACACCATCTGCCACTGCCATATGGGCTTCTTTCTTA 816
Db        676 ACCTCTCCTGCCAGGAGAAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAA 735

Qy        817 AAGGCGCCAAGTGCATCTCCTGTCATGATTGTAAGAA---CAAGGAGTGCGAGAAGTTAT 873
Db        736 GAGAAAACGAGTGTGTCTCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGT 795

Qy        874 GTCCAACCCGACCTTCAACTGGTAAAGACTCTCAGGACCCAGGCACTACAGTACTATTAC 933
Db        796 GCCTACCCCAGATTGAGAATGTTAAGGGCACTGAGGACTCAGGCACCACAGTGCTGTTGC 855

Qy        934 CCCTGGTGATTGTCTTCGGGCTTTGCCTGGCATCCTTCGCCTCTGTCGTCTTAGCATGTC 993
Db        856 CCCTGGTCATTTTCTTTGGTCTTTGCCTTTTATCCCTCCTCTTCATTGGTTTAATGTATC 915

Qy        994 GCTACCAGCGGTGGAAGCCCAAGCTCTACTCCATCATTTGCGGGCAGTCGACTCTGGTAA 1053
Db        916 GCTACCAACGGTGGAAGTCCAAGCTCTACTCCATTGTTTGTGGGAAATCGACACCTGAAA 975

Qy       1054 AAGAGGGGGAGCCAGAA---------CTCCTGGTCCCGGCCCCAGGCTTCAACCCCACCA 1104
Db        976 AAGAGGGGGAGCTTGAAGGAACTACTACTAAGCCCCTGGCCCCAAACCCAAGCTTCAGTC 1035

Qy       1105 CCACCATCTGCTTCAGCTCCACCCCAAGTTCCAGTCCTGTCTCCATTCCCCCTTACATCT 1164
Db       1036 CCACTCCAGGCTTCACCCCCACCCTGGGCTTCAGTCCCGTGCCCAGTTCCACCTTCACCT 1095

Qy       1165 CCTGTGACCGGTCCAACTTCGGAG---------CCGTCGCATCTCCCTCCAGCGAGACGG 1215
Db       1096 CCAGCTCCACCTATACCCCCGGTGACTGTCCCAACTTTGCGGCTCCCCGCAGAGAGGTGG 1155
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Qy       1216 CCCCGCCCCATCTAAAGGCTGGCCCCATCCTCCCGGGGCCTCCGGCCTCCACCCACCTCT 1275
Db       1156 CACCACCCTATCAGGGGGCTGACCCCATCCT---------------------------- 1186

Qy       1276 GTACCCCGGGGCCTCCGGCCTCCACCCACCTCTGTACCCCGGGGCCTCCGGCCTCCACCC 1335
Db       1187 -----------------------------------TGCGACAGCCCTCGCCTCCGACC 1209

Qy       1336 ACCTCTGCACCCCAGTTCAGAAGTGGGAAGCCAGCGCCCCCAGCGCCCCCGATCAGCTCG 1395
Db       1210 CCATCCCCAACCCCCTTCAGAAGTGGGAGGACAGCGCCCACA---AGCCACAGAGCCTAG 1266

Qy       1396 CGGATGCCGACCCCGCGACCCTGTACGCGGTGGTGGACGGCGTGCCCCCGTCGCGCTGGA 1455
Db       1267 ACACTGATGACCCCGCGACGCTGTACGCCGTGGTGGAGAACGTGCCCCCGTTGCGCTGGA 1326

Qy       1456 AGGAGTTGGTGCGGCGGCTGGGACTGAGCGAGCACGAGATCGAGCGGCTGGAGCTGGAGA 1515
Db       1327 AGGAATTCGTGCGGCGCCTAGGGCTGAGCGACCACGAGATCGATCGGCTGGAGCTGCAGA 1386

Qy       1516 ACGGGCGCCACCTGCGCGAGGCGCAGTACAGCATGCTGGCGGCCTGGCGGCGGCGCACGC 1575
Db       1387 ACGGGCGCTGCCTGCGCGAGGCGCAATACAGCATGCTGGCGACCTGGAGGCGGCGCACGC 1446

Qy       1576 CGCGCCGCGAGGCCACGCTGGAGCTGCTGGGCCGCGTGCTCAGGGACATGGACCTGCTGG 1635
Db       1447 CGCGGCGCGAGGCCACGCTGGAGCTGCTGGGACGCGTGCTCCGCGACATGGACCTGCTGG 1506

Qy       1636 GTTGCCTGGAAAACATAGAGGAGGCGCTGGGTGGCGCCGCCCGCCTCGCGTCCGAGCCCC 1695
Db       1507 GCTGCCTGGAGGACATCGAGGAGGCGCTTTGCGGCCCCGCCGCCCTCCCGCCCGCGCCCA 1566

Qy       1696 GCCTTCTCTGGTGAAGCCCCGCCCCTCCG 1724
Db       1567 GTCTTCTCAGATGAGGCTGCGCCCCTGCG 1595
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RESULT 5
US-09-792-356-16
; Sequence 16, Application US/09792356
; Publication No. US20020183485A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stratowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; TITLE OF INVENTION: Them
; FILE REFERENCE: 98,385-G
; CURRENT APPLICATION NUMBER: US/09/792,356
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 08/477,639
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 2141
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (213)..(1580)
; OTHER INFORMATION: Description of Artificial Sequence: human TNF-R in
; OTHER INFORMATION: lTNF-R2
US-09-792-356-16

Query Match 30.2%; Score 737; DB 10; Length 2141;
Best Local Similarity 69.9%; Pred. No. 8.2e-177;
Matches 1152; Conservative 1; Mismatches 401; Indels 95; Gaps 8;

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Qy        101 GGCCGCAGGGCTGGCCTTCCGGGTTTGAGGTCCTCCGGATTGGGCTGTG---TCCCCGCC 157
Db         17 GGCTCCAGTTCTGGCCTTTGGGGTTCAAGATCACTGGGACCAGGCCGTGATCTCTATGCC 76

Qy        158 CCAGTCTCAACCCTCCACTCCCCGACCCGAGGCCCGGGCTCCACTGGGCATACGCGAGGA 217
Db         77 CGAGTCTCAACCCTCAACTGTCACCCCAAGGCACTTGGGACGTCCTGGACAGACCGAGTC 136

Qy        218 CCGTGTTGCTGTCACTGTCGCGGGCCGCCACTGCCCC-AGCCCTGATGGGGGATTGAGAG 276
Db        137 CCGGGAAGCCCCAGCACTGCCGCTGCCACACTGCCCTGAGCCCAKATGGGGGAGTGAGAG 196

Qy        277 GCCACAGCTGGCCGGACATGGGCCTCCCCACCGTGCCTGGCCTGCTGCTGCCACTGGTGC 336
Db        197 GCCATAGCTGTCTGG-CATGGGCCTCTCCACCGTGCCTGACCTGCTGCTGCCACTGGTGC 255

Qy        337 TTCCAGCTCTGTTGGCAGATGTGTACCCCGCAGGGGTTCAGGGGCTGGTCCCTCACCCCG 396
Db        256 TCCTGGAGCTGTTGGTGGGAATATACCCCTCAGGGGTTATTGGACTGGTCCCTCACCTAG 315

Qy        397 GGGACCTGGAGAAGAGAGAGAGTCCCTGTCCCCAAGGAAAATATAACCACCCGCAAAATA 456
Db        316 GGGACAGGGAGAAGAGAGATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATA 375

Qy        457 GCACCATTTGCTGCACCAAGTGCCACAAAGGTACCTATCTGTACAATGACTGTCCGGGTC 516
Db        376 ATTCGATTTGCTGTACCAAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCC 435

Qy        517 CAGGGCGAGACACGGACTGCAGGGTGTGTGCCCCTGGCACCTACACTGCCTTGGAGAACC 576
Db        436 CGGGGCAGGATACGGACTGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACC 495

Qy        577 ATCTCAGACGATGCCTGAGCTGCTCCAGGTGCCGGGACGAAATGTTCCAGGTGGAGATTT 636
Db        496 ACCTCAGACACTGCCTCAGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCT 555

Qy        637 CGCCTTGTGTAGTGGACCGGGACACTGTGTGCGGCTGCAGGAAGAACCAGTACCGGGAAT 696
Db        556 CTTCTTGCACAGTGGACCGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATT 615

Qy        697 ACTGGGGTGAAACTGGCTTCCGGTGTCTGAACTGCAGCCTCTGTCCCAATGGCACAGTGA 756
Db        616 ATTGGAGTGAAAACCTTTTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGC 675

Qy        757 ATATCCCCTGCCAGGAGAGACAGGACACCATCTGCCACTGCCATATGGGCTTCTTTCTTA 816
Db        676 ACCTCTCCTGCCAGGAGAAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAA 735

Qy        817 AAGGCGCCAAGTGCATCTCCTGTCATGATTGTAAGAA---CAAGGAGTGCGAGAAGTTAT 873
Db        736 GAGAAAACGAGTGTGTCTCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGT 795

Qy        874 GTCCAACCCGACCTTCAACTGGTAAAGACTCTCAGGACCCAGGCACTACAGTACTATTAC 933
Db        796 GCCTACCCCAGATTGAGAATGTTAAGGGCACTGAGGACTCAGGCACCACAGTGCTGTTGC 855

Qy        934 CCCTGGTGATTGTCTTCGGGCTTTGCCTGGCATCCTTCGCCTCTGTCGTCTTAGCATGTC 993
Db        856 CCCTGGTCATTTTCTTTGGTCTTTGCCTTTTATCCCTCCTCTTCATTGGTTTAATGTATC 915

Qy        994 GCTACCAGCGGTGGAAGCCCAAGCTCTACTCCATCATTTGCGGGCAGTCGACTCTGGTAA 1053
Db        916 GCTACCAACGGTGGAAGTCCAAGCTCTACTCCATTGTTTGTGGGAAATCGACACCTGAAA 975

Qy       1054 AAGAGGGGGAGCCAGAA---------CTCCTGGTCCCGGCCCCAGGCTTCAACCCCACCA 1104
Db        976 AAGAGGGGGAGCTTGAAGGAACTACTACTAAGCCCCTGGCCCCAAACCCAAGCTTCAGTC 1035
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Qy       1105 CCACCATCTGCTTCAGCTCCACCCCAAGTTCCAGTCCTGTCTCCATTCCCCCTTACATCT 1164
             ||||     |||||| | ||||||   | | |||||| ||  ||| | || | | || ||
Db       1036 CCACTCCAGGCTTCACCCCCACCCTGGGCTTCAGTCCCGTGCCCAGTTCCACCTTCACCT 1095

Qy       1165 CCTGTGACCGGTCCAACTTCGGAG---------CCGTCGCATCTCCCTCCAGCGAGACGG 1215
             || |   |   | | |  ||| |         | | ||  |||||  ||| |||  ||
Db       1096 CCAGCTCCACCTATACCCCCGGTGACTGTCCCAACTTTGCGGCTCCCCGCAGAGAGGTGG 1155

Qy       1216 CCCCGCCCCATCTAAAGGCTGGCCCCATCCTCCCGGGGCCTCCGGCCTCCACCCACCTCT 1275
             | || ||| |||     ||||| |||||||||
Db       1156 CACCACCCTATCAGGGGGCTGACCCCATCCT---------------------------- 1186

Qy       1276 GTACCCCGGGGCCTCCGGCCTCCACCCACCTCTGTACCCCGGGGCCTCCGGCCTCCACCC 1335
                                                ||     | |  ||||||  ||
Db       1187 -----------------------------------TGCGACAGCCCTCGCCTCCGACC 1209

Qy       1336 ACCTCTGCACCCCAGTTCAGAAGTGGGAAGCCAGCGCCCCCAGCGCCCCCGATCAGCTCG 1395
              | ||  || |||  |||||||||||||| | |||||||| ||      ||  |    || |
Db       1210 CCATCCCCAACCCCCTTCAGAAGTGGGAGGACAGCGCCCACA---AGCCACAGAGCCTAG 1266

Qy       1396 CGGATGCCGACCCCGCGACCCTGTACGCGGTGGTGGACGGCGTGCCCCCGTCGCGCTGGA 1455
                ||  |||||||||| |||||||| ||||||||   |||||||||| |||||||||
Db       1267 ACACTGATGACCCCGCGACGCTGTACGCCGTGGTGGAGAACGTGCCCCCGTTGCGCTGGA 1326

Qy       1456 AGGAGTTGGTGCGGCGGCTGGGACTGAGCGAGCACGAGATCGAGCGGCTGGAGCTGGAGA 1515
              |||| || |||||||| || || |||||||| |||||||||| |||||||||||  |||
Db       1327 AGGAATTCGTGCGGCGCCTAGGGCTGAGCGACCACGAGATCGATCGGCTGGAGCTGCAGA 1386

Qy       1516 ACGGGCGCCACCTGCGCGAGGCGCAGTACAGCATGCTGGCGGCCTGGCGGCGGCGCACGC 1575
              ||||||||  |||||||||||||||| |||||||||||||||| ||||| ||||||||||||
Db       1387 ACGGGCGCTGCCTGCGCGAGGCGCAATACAGCATGCTGGCGACCTGGAGGCGGCGCACGC 1446

Qy       1576 CGCGCCGCGAGGCCACGCTGGAGCTGCTGGGCCGCGTGCTCAGGGACATGGACCTGCTGG 1635
              |||| |||||||||||||||||||||||||||||||| |||||||| | ||||||||||||||
Db       1447 CGCGGCGCGAGGCCACGCTGGAGCTGCTGGGACGCGTGCTCCGCGACATGGACCTGCTGG 1506

Qy       1636 GTTGCCTGGAAAACATAGAGGAGGCGCTGGGTGGCGCCGCCCGCCTCGCGTCCGAGCCCC 1695
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Db       1507 GCTGCCTGGAGGACATCGAGGAGGCGCTTTGCGGCCCCGCCGCCCTCCCGCCCGCGCCCA 1566

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RESULT 6
US-10-120-397-1
; Sequence 1, Application US/10120397
; Publication No. US20020142357A1
;   GENERAL INFORMATION:
;        APPLICANT: WALLACH, David
;                   BRAKEBUSCH, Cord
;        TITLE OF INVENTION: TNF RECEPTOR ACTION MODULATION
;        NUMBER OF SEQUENCES: 8
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W.
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/120,397
;             FILING DATE: 12-Apr-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/054,970
;             FILING DATE: 03-MAY-1993
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Townsend, Kevin G.
;             REGISTRATION NUMBER: 34,033
;             REFERENCE/DOCKET NUMBER: WALLACH=9
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;             TELEX: 248633
;   INFORMATION FOR SEQ ID NO: 1:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 2175 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  256..1620
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US-10-120-397-1

  Query Match             29.8%;  Score 727;  DB 13;  Length 2175;
  Best Local Similarity   69.6%;  Pred. No. 2.8e-174;
  Matches 1129;  Conservative    0;  Mismatches  400;  Indels   92;  Gaps    7;

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              ||||  ||| |  ||.   |  |  ||   |  ||||||||  |||||  |||||
Db        170 AGACCGAGTCCCGGGAAGCCCCAGCACTGCCGCTGCCACACTGCCCTGAGCCCAAATGGG 229

Qy        267 GGATTGAGAGGCCACAGCTGGCCGGACATGGGCCTCCCCACCGTGCCTGGCCTGCTGCTG 326
              ||| ||||||||||  |||||  || ||||||||||  ||||||||||  ||||||||||
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Qy        327 CCACTGGTGCTTCCAGCTCTGTTGGCAGATGTGTACCCCGCAGGGGTTCAGGGGCTGGTC 386
              || |||||||| |  |  |||||||  |   | ||||||  ||||||||   || ||||||
Db        289 CCGCTGGTGCTCCTGGAGCTGTTGGTGGGAATATACCCCTCAGGGGTTATTGGACTGGTC 348

Qy        387 CCTCACCCCGGGGACCTGGAGAAGAGAGAGAGTCCCTGTCCCCAAGGAAAATATAACCAC 446
              |||||||  ||||||  |||||||||||  |||  ||||||||||||||||||  ||||
Db        349 CCTCACCTAGGGGACAGGGAGAAGAGAGATAGTGTGTGTCCCCAAGGAAAATATATCCAC 408

Qy        447 CCGCAAAATAGCACCATTTGCTGCACCAAGTGCCACAAAGGTACCTATCTGTACAATGAC 506
              || |||||||  | |||||||| ||||||||||||||||||  |||||  ||||||||||
Db        409 CCTCAAAATAATTCGATTTGCTGTACCAAGTGCCACAAAGGAACCTACTTGTACAATGAC 468

Qy        507 TGTCCGGGTCCAGGGCGAGACACGGACTGCAGGGTGTGTGCCCCTGGCACCTACACTGCC 566
              ||||| || || ||||  || ||||||||||||| |||||      ||| ||| ||| ||
Db        469 TGTCCAGGCCCGGGGCAGGATACGGACTGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCT 528

Qy        567 TTGGAGAACCATCTCAGACGATGCCTGAGCTGCTCCAGGTGCCGGGACGAAATGTTCCAG 626
              |  || ||||| |||||||  |||||  |||||||||  |||||  | ||||||   |||
Db        529 TCAGAAAACCACCTCAGACACTGCCTCAGCTGCTCCAAATGCCGAAAGGAAATGGGTCAG 588

Qy        627 GTGGAGATTTCGCCTTGTGTAGTGGACCGGGACACTGTGTGCGGCTGCAGGAAGAACCAG 686
              |||||||| ||  ||||  |||||||||||||| ||||| ||||||||||||||||||||
Db        589 GTGGAGATCTCTTCTTGCACAGTGGACCGGGACACCGTGTGTGGCTGCAGGAAGAACCAG 648

Qy        687 TACCGGGAATACTGGGGTGAAACTGGCTTCCGGTGTCTGAACTGCAGCCTCTGTCCCAAT 746
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Db        649 TACCGGCATTATTGGAGTGAAAACCTTTTCCAGTGCTTCAATTGCAGCCTCTGCCTCAAT 708

Qy        747 GGCACAGTGAATATCCCCTGCCAGGAGAGACAGGACACCATCTGCCACTGCCATATGGGC 806
              || || ||| |  || |||||||||||| |||| ||||| | |||  |||||||   ||
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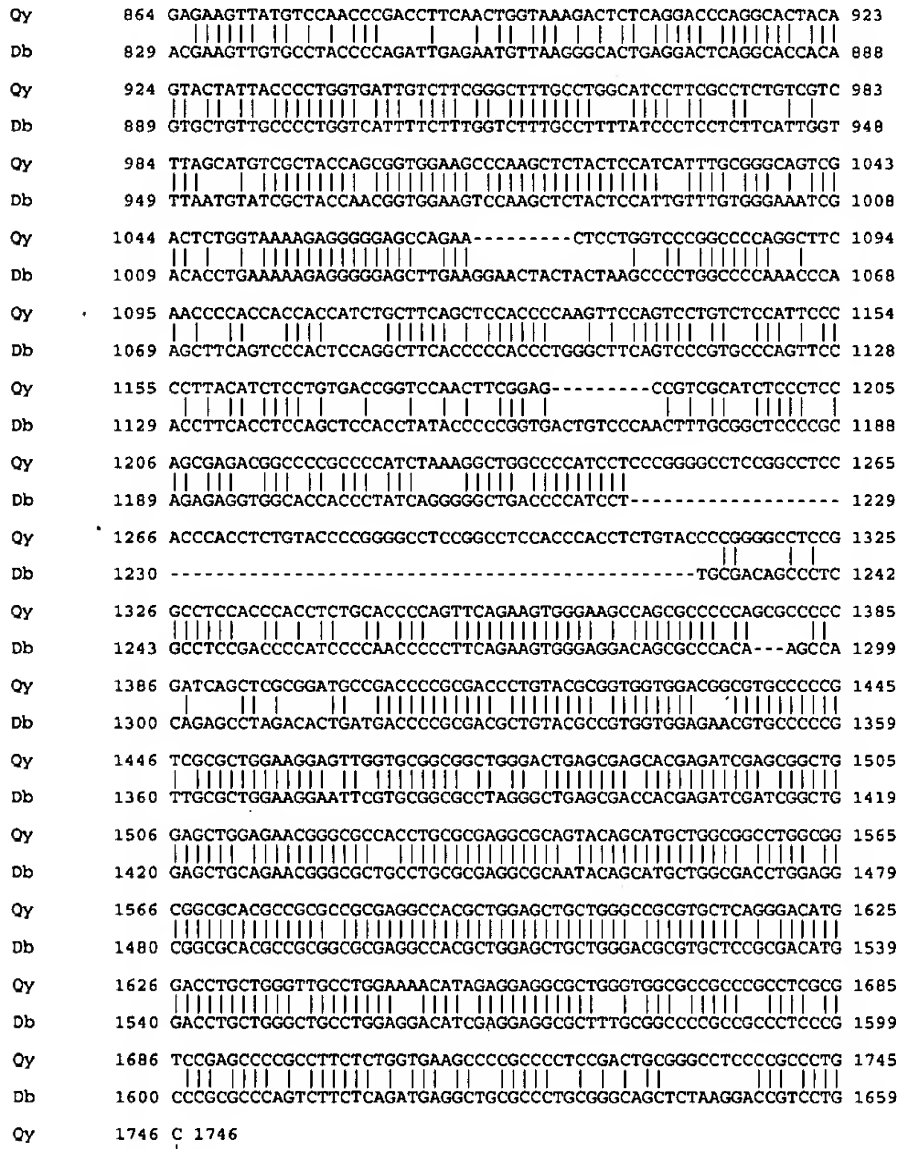

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RESULT 7
US-09-880-107-2360
; Sequence 2360, Application US/09880107
;.Patent No. US20020142981A1
; GENERAL INFORMATION:
;  APPLICANT: Horne, Darci T.
;  APPLICANT:  Vockley, Joseph G.
;  APPLICANT:  Scherf, Uwe
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;  APPLICANT:  Gene Logic, Inc.
;  TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
;  FILE REFERENCE: 44921-5028-WO
;  CURRENT APPLICATION NUMBER: US/09/880,107
;  CURRENT FILING DATE:  2001-06-14
;  PRIOR APPLICATION NUMBER: US 60/211,379
;  PRIOR FILING DATE: 2000-06-14
;  PRIOR APPLICATION NUMBER: US 60/237,054
;  PRIOR FILING DATE: 2000-10-02
;  NUMBER OF SEQ ID NOS: 3950
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2360
;   LENGTH: 2111
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Genbank Accession No. US20020142981A1 M58286
US-09-880-107-2360

  Query Match           29.7%;  Score 725.8;  DB 10;  Length 2111;
  Best Local Similarity  70.0%;  Pred. No. 5.6e-174;
  Matches 1120;  Conservative    0;  Mismatches  387;  Indels   92;  Gaps    7;
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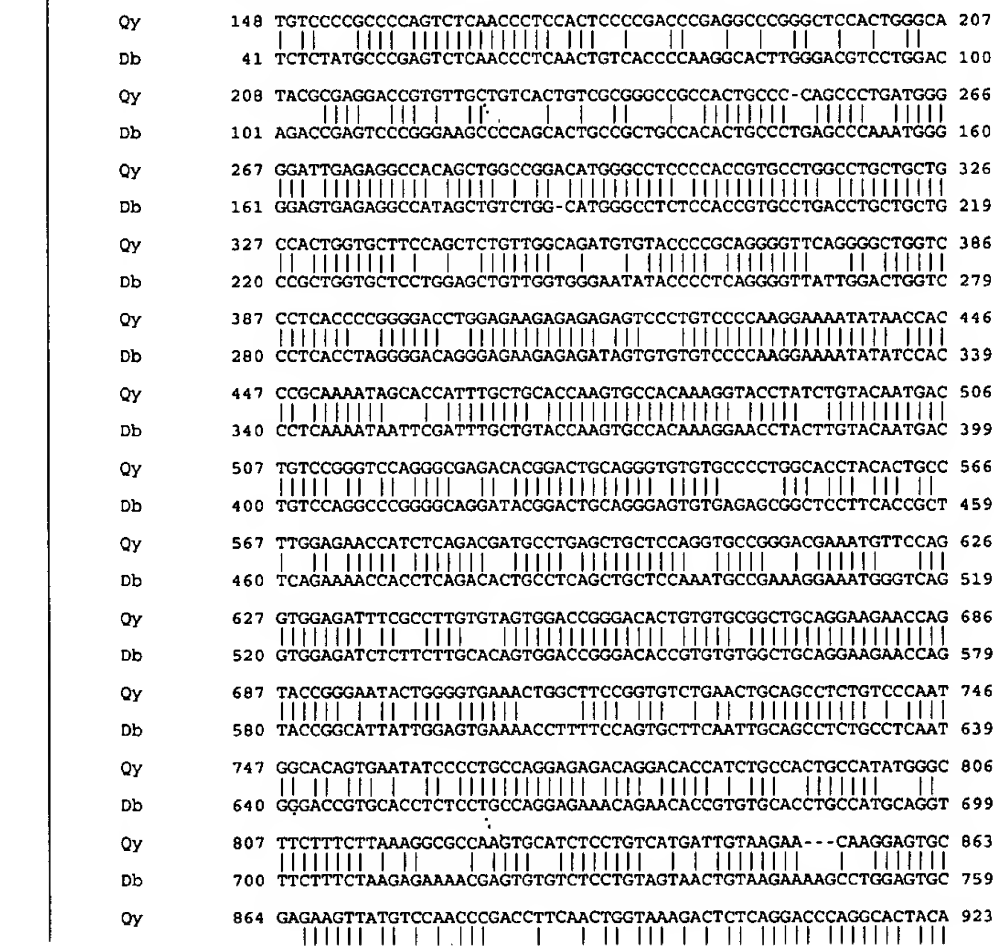

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Qy        924 GTACTATTACCCCTGGTGATTGTCTTCGGGCTTTGCCTGGCATCCTTCGCCTCTGTCGTC 983

Db        820 GTGCTGTTGCCCCTGGTCATTTTCTTTGGTCTTTGCCTTTTATCCCTCCTCTTCATTGGT 879

Qy        984 TTAGCATGTCGCTACCAGCGGTGGAAGCCCAAGCTCTACTCCATCATTTGCGGGCAGTCG 1043

Db        880 TTAATGTATCGCTACCAACGGTGGAAGTCCAAGCTCTACTCCATTGTTTGTGGGAAATCG 939

Qy       1044 ACTCTGGTAAAAGAGGGGGAGCCAGAA---------CTCCTGGTCCCGGCCCCAGGCTTC 1094

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Qy       1155 CCTTACATCTCCTGTGACCGGTCCAACTTCGGAG---------CCGTCGCATCTCCCTCC 1205

Db       1060 ACCTTCACCTCCAGCTCCACCTATACCCCCGGTGACTGTCCCAACTTTGCGGCTCCCCGC 1119

Qy       1206 AGCGAGACGGCCCCGCCCCATCTAAAGGCTGGCCCCATCCTCCCGGGGGCCTCCGGCCTCC 1265

Db       1120 AGAGAGGTGGCACCACCCTATCAGGGGGCTGACCCCATCCT------------------- 1160

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Qy       1386 GATCAGCTCGCGGATGCCGACCCCGCGACCCTGTACGCGGTGGTGGACGGCGTGCCCCCG 1445

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Qy       1446 TCGCGCTGGAAGGAGTTGGTGCGGCGGCTGGGACTGAGCGAGCACGAGATCGAGCGGCTG 1505

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Qy       1686 TCCGAGCCCCGCCTTCTCTGGTGAAGCCCCGCCCCTCCG 1724

Db       1531 CCCGCGCCCAGTCTTCTCAGATGAGGCTGCGCCCCTGCG 1569
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RESULT 8
US-09-899-422-1
; Sequence 1, Application US/09899422
; Patent No. US20020090676A1
; GENERAL INFORMATION:
;  APPLICANT: Hauptmann, Rudolph
;  APPLICANT:  Himmler, Adolph
;  APPLICANT:  Maurer-Fogy, Ingrid
;  APPLICANT:  Stratowa, Christian
;  TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
;  TITLE OF INVENTION:  Them
;  FILE REFERENCE: 98,385-H
;  CURRENT APPLICATION NUMBER: US/09/899,422
;  CURRENT FILING DATE:  2001-08-21
;  PRIOR APPLICATION NUMBER: 09/525,998
;  PRIOR FILING DATE: 2000-03-15
;  PRIOR APPLICATION NUMBER: 08/383,676
;  PRIOR FILING DATE: 1995-02-01
;  PRIOR APPLICATION NUMBER: 08/153,287
;  PRIOR FILING DATE: 1993-11-17
;  PRIOR APPLICATION NUMBER: 07/821,750
;  PRIOR FILING DATE: 1992-01-02
;  PRIOR APPLICATION NUMBER: 07/511,430
;  PRIOR FILING DATE: 1990-04-20
;  NUMBER OF SEQ ID NOS: 87
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;  LENGTH: 1368
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (1)..(1368)
;  NAME/KEY: sig_peptide
;  LOCATION: (1)..(87)
;  NAME/KEY: misc_feature
;  LOCATION: (88)..(120)
;  OTHER INFORMATION: Portion of TNF-BP pro protein cleaved by
;  OTHER INFORMATION: extracellular proteases following secretion.
;  NAME/KEY: misc_feature
;  LOCATION: (606)..(633)
;  OTHER INFORMATION: Portion of TNF-BP pro protein cleaved by
;  OTHER INFORMATION: extracellular proteases following secretion.
US-09-899-422-1

  Query Match           28.1%;  Score 685.4;  DB 9;  Length 1368;
  Best Local Similarity  71.1%;  Pred. No. 8.9e-164;
  Matches 1021;  Conservative    0;  Mismatches  326;  Indels   90;  Gaps    5;

Qy        294 ATGGGCCTCCCCACCGTGCCTGGCCTGCTGCTGCCACTGGTGCTTCCAGCTCTGTTGGCA 353

Db          1 ATGGGCCTCTCCACCGTGCCTGACCTGCTGCTGCCACTGGTGCTCCTGGAGCTGTTGGTG 60

Qy        354 GATGTGTACCCCGCAGGGGTTCAGGGGCTGGTCCCTCACCCCGGGGACCTGGAGAAGAGA 413

Db         61 GGAATATACCCCTCAGGGGTTATTGGACTGGTCCCTCACCTAGGGGACAGGGAGAAGAGA 120

Qy        414 GAGAGTCCCTGTCCCCAAGGAAAATATAACCACCCGCAAAATAGCACCATTTGCTGCACC 473

Db        121 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 180

Qy        474 AAGTGCCACAAAGGTACCTATCTGTACAATGACTGTCCGGGTCCAGGGCGAGACACGGAC 533

Db        181 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 240

Qy        534 TGCAGGGTGTGTGCCCCTGGCACCTACACTGCCTTGGAGAACCATCTCAGACGATGCCTG 593

Db        241 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 300

Qy        594 AGCTGCTCCAGGTGCCGGGACGAAATGTTCCAGGTGGAGATTTCGCCTTGTGTAGTGGAC 653

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Qy        654 CGGGACACTGTGTGCGGCTGCAGGAAGAACCAGTACCGGGAATACTGGGGTGAAACTGGC 713

Db        361 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 420

Qy        714 TTCCGGTGTCTGAACTGCAGCCTCTGTCCCAATGGCACAGTGAATATCCCCTGCCAGGAG 773

Db        421 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 480

Qy        774 AGACAGGACACCATCTGCCACTGCCATATGGGCTTCTTTCTTAAAGGCGCCAAGTGCATC 833

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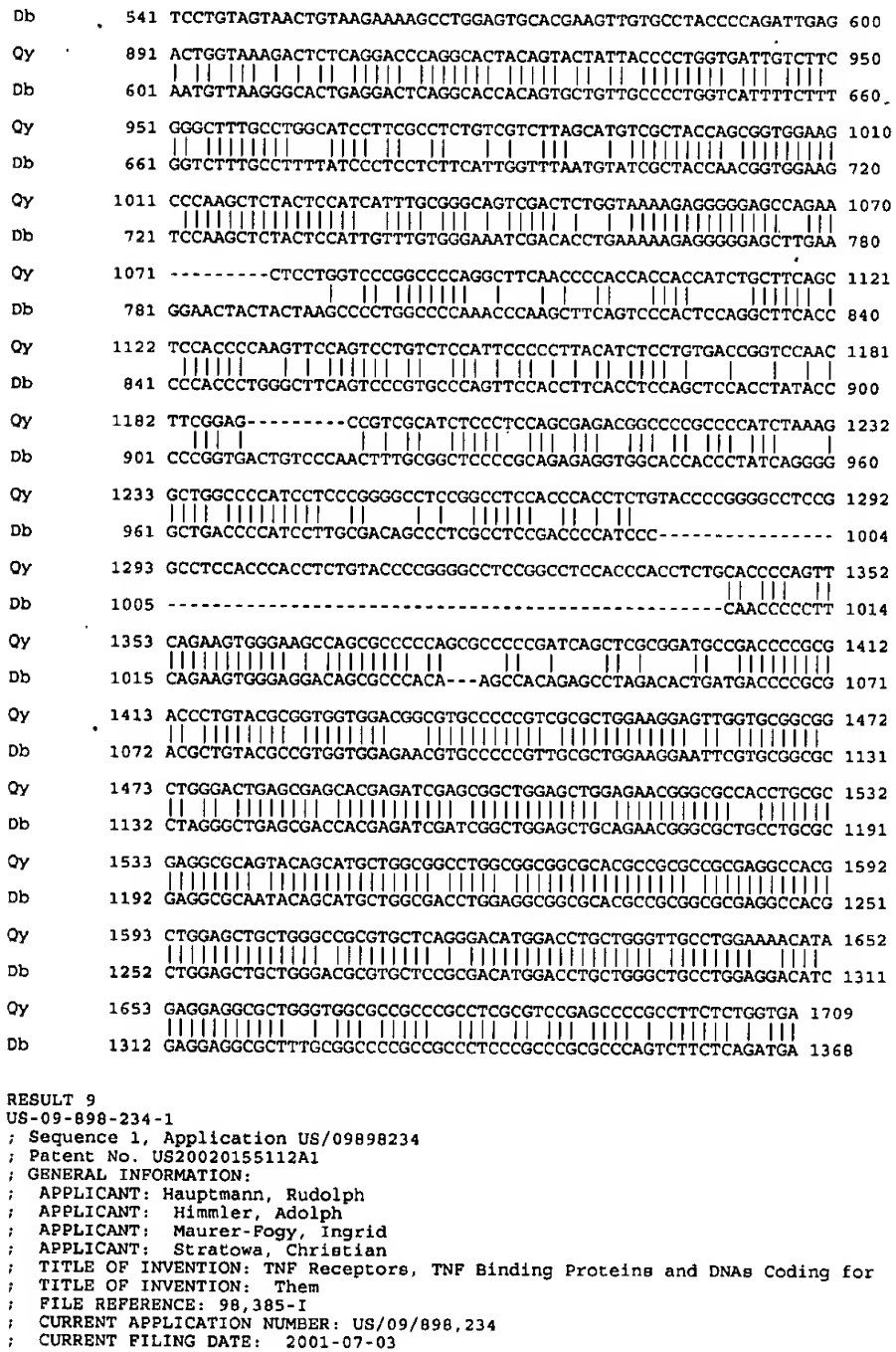
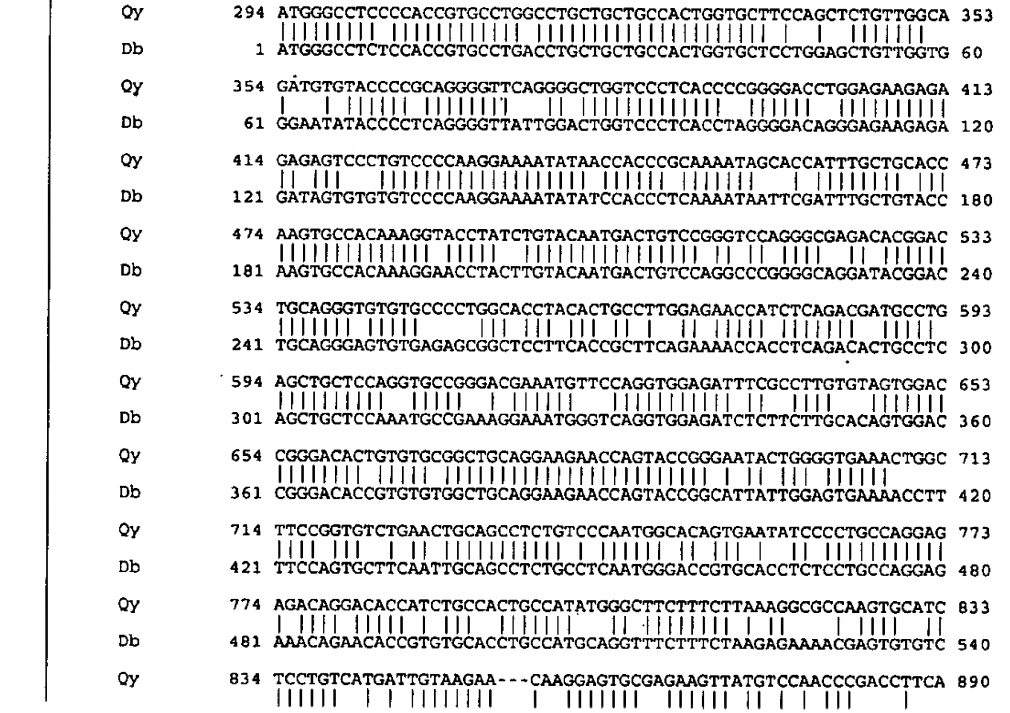


RESULT 9
US-09-898-234-1
; Sequence 1, Application US/09898234
; Patent No. US20020155112A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stratowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; TITLE OF INVENTION: Them
; FILE REFERENCE: 98,385-I
; CURRENT APPLICATION NUMBER: US/09/898,234
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/525,998
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1368
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1368)
; NAME/KEY: sig_peptide
; LOCATION: (1)..(87)
; NAME/KEY: misc_feature
; LOCATION: (88)..(120)
; OTHER INFORMATION: Portion of TNF-BP pro protein cleaved by
; OTHER INFORMATION: extracellular proteases following secretion.
; NAME/KEY: misc_feature
; LOCATION: (606)..(633)
; OTHER INFORMATION: Portion of TNF-BP pro protein cleaved by
; OTHER INFORMATION: extracellular proteases following secretion.
US-09-898-234-1

Query Match 28.1%; Score 685.4; DB 10; Length 1368;
Best Local Similarity 71.1%; Pred. No. 8.9e-164;
Matches 1021; Conservative 0; Mismatches 326; Indels 90; Gaps 5;



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Db        661 GGTCTTTGCCTTTTATCCCTCCTCTTCATTGGTTTAATGTATCGCTACCAACGGTGGAAG 720

Qy       1011 CCCAAGCTCTACTCCATCATTTGCGGGCAGTCGACTCTGGTAAAAGAGGGGGAGCCAGAA 1070

Db        721 TCCAAGCTCTACTCCATTGTTTGTGGGAAATCGACACCTGAAAAAGAGGGGGAGCTTGAA 780

Qy       1071 ---------CTCCTGGTCCCGGCCCCAGGCTTCAACCCCACCACCACCATCTGCTTCAGC 1121

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Qy       1122 TCCACCCCAAGTTCCAGTCCTGTCTCCATTCCCCCTTACATCTCCTGTGACCGGTCCAAC 1181

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Qy       1182 TTCGGAG---------CCGTCGCATCTCCCTCCAGCGAGACGGCCCCGCCCCATCTAAAG 1232

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Qy       1353 CAGAAGTGGGAAGCCAGCGCCCCCAGCGCCCCCGATCAGCTCGCGGATGCCGACCCCGCG 1412

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Db       1132 CTAGGGCTGAGCGACCACGAGATCGATCGGCTGGAGCTGCAGAACGGGCGCTGCCTGCGC 1191

Qy       1533 GAGGCGCAGTACAGCATGCTGGCGGCCTGGCGGCGGCGCACGCCGCGCCGCGAGGCCACG 1592

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; Sequence 1, Application US/09899429A
; Patent No. US20020169118A1
; GENERAL INFORMATION:
;  APPLICANT: Hauptmann, Rudolph
;  APPLICANT:  Himmler, Adolph
;  APPLICANT:  Maurer-Fogy, Ingrid
;  APPLICANT:  Stratowa, Christian
;  TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
;  TITLE OF INVENTION:  Them
;  FILE REFERENCE: 98-385-J
;  CURRENT APPLICATION NUMBER: US/09/899,429A
;  CURRENT FILING DATE:  2001-07-03
;  PRIOR APPLICATION NUMBER: 09/792,356
;  PRIOR FILING DATE: 2000-02-23
;  PRIOR APPLICATION NUMBER: 08/477,639
;  PRIOR FILING DATE: 1955-06-07
;  PRIOR APPLICATION NUMBER: 08/383,676
;  PRIOR FILING DATE: 1995-02-01
;  PRIOR APPLICATION NUMBER: 08/153,287
;  PRIOR FILING DATE: 1993-11-17
;  PRIOR APPLICATION NUMBER: 07/821,750
;  PRIOR FILING DATE: 1992-01-02
;  PRIOR APPLICATION NUMBER: 07/511,430
;  PRIOR FILING DATE: 1990-04-20
;  NUMBER OF SEQ ID NOS: 97
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;  LENGTH: 1368
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (1)..(1365)
;  NAME/KEY: sig_peptide
;  LOCATION: (1)..(87)
;  NAME/KEY: misc_feature
;  LOCATION: (88)..(120)
;  OTHER INFORMATION: portion of TNF-BP pro protein cleaved by
;  OTHER INFORMATION: extracellular proteases following secretion
;  NAME/KEY: misc_feature
;  LOCATION: (606)..(633)
;  OTHER INFORMATION: portion of TNF-BP pro protein cleaved by
;  OTHER INFORMATION: extracellular proteases following secretion
US-09-899-429A-1

  Query Match           28.1%;  Score 685.4;  DB 10;  Length 1368;
  Best Local Similarity  71.1%;  Pred. No. 8.9e-164;
  Matches 1021;  Conservative    0;  Mismatches  326;  Indels   90;  Gaps    5;

Qy        294 ATGGGCCTCCCCACCGTGCCTGGCCTGCTGCTGCCACTGGTGCTTCCAGCTCTGTTGGCA 353

Db          1 ATGGGCCTCTCCACCGTGCCTGACCTGCTGCTGCCACTGGTGCTCCTGGAGCTGTTGGTG 60

Qy        354 GATGTGTACCCCGCAGGGGTTCAGGGGCTGGTCCCTCACCCCGGGGACCTGGAGAAGAGA 413

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Qy        474 AAGTGCCACAAAGGTACCTATCTGTACAATGACTGTCCGGGTCCAGGGCGAGACACGGAC 533

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Qy        534 TGCAGGGTGTGTGCCCCTGGCACCTACACTGCCTTGGAGAACCATCTCAGACGATGCCTG 593

Db        241 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 300

Qy        594 AGCTGCTCCAGGTGCCGGGACGAAATGTTCCAGGTGGAGATTTCGCCTTGTGTAGTGGAC 653

Db        301 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 360

Qy        654 CGGGACACTGTGTGCGGCTGCAGGAAGAACCAGTACCGGGAATACTGGGGTGAAACTGGC 713

Db        361 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 420

Qy        714 TTCCGGTGTCTGAACTGCAGCCTCTGTCCCAATGGCACAGTGAATATCCCCTGCCAGGAG 773

Db        421 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 480

Qy        774 AGACAGGACACCATCTGCCACTGCCATATGGGCTTCTTTCTTAAAGGCGCCAAGTGCATC 833

Db        481 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 540
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Qy        834 TCCTGTCATGATTGTAAGAA---CAAGGAGTGCGAGAAGTTATGTCCAACCCGACCTTCA 890
Db        541 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 600

Qy        891 ACTGGTAAAGACTCTCAGGACCCAGGCACTACAGTACTATTACCCCTGGTGATTGTCTTC 950
Db        601 AATGTTAAGGGCACTGAGGACTCAGGCACCACAGTGCTGTTGCCCCTGGTCATTTTCTTT 660

Qy        951 GGGCTTTGCCTGGCATCCTTCGCCTCTGTCGTCTTAGCATGTCGCTACCAGCGGTGGAAG 1010
Db        661 GGTCTTTGCCTTTTATCCCTCCTCTTCATTGGTTTAATGTATCGCTACCAACGGTGGAAG 720

Qy       1011 CCCAAGCTCTACTCCATCATTTGCGGGCAGTCGACTCTGGTAAAAGAGGGGGAGCCAGAA 1070
Db        721 TCCAAGCTCTACTCCATTGTTTGTGGGAAATCGACACCTGAAAAAGAGGGGGAGCTTGAA 780

Qy       1071 ---------CTCCTGGTCCCGGCCCCAGGCTTCAACCCCACCACCACCATCTGCTTCAGC 1121
Db        781 GGAACTACTACTAAGCCCCTGGCCCCAAACCCAAGCTTCAGTCCCACTCCAGGCTTCACC 840

Qy       1122 TCCACCCCAAGTTCCAGTCCTGTCTCCATTCCCCCTTACATCTCCTGTGACCGGTCCAAC 1181
Db        841 CCCACCCTGGGCTTCAGTCCCGTGCCCAGTTCCACCTTCACCTCCAGCTCCACCTATACC 900

Qy       1182 TTCGGAG---------CCGTCGCATCTCCCTCCAGCGAGACGGCCCCGCCCCATCTAAAG 1232
Db        901 CCCGGTGACTGTCCCAACTTTGCGGCTCCCCGCAGAGAGGTGGCACCACCCTATCAGGGG 960

Qy       1233 GCTGGCCCCATCCTCCCGGGGCCTCCGGCCTCCACCCACCTCTGTACCCCGGGGCCTCCG 1292
Db        961 GCTGACCCCATCCTTGCGACAGCCCTCGCCTCCGACCCCATCCC---------------- 1004

Qy       1293 GCCTCCACCCACCTCTGTACCCCGGGGCCTCCGGCCTCCACCCACCTCTGCACCCCAGTT 1352
Db       1005 ----------------------------------}--------------CAACCCCCTT 1014

Qy       1353 CAGAAGTGGGAAGCCAGCGCCCCCAGCGCCCCCGATCAGCTCGCGGATGCCGACCCCGCG 1412
Db       1015 CAGAAGTGGGAGGACAGCGCCCACA---AGCCACAGAGCCTAGACACTGATGACCCCGCG 1071

Qy       1413 ACCCTGTACGCGGTGGTGGACGGCGTGCCCCCGTCGCGCTGGAAGGAGTTGGTGCGGCGG 1472
Db       1072 ACGCTGTACGCCGTGGTGGAGAACGTGCCCCCGTTGCGCTGGAAGGAATTCGTGCGGCGC 1131

Qy       1473 CTGGGACTGAGCGAGCACGAGATCGAGCGGCTGGAGCTGGAGAACGGGCGCCACCTGCGC 1532
Db       1132 CTAGGGCTGAGCGACCACGAGATCGATCGGCTGGAGCTGCAGAACGGGCGCTGCCTGCGC 1191

Qy       1533 GAGGCGCAGTACAGCATGCTGGCGGCCTGGCGGCGGCGCACGCCGCGCCGCGAGGCCACG 1592
Db       1192 GAGGCGCAATACAGCATGCTGGCGACCTGGAGGCGGCGCACGCCGCGGCGCGAGGCCACG 1251

Qy       1593 CTGGAGCTGCTGGGCCGCGTGCTCAGGGACATGGACCTGCTGGGTTGCCTGGAAAACATA 1652
Db       1252 CTGGAGCTGCTGGGACGCGTGCTCCGCGACATGGACCTGCTGGGCTGCCTGGAGGACATC 1311

Qy       1653 GAGGAGGCGCTGGGTGGCGCCGCCCGCCTCGCGTCCGAGCCCCGCCTTCTCTGGTGA 1709
Db       1312 GAGGAGGCGCTTTGCGGCCCCGCCGCCCTCCCGCCCGCGCCCAGTCTTCTCAGATGA 1368
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RESULT 11
US-09-792-356-1
; Sequence 1, Application US/09792356
; Publication No. US20020183485A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stratowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; TITLE OF INVENTION: Them
; FILE REFERENCE: 98,385-G
; CURRENT APPLICATION NUMBER: US/09/792,356
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 08/477,639
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1368
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1368)
; NAME/KEY: sig_peptide
; LOCATION: (1)..(87)
; NAME/KEY: misc_feature
; LOCATION: (88)..(120)
; OTHER INFORMATION: Portion of TNF-BP pro protein cleaved by
; OTHER INFORMATION: extracellular proteases following secretion.
; NAME/KEY: misc_feature
; LOCATION: (606)..(633)
; OTHER INFORMATION: Portion of TNF-BP pro protein cleaved by
; OTHER INFORMATION: extracellular proteases following secretion.
US-09-792-356-1

Query Match 28.1%; Score 685.4; DB 10; Length 1368;
Best Local Similarity 71.1%; Pred. No. 8.9e-164;
Matches 1021; Conservative 0; Mismatches 326; Indels 90; Gaps 5;

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Qy        294 ATGGGCCTCCCCACCGTGCCTGGCCTGCTGCTGCCACTGGTGCTTCCAGCTCTGTTGGCA 353
Db          1 ATGGGCCTCTCCACCGTGCCTGACCTGCTGCTGCCACTGGTGCTCCTGGAGCTGTTGGTG 60

Qy        354 GATGTGTACCCCGCAGGGGTTCAGGGGCTGGTCCCTCACCCCGGGGACCTGGAGAAGAGA 413
Db         61 GGAATATACCCCTCAGGGGTTATTGGACTGGTCCCTCACCTAGGGGACAGGGAGAAGAGA 120

Qy        414 GAGAGTCCCTGTCCCCAAGGAAAATATAACCACCCGCAAAATAGCACCATTTGCTGCACC 473
Db        121 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 180

Qy        474 AAGTGCCACAAAGGTACCTATCTGTACAATGACTGTCCGGGTCCAGGGCGAGACACGGAC 533
Db        181 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 240

Qy        534 TGCAGGGTGTGTGCCCCTGGCACCTACACTGCCTTGGAGAACCATCTCAGACGATGCCTG 593
Db        241 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 300

Qy        594 AGCTGCTCCAGGTGCCGGGACGAAATGTTCCAGGTGGAGATTTCGCCTTGTGTAGTGGAC 653
Db        301 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 360

Qy        654 CGGGACACTGTGTGCGGCTGCAGGAAGAACCAGTACCGGGAATACTGGGGTGAAACTGGC 713
Db        361 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 420

Qy        714 TTCCGGTGTCTGAACTGCAGCCTCTGTCCCAATGGCACAGTGAATATCCCCTGCCAGGAG 773
Db        421 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 480

Qy        774 AGACAGGACACCATCTGCCACTGCCATATGGGCTTCTTTCTTAAAGGCGCCAAGTGCATC 833
Db        481 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 540
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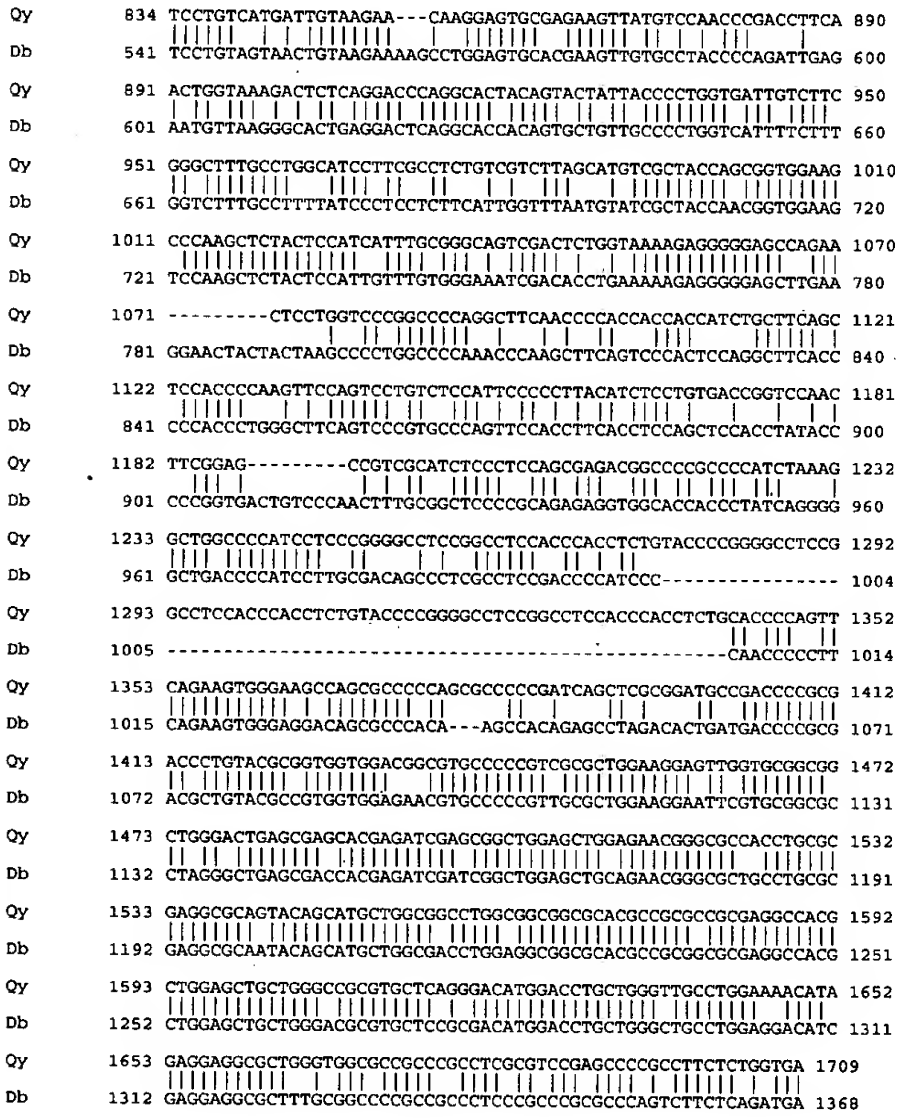
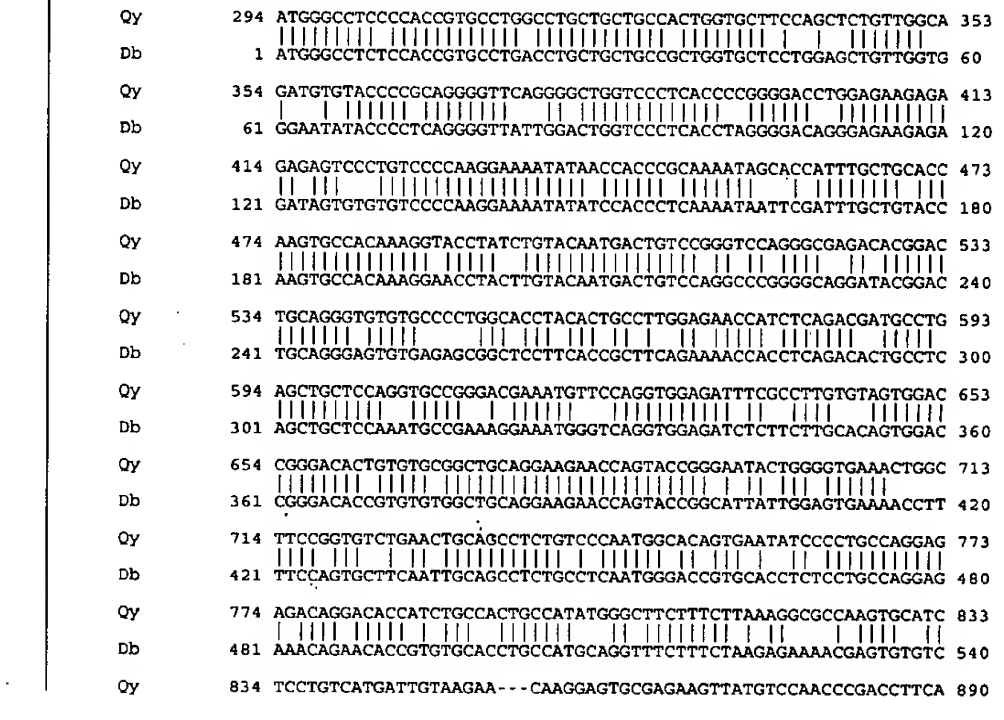


RESULT 12
US-10-252-408-3
; Sequence 3, Application US/10252408
; Publication No. US20030082736A1
; GENERAL INFORMATION:
; APPLICANT: SMITH, Craig A.
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR-ALPHA AND BETA-RECEPTORS
; FILE REFERENCE: A-71592
; CURRENT APPLICATION NUMBER: US/10/252,408
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: US/08/406,824
; PRIOR FILING DATE: 1995-03-20
; PRIOR APPLICATION NUMBER: US 08/255,849
; PRIOR FILING DATE: 1994-06-08
; PRIOR APPLICATION NUMBER: US 07/860,710
; PRIOR FILING DATE: 1992-03-30
; PRIOR APPLICATION NUMBER: US 07/523,635
; PRIOR FILING DATE: 1990-05-10
; PRIOR APPLICATION NUMBER: US 07/421,417
; PRIOR FILING DATE: 1989-10-13
; PRIOR APPLICATION NUMBER: US 07/405,370
; PRIOR FILING DATE: 1989-09-11
; PRIOR APPLICATION NUMBER: US 07/403,241
; PRIOR FILING DATE: 1989-09-05
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1368
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1365)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (121)..()
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (1)..(120)
; OTHER INFORMATION:
US-10-252-408-3

Query Match 28.0%; Score 683.8; DB 14; Length 1368;
Best Local Similarity 71.0%; Pred. No. 2.3e-163;
Matches 1020; Conservative 0; Mismatches 327; Indels 90; Gaps 5;



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Db        541 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 600

Qy        891 ACTGGTAAAGACTCTCAGGACCCAGGCACTACAGTACTATTACCCCTGGTGATTGTCTTC 950

Db        601 AATGTTAAGGGCACTGAGGACTCAGGCACCACAGTGCTGTTGCCCCTGGTCATTTTCTTT 660

Qy        951 GGGCTTTGCCTGGCATCCTTCGCCTCTGTCGTCTTAGCATGTCGCTACCAGCGGTGGAAG 1010

Db        661 GGTCTTTGCCTTTTATCCCTCCTCTTCATTGGTTTAAGTTATCGCTACCAACGGTGGAAG 720

Qy       1011 CCCAAGCTCTACTCCATCATTTGCGGGCAGTCGACTCTGGTAAAAGAGGGGGAGCCAGAA 1070

Db        721 TCCAAGCTCTACTCCATTGTTTGTGGGAAATCGACACCTGAAAAAGAGGGGGAGCTTGAA 780

Qy       1071 ---------CTCCTGGTCCCGGCCCCAGGCTTCAACCCCACCACCACCATCTGCTTCAGC 1121

Db        781 GGAACTACTACTAAGCCCCTGGCCCCAAACCCAAGCTTCAGTCCCACTCCAGGCTTCACC 840

Qy       1122 TCCACCCCAAGTTCCAGTCCTGTCTCCATTCCCCCTTACATCTCCTGTGACCGGTCCAAC 1181

Db        841 CCCACCCTGGGCTTCAGTCCCGTGCCCAGTTCCACCTTCACCTCCAGCTCCACCTATACC 900

Qy       1182 TTCGGAG---------CCGTCGCATCTCCCTCCAGCGAGACGGCCCCGCCCCATCTAAAG 1232

Db        901 CCCGGTGACTGTCCCAACTTTGCGGCTCCCCGCAGAGAGGTGGCACCACCCTATCAGGGG 960

Qy       1233 GCTGGCCCCATCCTCCCGGGGCCTCCGGCCTCCACCCACCTCTGTACCCCGGGGCCTCCG 1292

Db        961 GCTGACCCCATCCTTGCGACAGCCCTCGCCTCCGACCCCATCCC---------------- 1004

Qy       1293 GCCTCCACCCACCTCTGTACCCCGGGGCCTCCGGCCTCCACCCACCTCTGCACCCCAGTT 1352

Db       1005 ----------------------------------------------------CAACCCCCTT 1014

Qy       1353 CAGAAGTGGGAAGCCAGCGCCCCCAGCGCCCCCGATCAGCTCGCGGATGCCGACCCCGCG 1412

Db       1015 CAGAAGTGGGAGGACAGCGCCCACA---AGCCACAGAGCCTAGACACTGATGACCCCGCG 1071

Qy       1413 ACCCTGTACGCGGTGGTGGACGGCGTGCCCCCGTCGCGCTGGAAGGAGTTGGTGCGGCGG 1472

Db       1072 ACGCTGTACGCCGTGGTGGAGAACGTGCCCCCGTTGCGCTGGAAGGAATTCGTGCGGCGC 1131

Qy       1473 CTGGGACTGAGCGAGCACGAGATCGAGCGGCTGGAGCTGGAGAACGGGCGCCACCTGCGC 1532

Db       1132 CTAGGGCTGAGCGACCACGAGATCGATCGGCTGGAGCTGCAGAACGGGCGCTGCCTGCGC 1191

Qy       1533 GAGGCGCAGTACAGCATGCTGGCGGCCTGGCGGCGGCGCACGCCGCGCCGCGAGGCCACG 1592

Db       1192 GAGGCGCAATACAGCATGCTGGCGACCTGGAGGCGGCGCACGCCGCGGCGCGAGGCCACG 1251

Qy       1593 CTGGAGCTGCTGGGCCGCGTGCTCAGGGACATGGACCTGCTGGGTTGCCTGGAAAACATA 1652

Db       1252 CTGGAGCTGCTGGGACGCGTGCTCCGCGACATGGACCTGCTGGGCTGCCTGGAGGACATC 1311

Qy       1653 GAGGAGGCGCTGGGTGGCGCCGCCCGCCTCGCGTCCGAGCCCCGCCTTCTCTGGTGA 1709

Db       1312 GAGGAGGCGCTTTGCGGCCCCGCCGCCCTCCCGCCCGCGCCCAGTCTTCTCAGATGA 1368


RESULT 13
US-09-945-505-2
; Sequence 2, Application US/09945505
; Publication No. US20030165844A1
; GENERAL INFORMATION:
;  APPLICANT: Anastasio, Alison E.
;  APPLICANT:  Chew, Anne
;  APPLICANT:  Denton, R. Rex
;  APPLICANT:  Nandabalan, Krishnan
;  APPLICANT:  Parks, Katie E.
;  APPLICANT:  Stephens, J. Claiborne
;  TITLE OF INVENTION: Haplotypes of the TNFRSF1A Gene
;  FILE REFERENCE: MWH-0030US
;  CURRENT APPLICATION NUMBER: US/09/945,505
;  CURRENT FILING DATE:  2001-08-31
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 1368
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-945-505-2

  Query Match             28.0%;  Score 682.2;  DB 12;  Length 1368;
  Best Local Similarity   70.9%;  Pred. No. 5.7e-163;
  Matches 1019;  Conservative    0;  Mismatches  328;  Indels   90;  Gaps    5;

Qy        294 ATGGGCCTCCCCACCGTGCCTGGCCTGCTGCTGCCACTGGTGCTTCCAGCTCTGTTGGCA 353

Db          1 ATGGGCCTCTCCACCGTGCCTGACCTGCTGCTGCCCCAGGTGCTCCTGGAGCTGTTGGTG 60

Qy        354 GATGTGTACCCCGCAGGGGTTCAGGGGCTGGTCCCTCACCCCGGGGACCTGGAGAAGAGA 413

Db         61 GGAATATACCCCTCAGGGGTTATTGGACTGGTCCCTCACCTAGGGGACAGGGAGAAGAGA 120

Qy        414 GAGAGTCCCTGTCCCCAAGGAAAATATAACCACCCGCAAAATAGCACCATTTGCTGCACC 473

Db        121 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 180

Qy        474 AAGTGCCACAAAGGTACCTATCTGTACAATGACTGTCCGGGTCCAGGGCGAGACACGGAC 533

Db        181 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 240

Qy        534 TGCAGGGTGTGTGCCCCTGGCACCTACACTGCCTTGGAGAACCATCTCAGACGATGCCTG 593

Db        241 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 300

Qy        594 AGCTGCTCCAGGTGCCGGGACGAAATGTTCCAGGTGGAGATTTCGCCTTGTGTAGTGGAC 653

Db        301 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 360

Qy        654 CGGGACACTGTGTGCGGCTGCAGGAAGAACCAGTACCGGGAATACTGGGGTGAAACTGGC 713

Db        361 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 420

Qy        714 TTCCGGTGTCTGAACTGCAGCCTCTGTCCCAATGGCACAGTGAATATCCCCTGCCAGGAG 773

Db        421 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 480

Qy        774 AGACAGGACACCATCTGCCACTGCCATATGGGCTTCTTTCTTAAAGGCGCCAAGTGCATC 833

Db        481 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 540

Qy        834 TCCTGTCATGATTGTAAGAA---CAAGGAGTGCGAGAAGTTATGTCCAACCCGACCTTCA 890

Db        541 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 600

Qy        891 ACTGGTAAAGACTCTCAGGACCCAGGCACTACAGTACTATTACCCCTGGTGATTGTCTTC 950

Db        601 AATGTTAAGGGCACTGAGGACTCAGGCACCACAGTGCTGTTGCCCCTGGTCATTTTCTTT 660

Qy        951 GGGCTTTGCCTGGCATCCTTCGCCTCTGTCGTCTTAGCATGTCGCTACCAGCGGTGGAAG 1010

Db        661 GGTCTTTGCCTTTTATCCCTCCTCTTCATTGGTTTAATGTATCGCTACCAACGGTGGAAG 720

Qy       1011 CCCAAGCTCTACTCCATCATTTGCGGGCAGTCGACTCTGGTAAAAGAGGGGGAGCCAGAA 1070

Db        721 TCCAAGCTCTACTCCATTGTTTGTGGGAAATCGACACCTGAAAAAGAGGGGGAGCTTGAA 780

Qy       1071 ---------CTCCTGGTCCCGGCCCCAGGCTTCAACCCCACCACCACCATCTGCTTCAGC 1121

Db        781 GGAACTACTACTAAGCCCCTGGCCCCAAACCCAAGCTTCAGTCCCACTCCAGGCTTCACC 840

Qy       1122 TCCACCCCAAGTTCCAGTCCTGTCTCCATTCCCCCTTACATCTCCTGTGACCGGTCCAAC 1181

Db        841 CCCACCCTGGGCTTCAGTCCCGTGCCCAGTTCCACCTTCACCTCCAGCTCCACCTATACC 900
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Qy       1182 TTCGGAG---------CCGTCGCATCTCCCTCCAGCGAGACGGCCCCGCCCCATCTAAAG 1232
Db        901 CCCGGTGACTGTCCCAACTTTGCGGCTCCCCGCAGAGAGGTGGCACCACCCTATCAGGGG 960

Qy       1233 GCTGGCCCCATCCTCCCGGGGCCTCCGGCCTCCACCCACCTCTGTACCCCGGGGCCTCCG 1292
Db        961 GCTGACCCCATCCTTGCGACAGCCCTCGCCTCCGACCCCATCCC---------------- 1004

Qy       1293 GCCTCCACCCACCTCTGTACCCCGGGGCCTCCGGCCTCCACCCACCTCTGCACCCCAGTT 1352
Db       1005 ----------------------------------------------------CAACCCCCTT 1014

Qy       1353 CAGAAGTGGGAAGCCAGCGCCCCCAGCGCCCCCGATCAGCTCGCGGATGCCGACCCCGCG 1412
Db       1015 CAGAAGTGGGAGGACAGCGCCCACA---AGCCACAGAGCCTAGACACTGATGACCCCGCG 1071

Qy       1413 ACCCTGTACGCGGTGGTGGACGGCGTGCCCCCGTCGCGCTGGAAGGAGTTGGTGCGGCGG 1472
Db       1072 ACGCTGTACGCCGTGGTGGAGAACGTGCCCCCGTTGCGCTGGAAGGAATTCGTGCGGCGC 1131

Qy       1473 CTGGGACTGAGCGAGCACGAGATCGAGCGGCTGGAGCTGGAGAACGGGCGCCACCTGCGC 1532
Db       1132 CTAGGGCTGAGCGACCACGAGATCGATCGGCTGGAGCTGCAGAACGGGCGCTGCCTGCGC 1191

Qy       1533 GAGGCGCAGTACAGCATGCTGGCGGCCTGGCGGCGGCGCACGCCGCGCCGCGAGGCCACG 1592
Db       1192 GAGGCGCAATACAGCATGCTGGCGACCTGGAGGCGGCGCACGCCGCGGCGCGAGGCCACG 1251

Qy       1593 CTGGAGCTGCTGGGCCGCGTGCTCAGGGACATGGACCTGCTGGGTTGCCTGGAAAACATA 1652
Db       1252 CTGGAGCTGCTGGGACGCGTGCTCCGCGACATGGACCTGCTGGGCTGCCTGGAGGACATC 1311

Qy       1653 GAGGAGGCGCTGGGTGGCGCCGCCCGCCTCGCGTCCGAGCCCCGCCTTCTCTGGTGA 1709
Db       1312 GAGGAGGCGCTTTGCGGCCCCGCCGCCCTCCCGCCCGCGCCCAGTCTTCTCAGATGA 1368
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RESULT 14
US-10-157-305A-18
; Sequence 18, Application US/10157305A
; Publication No. US20030166099A1
; GENERAL INFORMATION:
; APPLICANT: Sabbadini, Roger A.
; APPLICANT: Surber, Mark W.
; APPLICANT: Neil Berkley
; APPLICANT: Anca M. Segall
; APPLICANT: Robert Klepper
; TITLE OF INVENTION: MINICELL COMPRISING MEMBRANE PROTEINS
; FILE REFERENCE: MPEX.008DV1
; CURRENT APPLICATION NUMBER: US/10/157,305A
; CURRENT FILING DATE: 2002-05-28
; PRIOR APPLICATION NUMBER: 60/293,566
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/359,843
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 10/154,951
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 258
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 1380
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-157-305A-18

Query Match 25.7%; Score 628; DB 12; Length 1380;
Best Local Similarity 70.5%; Pred. No. 3.1e-149;
Matches 954; Conservative 0; Mismatches 310; Indels 90; Gaps 5;

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Qy        377 GGGGCTGGTCCCTCACCCGGGGACCTGGAGAAGAGAGAGAGTCCCTGTCCCCAAGGAAA 436
Db         53 GGGACTGGTCCCTCACCTAGGGGACAGGGAGAAGAGAGATAGTGTGTGTCCCCAAGGAAA 112

Qy        437 ATATAACCACCCGCAAAATAGCACCATTTGCTGCACCAAGTGCCACAAAGGTACCTATCT 496
Db        113 ATATATCCACCCTCAAAATAATTCGATTTGCTGTACCAAGTGCCACAAAGGAACCTACTT 172

Qy        497 GTACAATGACTGTCCGGGTCCAGGGCGAGACACGGACTGCAGGGTGTGTGCCCCTGGCAC 556
Db        173 GTACAATGACTGTCCAGGCCCGGGGCAGGATACGGACTGCAGGGAGTGTGAGAGCGGCTC 232

Qy        557 CTACACTGCCTTGGAGAACCATCTCAGACGATGCCTGAGCTGCTCCAGGTGCCGGGACGA 616
Db        233 CTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTCAGCTGCTCCAAATGCCGAAAGGA 292

Qy        617 AATGTTCCAGGTGGAGATTTCGCCTTGTGTAGTGGACCGGGACACTGTGTGCGGCTGCAG 676
Db        293 AATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGACCGGGACACCGTGTGTGGCTGCAG 352

Qy        677 GAAGAACCAGTACCGGGAATACTGGGGTGAAACTGGCTTCCGGTGTCTGAACTGCAGCCT 736
Db        353 GAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTTTTCCAGTGCTTCAATTGCAGCCT 412

Qy        737 CTGTCCCAATGGCACAGTGAATATCCCCTGCCAGGAGAGACAGGACACCATCTGCCACTG 796
Db        413 CTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAGAAACAGAACACCGTGTGCACCTG 472

Qy        797 CCATATGGGCTTCTTTCTTAAAGGCGCCAAGTGCATCTCCTGTCATGATTGTAAGAA--- 853
Db        473 CCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTCTCCTGTAGTAACTGTAAGAAAAG 532

Qy        854 CAAGGAGTGCGAGAAGTTATGTCCAACCCGACCTTCAACTGGTAAAGACTCTCAGGACCC 913
Db        533 CCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAGAATGTTAAGGGCACTGAGGACTC 592

Qy        914 AGGCACTACAGTACTATTACCCCTGGTGATTGTCTTCGGGCTTTGCCTGGCATCCTTCGC 973
Db        593 AGGCACCACAGTGCTGTTGCCCCTGGTCATTTTCTTTGGTCTTTGCCTTTTATCCCTCCT 652

Qy        974 CTCTGTCGTCTTAGCATGTCGCTACCAGCGGTGGAAGCCCAAGCTCTACTCCATCATTTG 1033
Db        653 CTTCATTGGTTTAATGTATCGCTACCAACGGTGGAAGTCCAAGCTCTACTCCATTGTTTG 712

Qy       1034 CGGGCAGTCGACTCTGGTAAAAGAGGGGGAGCCAGAACTCCT---------GGTCCCGGC 1084
Db        713 TGGGAAATCGACACCTGAAAAAGAGGGGGAGCTTGAAGGAACTACTACTAAGCCCCTGGC 772

Qy       1085 CCCAGGCTTCAACCCCACCACCACCATCTGCTTCAGCTCCACCCCAAGTTCCAGTCCTGT 1144
Db        773 CCCAAACCCAAGCTTCAGTCCCACTCCAGGCTTCACCCCCACCCTGGGCTTCAGTCCCGT 832

Qy       1145 CTCCATTCCCCCTTACATCTCCTGTGACCGGTCCAACTTCGGAGCCG---------TCGC 1195
Db        833 GCCCAGTTCCACCTTCACCTCCAGCTCCACCTATACCCCCGGTGACTGTCCCAACTTTGC 892

Qy       1196 ATCTCCCTCCAGCGAGACGGCCCCGCCCCATCTAAAGGCTGGCCCCATCCTCCCGGGGCC 1255
Db        893 GGCTCCCCGCAGAGAGGTGGCACCACCCTATCAGGGGGCTGACCCCATCCTTGCGACAGC 952

Qy       1256 TCCGGCCTCCACCCACCTCTGTACCCCGGGGCCTCCGGCCTCCACCCACCTCTGTACCCC 1315
Db        953 CCTCGCCTCCGACCCCATCCC---------------------------------------- 973

Qy       1316 GGGGCCTCCGGCCTCCACCCACCTCTGCACCCCAGTTCAGAAGTGGGAAGCCAGCGCCCC 1375
Db        974 --------------------------CAACCCCCTTCAGAAGTGGGAGGACAGCGCCCA 1006

Qy       1376 CAGCGCCCCCGATCAGCTCGCGGATGCCGACCCCGCGACCCTGTACGCGGTGGTGGACGG 1435
Db       1007 CA---AGCCACAGAGCCTAGACACTGATGACCCCGCGACGCTGTACGCCGTGGTGGAGAA 1063

Qy       1436 CGTGCCCCCGTCGCGCTGGAAGGAGTTGGTGCGGCGGCTGGGACTGAGCGAGCACGAGAT 1495
Db       1064 CGTGCCCCCGTTGCGCTGGAAGGAATTCGTGCGGCGCCTAGGGCTGAGCGACCACGAGAT 1123
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Qy       1496 CGAGCGGCTGGAGCTGGAGAACGGGCGCCACCTGCGCGAGGCGCAGTACAGCATGCTGGC 1555
Db       1124 CGATCGGCTGGAGCTGCAGAACGGGCGCTGCCTGCGCGAGGCGCAATACAGCATGCTGGC 1183

Qy       1556 GGCCTGGCGGCGGCGCACGCCGCGCCGCGAGGCCACGCTGGAGCTGCTGGGCCGCGTGCT 1615
Db       1184 GACCTGGAGGCGGCGCACGCCGCGGCGCGAGGCCACGCTGGAGCTGCTGGGACGCGTGCT 1243

Qy       1616 CAGGGACATGGACCTGCTGGGTTGCCTGGAAAACATAGAGGAGGCGCTGGGTGGCGCCGC 1675
Db       1244 CCGCGACATGGACCTGCTGGGCTGCCTGGAGGACATCGAGGAGGCGCTTTGCGGCCCCGC 1303

Qy       1676 CCGCCTCGCGTCCGAGCCCCGCCTTCTCTGGTGA 1709
Db       1304 CGCCCTCCCGCCCGCGCCCAGTCTTCTCAGATAA 1337


RESULT 15
US-10-157-391-18
; Sequence 18, Application US/10157391
; Publication No. US20030166279A1
; GENERAL INFORMATION:
;  APPLICANT: Sabbadini, Roger A.
;  APPLICANT:  Neil Berkley
;  TITLE OF INVENTION: MINICELL-BASED TRANSFECTION
;  FILE REFERENCE: MPEX.008DV14
;  CURRENT APPLICATION NUMBER: US/10/157,391
;  CURRENT FILING DATE:  2002-05-28
;  PRIOR APPLICATION NUMBER: 60/293,566
;  PRIOR FILING DATE: 2001-05-24
;  PRIOR APPLICATION NUMBER: 60/359,843
;  PRIOR FILING DATE: 2002-02-25
;  PRIOR APPLICATION NUMBER: 10/154,951
;  PRIOR FILING DATE: 2002-05-24
;  NUMBER OF SEQ ID NOS: 257
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
;   LENGTH: 1380
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Fusion protein
US-10-157-391-18

  Query Match             25.7%;  Score 628;  DB 12;  Length 1380;
  Best Local Similarity   70.5%;  Pred. No. 3.1e-149;
  Matches  954;  Conservative    0;  Mismatches  310;  Indels   90;  Gaps    5;

Qy        377 GGGGCTGGTCCCTCACCCCGGGGACCTGGAGAAGAGAGAGAGTCCCTGTCCCCAAGGAAA 436
Db         53 GGGACTGGTCCCTCACCTAGGGGACAGGGAGAAGAGAGATAGTGTGTGTCCCCAAGGAAA 112

Qy        437 ATATAACCACCCGCAAAATAGCACCATTTGCTGCACCAAGTGCCACAAAGGTACCTATCT 496
Db        113 ATATATCCACCCTCAAAATAATTCGATTTGCTGTACCAAGTGCCACAAAGGAACCTACTT 172

Qy        497 GTACAATGACTGTCCGGGTCCAGGGCGAGACACGGACTGCAGGGTGTGTGCCCCTGGCAC 556
Db        173 GTACAATGACTGTCCAGGCCCGGGGCAGGATACGGACTGCAGGGAGTGTGAGAGCGGCTC 232

Qy        557 CTACACTGCCTTGGAGAACCATCTCAGACGATGCCTGAGCTGCTCCAGGTGCCGGGACGA 616
Db        233 CTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTCAGCTGCTCCAAATGCCGAAAGGA 292

Qy        617 AATGTTCCAGGTGGAGATTTCGCCTTGTGTAGTGGACCGGGACACTGTGTGCGGCTGCAG 676
Db        293 AATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGACCGGGACACCGTGTGTGGCTGCAG 352

Qy        677 GAAGAACCAGTACCGGGAATACTGGGGTGAAACTGGCTTCCGGTGTCTGAACTGCAGCCT 736
Db        353 GAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTTTTCCAGTGCTTCAATTGCAGCCT 412

Qy        737 CTGTCCCAATGGCACAGTGAATATCCCCTGCCAGGAGAGACAGGACACCATCTGCCACTG 796
Db        413 CTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAGAAACAGAACACCGTGTGCACCTG 472

Qy        797 CCATATGGGCTTCTTTCTTAAAGGCGCCAAGTGCATCTCCTGTCATGATTGTAAGAA--- 853
Db        473 CCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTCTCCTGTAGTAACTGTAAGAAAAG 532

Qy        854 CAAGGAGTGCGAGAAGTTATGTCCAACCCGACCTTCAACTGGTAAAGACTCTCAGGACCC 913
Db        533 CCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAGAATGTTAAGGGCACTGAGGACTC 592

Qy        914 AGGCACTACAGTACTATTACCCCTGGTGATTGTCTTCGGGCTTTGCCTGGCATCCTTCGC 973
Db        593 AGGCACCACAGTGCTGTTGCCCCTGGTCATTTTCTTTGGTCTTTGCCTTTTATCCCTCCT 652

Qy        974 CTCTGTCGTCTTAGCATGTCGCTACCAGCGGTGGAAGCCCAAGCTCTACTCCATCATTTG 1033
Db        653 CTTCATTGGTTTAATGTATCGCTACCAACGGTGGAAGTCCAAGCTCTACTCCATTGTTTG 712

Qy       1034 CGGGCAGTCGACTCTGGTAAAAGAGGGGGAGCCAGAACTCCT---------GGTCCCGGC 1084
Db        713 TGGGAAATCGACACCTGAAAAAGAGGGGGAGCTTGAAGGAACTACTACTAAGCCCCTGGC 772

Qy       1085 CCCAGGCTTCAACCCCACCACCACCATCTGCTTCAGCTCCACCCCAAGTTCCAGTCCTGT 1144
Db        773 CCCAAACCCAAGCTTCAGTCCCACTCCAGGCTTCACCCCCACCCTGGGCTTCAGTCCCGT 832

Qy       1145 CTCCATTCCCCCTTACATCTCCTGTGACCGGTCCAACTTCGGAGCCG---------TCGC 1195
Db        833 GCCCAGTTCCACCTTCACCTCCAGCTCCACCTATACCCCCGGTGACTGTCCCAACTTTGC 892

Qy       1196 ATCTCCCTCCAGCGAGACGGCCCCCGCCCCATCTAAAGGCTGGCCCCATCCTCCCGGGGCC 1255
Db        893 GGCTCCCCGCAGAGAGGTGGCACCACCCTATCAGGGGGCTGACCCCATCCTTGCGACAGC 952

Qy       1256 TCCGGCCTCCACCCACCTCTGTACCCCGGGGCCTCCGGCCTCCACCCACCTCTGTACCCC 1315
Db        953 CCTCGCCTCCGACCCCATCCC---------------------------------------- 973

Qy       1316 GGGGCCTCCGGCCTCCACCCACCTCTGCACCCCAGTTCAGAAGTGGGAAGCCAGCGCCCC 1375
Db        974 ----------------------------CAACCCCCTTCAGAAGTGGGAGGACAGCGCCCA 1006

Qy       1376 CAGCGCCCCCGATCAGCTCGCGGATGCCGACCCCGCGACCCTGTACGCGGTGGTGGACGG 1435
Db       1007 CA---AGCCACAGAGCCTAGACACTGATGACCCCGCGACGCTGTACGCCGTGGTGGAGAA 1063

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Db       1124 CGATCGGCTGGAGCTGCAGAACGGGCGCTGCCTGCGCGAGGCGCAATACAGCATGCTGGC 1183

Qy       1556 GGCCTGGCGGCGGCGCACGCCGCGCCGCGAGGCCACGCTGGAGCTGCTGGGCCGCGTGCT 1615
Db       1184 GACCTGGAGGCGGCGCACGCCGCGGCGCGAGGCCACGCTGGAGCTGCTGGGACGCGTGCT 1243

Qy       1616 CAGGGACATGGACCTGCTGGGTTGCCTGGAAAACATAGAGGAGGCGCTGGGTGGCGCCGC 1675
Db       1244 CCGCGACATGGACCTGCTGGGCTGCCTGGAGGACATCGAGGAGGCGCTTTGCGGCCCCGC 1303

Qy       1676 CCGCCTCGCGTCCGAGCCCCGCCTTCTCTGGTGA 1709
Db       1304 CGCCCTCCCGCCCGCGCCCAGTCTTCTCAGATAA 1337


Search completed: September 15, 2003, 09:29:04
Job time : 454 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 15, 2003, 04:48:19 ; Search time 3429 Seconds
(without alignments)
17294.524 Million cell updates/sec

Title: US-09-970-532-1
Perfect score: 2440
Sequence: 1 ttttttattttttttttctt.....ttaaaaaaaaaaaaaaaaa 2440

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
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5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
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23: em_gss_mus:*
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25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	740.8	30.4	752	14	CB169515	CB169515 RUC603000
	2	630	25.8	630	14	CB438921	CB438921 687819 MA
c	3	627.4	25.7	632	14	CB439280	CB439280 688899 MA
c	4	622.8	25.5	659	14	CB169950	CB169950 CZI603001
	5	616	25.2	631	14	CB455341	CB455341 712479 MA
	6	612.2	25.1	621	14	CB467525	CB467525 733277 MA
c	7	604.6	24.8	611	14	CB456735	CB456735 714023 MA
	8	603	24.7	612	14	CB430512	CB430512 606411 MA
	9	584.6	24.0	591	14	CB437215	CB437215 684659 MA
c	10	559.2	22.9	586	14	CB431220	CB431220 607179 MA
	11	522	21.4	1042	9	AL559050	AL559050 AL559050
c	12	514.2	21.1	519	14	CB536686	CB536686 771726 MA
	13	513	21.0	545	14	CD288290	CD288290 3_P15.abd
	14	511.8	21.0	1096	13	BX377601	BX377601 BX377601
	15	500.4	20.5	502	12	BI898540	BI898540 479493 MA
	16	499.4	20.5	1201	13	BX417436	BX417436 BX417436
c	17	486.4	19.9	493	14	CB536490	CB536490 770877 MA
	18	485.6	19.9	1201	9	AL529836	AL529836 AL529836
	19	483	19.8	1064	13	BX397891	BX397891 BX397891
	20	478.8	19.6	490	12	BM107558	BM107558 511820 MA
	21	475.4	19.5	481	10	BF775926	BF775926 286207 MA
	22	472.4	19.4	474	10	BF775927	BF775927 286208 MA
	23	464.8	19.0	1201	13	BX399373	BX399373 BX399373
	24	461.8	18.9	962	13	BX386459	BX386459 BX386459
	25	457.2	18.7	1201	9	AL577008	AL577008 AL577008
	26	455.8	18.7	1022	13	BX383344	BX383344 BX383344
	27	450.6	18.5	1201	13	BX343994	BX343994 BX343994
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	29	444.6	18.2	477	9	AW315304	AW315304 12506 MAR
	30	444.4	18.2	1070	12	BM546826	BM546826 AGENCOURT
	31	441.8	18.1	1084	13	BX325404	BX325404 BX325404
	32	439.6	18.0	878	14	CD515445	CD515445 AGENCOURT
	33	431.4	17.7	912	9	AL522989	AL522989 AL522989
	34	430.8	17.7	872	13	BU189221	BU189221 AGENCOURT
	35	424.4	17.4	761	9	AU131978	AU131978 AU131978
	36	424.2	17.4	994	12	BM800044	BM800044 AGENCOURT
	37	420.8	17.2	883	13	BU181102	BU181102 AGENCOURT
	38	415.6	17.0	448	10	BF775033	BF775033 285072 MA
	39	411.6	16.9	1201	13	BX394822	BX394822 BX394822
	40	411.4	16.9	859	12	BI870917	BI870917 603394462
	41	411	16.8	1201	13	BX420583	BX420583 BX420583
	42	410.4	16.8	872	12	BI769006	BI769006 603058164
	43	410.2	16.8	859	9	AU124446	AU124446 AU124446
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ALIGNMENTS

RESULT 1
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LOCUS CB169515 752 bp mRNA linear EST 30-JAN-2003
DEFINITION RUC603000712.R1 CSEQFXN20 testes Bos taurus cDNA, mRNA sequence.
ACCESSION CB169515
VERSION CB169515.1 GI:28155642
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 752)
AUTHORS Adelson,D.L. and Gill,C.A.
TITLE Bovine ESTs (Adelson and Gill)
JOURNAL Unpublished
COMMENT Contact: David L. Adelson
Animal Breeding and Genetics
Texas A&M University
Animal Science Dept., TAMU-2471, College Station, TX 77843-2471, USA
Tel: 9798452616
Fax: 9798456970
Email: david.adelson@tamu.edu.
FEATURES Location/Qualifiers
source 1. .752
/organism="Bos taurus"

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                     /mol_type="mRNA"
                     /db_xref="taxon:9913"
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                     NotI; Site_2: EcoRI; sequence 5' of the insert
                     (5'-NNN. . .NNNinsert)
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                     the inserts (AAGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG.
                     normalized Rd 1 library, sequenced 3' with M13R primer."
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ORIGIN

  Query Match           30.4%;  Score 740.8;  DB 14;  Length 752;
  Best Local Similarity   99.7%;  Pred. No. 4.4e-117;
  Matches  742;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

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Db        752 GGTGGCGCCGCCCGCCTCGCGTCCGAGCCCCGCCTTCTCCGGTGAAGCCCCGCCCCTCCG 693

Qy       1725 ACTGCGGGCCTCCCCGCCCTGCAGACGGCTGCTTCCTTCCTGTGCCAGGCAGCCCGGAAG 1784
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Db        692 ACTGCGGGCCTCCCCGCCCTGCAGACGGCTGCTTCCTTCCTGTGCCAGGCAGCCCGGAAG 633

Qy       1785 GATCTGCGAGATGCCCTGTGGACCTCCTGTTTTGTTTTGTTTTTTTTCTGGAGAGGAAGTC 1844
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Db        632 GATCTGCGAGATGCCCTGTGGACCTCCTGTTTTGTTTTGTTTTTTTTCTGGAGAGGAAGTC 573

Qy       1845 TTGGAGGAGCAGGCACGATCTGGCAGCCACTGACCTGGTGCTACTCACTCAGTGTACATA 1904
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        572 TTGGAGGAGCAGGCACGATCTGGCAGCCACTGACCTGGTGCTACTCACTCAGTGTACATA 513

Qy       1905 GCTTTTCTCAGCTGCCTGAGTGTGTGTCTGTGTGTAGTGTGTGTCTGCGTGCAGTGCGTG 1964
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Db        512 GCTTTTCTCAGCTGCCTGAGTGTGTGTCTGTGTGTAGTGTGTGTCTGCGTGCAGTGCGTG 453

Qy       1965 TGTTTGTGTCTCTGTATGTGCGTCTGTGTGATGTGGAGTGTGTGTACTCGTGAGAGAGGC 2024
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Db        452 TGTTTGTGTCTCTGTATGTGCGTCTGTGTGATGTGGAGTGTGTGTACTCGTGAGAGAGGC 393

Qy       2025 CGAGTGTGCCCGGAGCCCAAGGCAGTGGTTGCGAAGATGAGGGGCGCCCTGCCTTATTGC 2084
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Db        392 CGAGTGTGCCCGGAGCCCAAGGCAGCGGTTGCGAAGATGAGGGGCGCCCTGCCTTATTGC 333

Qy       2085 CTGTTTTTTGGGCTTGGAGAACTCAGCAAGGCGACTTGGGGAACCTACGTCGGTCCCTGA 2144
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Db        332 CTGTTTTTTGGGCTTGGAGAACTCAGCAAGGCGACTTGGGGAACCTACGTCGGTCCCTGA 273

Qy       2145 GCCGGTTTCGCAGTAGATAAGCCATCTTTGTATCCACTCTGCACATCCACTCATCCACTC 2204
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Db        272 GCCGGTTTCGCAGTAGATAAGCCATCTTTGTATCCACTCTGCACATCCACTCATCCACTC 213

Qy       2205 TGTACACTAATAGAAACTTTGTTGCCCTGCCTGGACCAGCTGAACTGTCCCCAGGCAGCG 2264
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Qy       2265 GGGGAGCACAGAAAAATGGGGCCTCCCAAGGGAGCTAGCTGTTCAGTTCAGTTCAGTCGC 2324
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Qy       2325 TCAGTCGTGTCCGACTCTTTGCGACCCTGTGAATCGCAGGGACTTCTGTAAATACACTAA 2384
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Qy       2385 AATCTTCCAATTAAAGCTCTGCCC 2408
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Db         32 AATCTTCCAATTAAAGCTCTGCCC 9


RESULT 2
CB438921
LOCUS       CB438921                630 bp    mRNA    linear   EST 25-MAR-2003
DEFINITION  687819 MARC 6BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION   CB438921
VERSION     CB438921.1  GI:29223414
KEYWORDS    EST.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 630)
  AUTHORS   Smith,T.P.L., Roberts,A.J., Echternkamp,S.E., Chitko-McKown,C.G.,
            Wray,J.E. and Keele,J.W.
  TITLE     A second set of bovine ESTs from pooled-tissue normalized libraries
  JOURNAL   Unpublished
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called with phred v0.020425.c and
            trimmed with the aid of the trim_alt option. Vector identified with
            cross_match v0.990329.
            Plate: FQY8044  row: N  column: 10
            Seq primer: GTAATACGACTCACTATAGGG.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9913"
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                     /lab_host="DH10B"
                     /clone_lib="MARC 6BOV"
                     /note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: NotI;
                     Library made with RNA pooled from multiple tissues
                     including liver, lung, hypothalamus, pituitary, and
                     placenta/endometrium."
BASE COUNT       89 a    211 c    215 g    115 t
ORIGIN

  Query Match           25.8%;  Score 630;  DB 14;  Length 630;
  Best Local Similarity   100.0%;  Pred. No. 4.6e-98;
  Matches  630;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy       1370 CGCCCCCAGCGCCCCCGATCAGCTCGCGGATGCCGACCCCGCGACCCTGTACGCGGTGGT 1429
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1430 GGACGGCGTGCCCCCGTCGCGCTGGAAGGAGTTGGTGCGGCGGCTGGGACTGAGCGAGCA 1489
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Qy       1490 CGAGATCGAGCGGCTGGAGCTGGAGAACGGGCGCCACCTGCGCGAGGCGCAGTACAGCAT 1549
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Qy       1550 GCTGGCGGCCTGGCGGCGGCGCACGCCGCGCCGCGAGGCCACGCTGGAGCTGCTGGGCCG 1609
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Qy       1610 CGTGCTCAGGGACATGGACCTGCTGGGTTGCCTGGAAAACATAGAGGAGGCGCTGGGTGG 1669
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Qy       1670 CGCCGCCCGCCTCGCGTCCGAGCCCCGCCTTCTCTGGTGAAGCCCCGCCCCTCCGACTGC 1729
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Db        481 GCGAGATGCCCTGTGGACCTCCTGTTTTGTTTTGTTTTTTTCTGGAGAGGAAGTCTTGGA 540

Qy       1850 GGAGCAGGCACGATCTGGCAGCCACTGACCTGGTGCTACTCACTCAGTGTACATAGCTTT 1909
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Qy       1910 TCTCAGCTGCCTGAGTGTGTGTCTGTGTGT 1939
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RESULT 3
CB439280/c
LOCUS       CB439280                632 bp    mRNA    linear   EST 25-MAR-2003
DEFINITION  688899 MARC 6BOV Bos taurus cDNA 3', mRNA sequence.
ACCESSION   CB439280
VERSION     CB439280.1  GI:29224127
KEYWORDS    EST.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 632)
  AUTHORS   Smith,T.P.L., Roberts,A.J., Echternkamp,S.E., Chitko-McKown,C.G.,
            Wray,J.E. and Keele,J.W.
  TITLE     A second set of bovine ESTs from pooled-tissue normalized libraries
  JOURNAL   Unpublished
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called with phred v0.020425.c and
            trimmed with the aid of the trim_alt option. Vector identified with
            cross_match v0.990329.
            Plate: FQY8044  row: N  column: 10
            Seq primer: TAGAAGGCACAGTCGAGG.
FEATURES             Location/Qualifiers
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                     /organism="Bos taurus"
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                     /db_xref="taxon:9913"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /clone_lib="MARC 6BOV"
                     /note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: NotI;
                     Library made with RNA pooled from multiple tissues
                     including liver, lung, hypothalamus, pituitary, and
                     placenta/endometrium."
BASE COUNT      172 a    185 c    154 g    121 t
ORIGIN

  Query Match             25.7%;  Score 627.4;  DB 14;  Length 632;
  Best Local Similarity   99.8%;  Pred. No. 1.3e-97;
  Matches  628;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1766 GTGCCAGGCAGCCCGGAAGGATCTGCGAGATGCCCTGTGGACCTCCTGTTTTGTTTTGTT 1825
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        632 GTGCCAGGCAGCCCGGAAGGATCTGCGAGATGCCCTGTGGACCTCCTGTTTTGTTTTGTT 573

Qy       1826 TTTTTCTGGAGAGGAAGTCTTGGAGGAGCAGGCACGATCTGGCAGCCACTGACCTGGTGC 1885
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        572 TTTTTCTGGAGAGGAAGTCTTGGAGGAGCAGGCACGATCTGGCAGCCACTGACCTGGTGC 513

Qy       1886 TACTCACTCAGTGTACATAGCTTTTCTCAGCTGCCTGAGTGTGTGTCTGTGTGTAGTGTG 1945
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        512 TACTCACTCAGTGTACATAGCTTTTCTCAGCTGCCTGAGTGTGTGTCTGTGTGTAGTGTG 453

Qy       1946 TGTCTGCGTGCAGTGCGTGTGTTTGTGTCTCTGTATGTGCGTCTGTGTGATGTGGAGTGT 2005
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        452 TGTCTGCGTGCAGTGCGTGTGTTTGTGTCTCTGTATGTGCGTCTGTGTGATGTGGAGTGT 393

Qy       2006 GTGTACTCGTGAGAGAGGCCGAGTGTGCCCGGAGCCCAAGGCAGTGGTTGCGAAGATGAG 2065
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 GTGTACTCGTGAGAGAGGCCGAGTGTGCCCGGAGCCCAAGGCAGTGGTTGCGAAGATGAG 333

Qy       2066 GGGCGCCCTGCCTTATTGCCTGTTTTTTGGGCTTGGAGAACTCAGCAAGGCGACTTGGGG 2125
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 GGGCGCCCTGCCTTATTGCCTGTTTTTTGGGCTTGGAGAACTCAGCAAGGCGACTTGGGG 273

Qy       2126 AACCTACGTCGGTCCCTGAGCCGGTTTCGCAGTAGATAAGCCATCTTTGTATCCACTCTG 2185
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 AACCTACGTCGGTCCCTGAGCCGGTTTCGCAGTAGATAAGCCATCTTTGTATCCACTCTG 213

Qy       2186 CACATCCACTCATCCACTCTGTACACTAATAGAAACTTTGTTGCCCTGCCTGGACCAGCT 2245
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 CACATCCACTCATCCACTCTGTACACTAATAGAAACTTTGTTGCCCTGCCTGGACCAGCT 153

Qy       2246 GAACTGTCCCCAGGCAGCGGGGGAGCACAGAAAAATGGGGCCTCCCAAGGGAGCTAGCTG 2305
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 GAACTGTCCCCAGGCAGCGGGGGAGCACAGAAAAATGGGGCCTCCCAAGGGAGCTAGCTG 93

Qy       2306 TTCAGTTCAGTTCAGTCGCTCAGTCGTGTCCGACTCTTTGCGACCCTGTGAATCGCAGGG 2365
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 TTCAGTTCAGTTCAGTCGCTCAGTCGTGTCCGACTCTTTGCGACCCTGTGAATCGCAGGG 33

Qy       2366 ACTTCTGTAAATACACTAAAATCTTCCAA 2394
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Db         32 ACTTCTGTAAATACACTAAAATCTCCCAA 4


RESULT 4
CB169950/c
LOCUS       CB169950                659 bp    mRNA    linear   EST 30-JAN-2003
DEFINITION  CZI603001005.R1 CSEQFXN21 testes Bos taurus cDNA, mRNA sequence.
ACCESSION   CB169950
VERSION     CB169950.1  GI:28156078
KEYWORDS    EST.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 659)
  AUTHORS   Adelson,D.L. and Gill,C.A.
  TITLE     Bovine ESTs (Adelson and Gill)
  JOURNAL   Unpublished
COMMENT     Contact: David L. Adelson
            Animal Breeding and Genetics
            Texas A&M University
            Animal Science Dept., TAMU-2471, College Station, TX 77843-2471,
            USA
            Tel: 9798452616
            Fax: 9798456970
            Email: david.adelson@tamu.edu.
FEATURES             Location/Qualifiers
     source          1. .659
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9913"
                     /tissue_type="testes"
                     /clone_lib="CSEQFXN21 testes"
                     /note="Organ: testes; Vector: pBluescript SK+; Site_1:
                     NotI; Site_2: EcoRI; sequence 5' of the insert
                     (5'-NNN. . .NNNinsert)
                     GCGAATTGGAGCTCCACCGCGGTGGCGGCCGCGGCTCGAG. Sequence 3' of
                     the inserts (AAGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG.
                     normalized Rd 2 library, sequenced 3' with M13R primer."
BASE COUNT      179 a    192 c    159 g    129 t
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ORIGIN

Query Match 25.5%; Score 622.8; DB 14; Length 659;
Best Local Similarity 98.5%; Pred. No. 7.7e-97;
Matches 640; Conservative 0; Mismatches 7; Indels 3; Gaps 1;

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Qy       1769 CCAGGCAGCCCGGAAGGATCTGCGAGATGCCCTGTGGACCTCCTGTTTTGTTTTGTTTTT 1828
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Db        659 CCAGGCAGCCCGGAAGGATCTGCGAGATGCCCTGTGGACCTCCTGTTTTGTTTTGTTGTT 600

Qy       1829 TTCT---GGAGAGGAAGTCTTGGAGGAGCAGGCACGATCTGGCAGCCACTGACCTGGTGC 1885
                |  |   |  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        599 GTTTCTGGAGTAGGAAGTCTTGGAGGAGCAGGCACGATCTGGCAGCCACTGACCTGGTGC 540

Qy       1886 TACTCACTCAGTGTACATAGCTTTTCTCAGCTGCCTGAGTGTGTGTCTGTGTGTAGTGTG 1945
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Db        539 TACTCACTCAGTGTACATAGCTTTTCTCAGCTGCCTGAGTGTGTGTCTGTGTGTAGTGTG 480

Qy       1946 TGTCTGCGTGCAGTGCGTGTGTTTGTGTCTCTGTATGTGCGTCTGTGTGATGTGGAGTGT 2005
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Db        479 TGTCTGCGTGCAGTGCGTGTGTTTGTGTCTCTGTATGTGCGTCTGTGTGATGTGGAGTGT 420

Qy       2006 GTGTACTCGTGAGAGAGGCCGAGTGTGCCCGGAGCCCAAGGCAGTGGTTGCGAAGATGAG 2065
             ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        419 GTGTACTCGTGAGAGAGGCCGAGTGTGCCCGGAGCCCAAGGCAGCGGTTGCGAAGATGAG 360

Qy       2066 GGGCGCCCTGCCTTATTGCCTGTTTTTTGGGCTTGGAGAACTCAGCAAGGCGACTTGGGG 2125
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        359 GGGCGCCCTGCCTTATTGCCTGTTTTTTGGGCTTGGAGAACTCAGCAAGGCGACTTGGGG 300

Qy       2126 AACCTACGTCGGTCCCTGAGCCGGTTTCGCAGTAGATAAGCCATCTTTGTATCCACTCTG 2185
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Db        299 AACCTACGTCGGTCCCTGAGCCGGTTTCGCAGTAGATAAGCCATCTTTGTATCCACTCTG 240

Qy       2186 CACATCCACTCATCCACTCTGTACACTAATAGAAACTTTGTTGCCCTGCCTGGACCAGCT 2245
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        239 CACATCCACTCATCCACTCTGTACACTAATAGAAACTTTGTTGCCCTGCCTGGACCAGCT 180

Qy       2246 GAACTGTCCCCAGGCAGCGGGGGAGCACAGAAAAATGGGGCCTCCCAAGGGAGCTAGCTG 2305
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Db        179 GAACTGTCCCCAGGCAGCGGGGGAGCACAGAAAAATGGGGCCTCCCAAGGGAGCTAGCTG 120

Qy       2306 TTCAGTTCAGTTCAGTCGCTCAGTCGTGTCCGACTCTTTGCGACCCTGTGAATCGCAGGG 2365
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Db        119 TTCAGTTCAGTTCAGTCGCTCAGTCGTGTCCGACTCTTTGCGACCCTGTGAATCGCAGGG 60

Qy       2366 ACTTCTGTAAATACACTAAAATCTTCCAATTAAAGCTCTGCCCTGGAGGG 2415
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Db          59 ACTTCTGTAAATACACTAAAATCTTCCAATTAAAGCTCTGCCCTGGAGGG 10
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RESULT 5
CB455341
LOCUS CB455341 631 bp mRNA linear EST 26-MAR-2003
DEFINITION 712479 MARC 6BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION CB455341
VERSION CB455341.1 GI:29261723
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 631)
AUTHORS Smith,T.P.L., Roberts,A.J., Echternkamp,S.E., Chitko-McKown,C.G., Wray,J.E. and Keele,J.W.
TITLE A second set of bovine ESTs from pooled-tissue normalized libraries
JOURNAL Unpublished
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified with cross_match v0.990329.
Plate: FQY8070 row: E column: 3
Seq primer: GTAATACGACTCACTATAGGG.
FEATURES Location/Qualifiers
source 1. .631
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 6BOV"
/note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: NotI; Library made with RNA pooled from multiple tissues including liver, lung, hypothalamus, pituitary, and placenta/endometrium."
BASE COUNT 99 a 174 c 193 g 164 t 1 others
ORIGIN

Query Match 25.2%; Score 616; DB 14; Length 631;
Best Local Similarity 99.0%; Pred. No. 1.1e-95;
Matches 619; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy       1644 GAAAACATAGAGGAGGCGCTGGGTGGCGCCGCCCGCCTCGCGTCCGAGCCCCGCCTTCTC 1703
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Db          7 GGAAACATATAGGAGGCGCTGGGTGGCGCCGCCCGCCTCGCGTCCGAGCCCCGCCTTCTC 66

Qy       1704 TGGTGAAGCCCCGCCCCTCCGACTGCGGGCCTCCCCGCCCTGCAGACGGCTGCTTCCTTC 1763
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 TGGTGAAGCCCCGCCCCTCCGACTGCGGGCCTCCCCGCCCTGCAGACGGCTGCTTCCTTC 126

Qy       1764 CTGTGCCAGGCAGCCCGGAAGGATCTGCGAGATGCCCTGTGGACCTCCTGTTTTGTTTTG 1823
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  ||
Db        127 CTGTGCCAGGCAGCCCGGAAGGATCTGCGAGATGCCCTGTGGACCTCCTGTTTTGTGGTG 186

Qy       1824 TTTTTTTCTGGAGAGGAAGTCTTGGAGGAGCAGGCACGATCTGGCAGCCACTGACCTGGT 1883
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 TTTTTTTCTGGAGAGGAAGTCTTGGAGGAGCAGGCACGATCTGGCAGCCACTGACCTGGT 246

Qy       1884 GCTACTCACTCAGTGTACATAGCTTTTCTCAGCTGCCTGAGTGTGTGTCTGTGTGTAGTG 1943
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCTACTCACTCAGTGTACATAGCTTTTCTCAGCTGCCTGAGTGTGTGTCTGTGTGTAGTG 306

Qy       1944 TGTGTCTGCGTGCAGTGCGTGTGTTTGTGTCTCTGTATGTGCGTCTGTGTGATGTGGAGT 2003
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 TGTGTCTGCGTGCAGTGCGTGTGTTTGTGTCTCTGTATGTGCGTCTGTGTGATGTGGAGT 366

Qy       2004 GTGTGTACTCGTGAGAGAGGCCGAGTGTGCCCGGAGCCCAAGGCAGTGGTTGCGAAGATG 2063
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 GTGTGTACTCGTGAGAGAGGCCGAGTGTGCCCGGAGCCCAAGGCAGTGGTTGCGAAGATG 426

Qy       2064 AGGGGCGCCCTGCCTTATTGCCTGTTTTTTGGGCTTGGAGAACTCAGCAAGGCGACTTGG 2123
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 AGGGGCGCCCTGCCTTATTGCCTGTTTTTTGGGCTTGGAGAACTCAGCAAGGCGACTTGN 486

Qy       2124 GGAACCTACGTCGGTCCCTGAGCCGGTTTCGCAGTAGATAAGCCATCTTTGTATCCACTC 2183
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 GGAACCTACGTCGGTCCCTGAGCCGGTTTCGCAGTAGATAAGCCATCTTTGTATCCACTC 546

Qy       2184 TGCACATCCACTCATCCACTCTGTACACTAATAGAAACTTTGTTGCCCTGCCTGGACCAG 2243
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 TGCACATCCACTCATCCACTCTGTACACTAATAGAAACTTTGTTGCCCTGCCTGGACCAG 606

Qy       2244 CTGAACTGTCCCCAGGCAGCGGGGG 2268
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Db        607 CTGAACTGTCCCCAAGCAGCGGGGG 631
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RESULT 6
CB467525
LOCUS CB467525 621 bp mRNA linear EST 26-MAR-2003

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DEFINITION  733277 MARC 6BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION   CB467525
VERSION     CB467525.1  GI:29273910
KEYWORDS    EST.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 621)
  AUTHORS   Smith,T.P.L., Roberts,A.J., Echternkamp,S.E., Chitko-McKown,C.G.,
            Wray,J.E. and Keele,J.W.
  TITLE     A second set of bovine ESTs from pooled-tissue normalized libraries
  JOURNAL   Unpublished
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called with phred v0.020425.c and
            trimmed with the aid of the trim_alt option. Vector identified with
            cross_match v0.990329.
            Plate: LAM8011  row: F  column: 9
            Seq primer: GTAATACGACTCACTATAGGG.
FEATURES             Location/Qualifiers
     source          1. .621
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9913"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /clone_lib="MARC 6BOV"
                     /note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: NotI;
                     Library made with RNA pooled from multiple tissues
                     including liver, lung, hypothalamus, pituitary, and
                     placenta/endometrium."
BASE COUNT      117 a    152 c    177 g    173 t      2 others
ORIGIN

  Query Match           25.1%;  Score 612.2;  DB 14;  Length 621;
  Best Local Similarity  99.2%;  Pred. No. 5.2e-95;
  Matches  614;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       1798 CCCTGTGGACCTCCTGTTTTGTTTTGTTTTTTTCTGGAGAGGAAGTCTTGGAGGAGCAGG 1857
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Db          1 CCCTGTGGACCTCCTGTTTTGTTTTGTTTTTTTCTGGAGAGGAAGTCTTGGAGGAGCAGG 60

Qy       1858 CACGATCTGGCAGCCACTGACCTGGTGCTACTCACTCAGTGTACATAGCTTTTCTCAGCT 1917
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACGATCTGGCAGCCACTGACCTGGTGCTACTCACTCAGTGTACATAGCTTTTCTCAGCT 120

Qy       1918 GCCTGAGTGTGTGTCTGTGTGTAGTGTGTGTCTGCGTGCAGTGCGTGTGTTTGTGTCTCT 1977
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCTGAGTGTGTGTCTGTGTGTAGTGTGTGTCTGCGTGCAGTGCGTGTGTTTGTGTCTCT 180

Qy       1978 GTATGTGCGTCTGTGTGATGTGGAGTGTGTGTACTCGTGAGAGAGGCCGAGTGTGCCCGG 2037
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTATGTGCGTCTGTGTGATGTGGAGTGTGTGTACTCGTGAGAGAGGCCGAGTGTGCCCGG 240

Qy       2038 AGCCCAAGGCAGTGGTTGCGAAGATGAGGGGCGCCCTGCCTTATTGCCTGTTTTTTGGGC 2097
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGCCCAAGGCAGCGGTTGCGAAGATGAGGGGCGCCCTGCCTTATTGCCTGTTTTTTGGGC 300

Qy       2098 TTGGAGAACTCAGCAAGGCGACTTGGGGAACCTACGTCGGTCCCTGAGCCGGTTTCGCAG 2157
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Db        301 TTGGAGAACTCAGCAAGGCGACTTGGGGAACCTACGTCGGTCCCTGAGCCGGTTTCGCAG 360

Qy       2158 TAGATAAGCCATCTTTGTATCCACTCTGCACATCCACTCATCCACTCTGTACACTAATAG 2217
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Db        361 TAGATAAGCCATCTTTGTATCCACTCTGCACATCCACTCATCCACTCTGTACACTAATAG 420

Qy       2218 AAACTTTGTTGCCCTGCCTGGACCAGCTGAACTGTCCCCAGGCAGCGGGGGAGCACAGAA 2277
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Db        421 AAACTNTGTTGCCCTGCCTGGACCAGCTGAACTGTCCCCAGGCAGCGGGGGAGCACAGAA 480

Qy       2278 AAATGGGGCCTCCCAAGGGAGCTAGCTGTTCAGTTCAGTTCAGTCGCTCAGTCGTGTCCG 2337
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Db        481 AAATGGGGCCTCCCAAGGGAGCTAGCTGTTCAGTTCAGTTCAGTCGCTCAGTCGTGTCCG 540

Qy       2338 ACTCTTTGCGACCCTGTGAATCGCAGGGACTTCTGTAAATACACTAAAATCTTCCAATTA 2397
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Db        541 ACTCTTTGCGACCCTGTGAATCGCNAGGACTTCTGTAAATACACTAAAATCTTCCAATTA 600

Qy       2398 AAGCTCTGCCCTGGAGGGA 2416
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Db        601 AAGCTCTGCCCTGTAGGGA 619


RESULT 7
CB456735/c
LOCUS       CB456735                611 bp    mRNA    linear   EST 26-MAR-2003
DEFINITION  714023 MARC 6BOV Bos taurus cDNA 3', mRNA sequence.
ACCESSION   CB456735
VERSION     CB456735.1  GI:29263117
KEYWORDS    EST.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 611)
  AUTHORS   Smith,T.P.L., Roberts,A.J., Echternkamp,S.E., Chitko-McKown,C.G.,
            Wray,J.E. and Keele,J.W.
  TITLE     A second set of bovine ESTs from pooled-tissue normalized libraries
  JOURNAL   Unpublished
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called with phred v0.020425.c and
            trimmed with the aid of the trim_alt option. Vector identified with
            cross_match v0.990329.
            Plate: FQY8070  row: E  column: 3
            Seq primer: TAGAAGGCACAGTCGAGG.
FEATURES             Location/Qualifiers
     source          1. .611
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9913"
                     /tissue_type="pooled"
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                     /clone_lib="MARC 6BOV"
                     /note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: NotI;
                     Library made with RNA pooled from multiple tissues
                     including liver, lung, hypothalamus, pituitary, and
                     placenta/endometrium."
BASE COUNT      170 a    178 c    143 g    120 t
ORIGIN

  Query Match           24.8%;  Score 604.6;  DB 14;  Length 611;
  Best Local Similarity  99.3%;  Pred. No. 1e-93;
  Matches  607;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1818 GTTTTGTTTTTTTTCTGGAGAGGAAGTCTTGGAGGAGCAGGCACGATCTGGCAGCCACTGA 1877
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         611 GTTTTGTTTTTTTTCTGGAGAGGAAGTCTTGGAGGAGCAGGCACGATCTGGCAGCCACTGA 552

Qy       1878 CCTGGTGCTACTCACTCAGTGTACATAGCTTTTCTCAGCTGCCTGAGTGTGTGTCTGTGT 1937
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         551 CCTGGTGCTACTCACTCAGTGTACATAGCTTTTCTCAGCTGCCTGAGTGTGTGTCTGTGT 492

Qy       1938 GTAGTGTGTGTCTGCGTGCAGTGCGTGTGTTTGTGTCTCTGTATGTGCGTCTGTGTGATG 1997
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        491 GTAGTGTGTGTCTGCGTGCAGTGCGTGTGTTTGTGTCTCTGTATGTGCGTCTGTGTGATG 432

Qy       1998 TGGAGTGTGTGTACTCGTGAGAGAGGCCGAGTGTGCCCGGAGCCCAAGGCAGTGGTTGCG 2057
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        431 TGGAGTGTGTGTACTCGTGAGAGAGGCCGAGTGTGCCCGGAGCCCAAGGCAGTGGTTGCG 372

Qy       2058 AAGATGAGGGGCGCCCTGCCTTATTGCCTGTTTTTTGGGCTTGGAGAACTCAGCAAGGCG 2117
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        371 AAGATGAGGGGCGCCCTGCCTTATTGCCTGTTTTTTGGGCTTGGAGAACTCAGCAAGGCG 312

Qy       2118 ACTTGGGGAACCTACGTCGGTCCCTGAGCCGGTTTCGCAGTAGATAAGCCATCTTTGTAT 2177
              |||||||||||| |||||||||| ||||||||||||||||||||||||||||||||||||
Db        311 ACTTGGGGAACTTACGTCGGTCCTTGAGCCGGTTTCGCAGTAGATAAGCCATCTTTGTAT 252

Qy       2178 CCACTCTGCACATCCACTCATCCACTCTGTACACTAATAGAAACTTTGTTGCCCTGCCTG 2237
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        251 CCACTCTGCACATCCACTCATCCACTCTGTACACTAATAGAAACTTTGTTGCCCTGCCTG 192

Qy       2238 GACCAGCTGAACTGTCCCCAGGCAGCGGGGGAGCACAGAAAAATGGGGCCTCCCAAGGGA 2297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        191 GACCAGCTGAACTGTCCCCAGGCAGCGGGGGAGCACAGAAAAATGGGGCCTCCCAAGGGA 132

Qy       2298 GCTAGCTGTTCAGTTCAGTTCAGTCGCTCAGTCGTGTCCGACTCTTTGCGACCCTGTGAA 2357
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        131 GCTAGCTGTTCAGTTCAGTTCAGTCGCTCAGTCGTGTCCGACTCTTTGCGACCCTGTGAA 72

Qy       2358 TCGCAGGGACTTCTGTAAATACACTAAAATCTTCCAATTAAAGCTCTGCCCTGGAGGGAC 2417
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          71 TCGCAGGGACTTCTGTAAATACACTAAAATCTTCCAATTAAAGCTCTGCCCTGGAGGGAC 12

Qy       2418 TGGTTAAAAAA 2428
              ||| | |||||
Db          11 TGGCTGAAAAA 1
```

RESULT 8
CB430512

```
LOCUS       CB430512                612 bp    mRNA    linear   EST 25-MAR-2003
DEFINITION  606411 MARC 6BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION   CB430512
VERSION     CB430512.1  GI:29206632
KEYWORDS    EST.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 612)
  AUTHORS   Smith,T.P.L., Roberts,A.J., Echternkamp,S.E., Chitko-McKown,C.G.,
            Wray,J.E. and Keele,J.W.
  TITLE     A second set of bovine ESTs from pooled-tissue normalized libraries
  JOURNAL   Unpublished
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called with phred v0.020425.c and
            trimmed with the aid of the trim_alt option. Vector identified with
            cross_match v0.990329.
            Plate: FQY8024  row: F  column: 24
            Seq primer: GTAATACGACTCACTATAGGG.
FEATURES             Location/Qualifiers
     source          1. .612
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9913"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /clone_lib="MARC 6BOV"
                     /note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: NotI;
                     Library made with RNA pooled from multiple tissues
                     including liver, lung, hypothalamus, pituitary, and
                     placenta/endometrium."
BASE COUNT      113 a    151 c    171 g    176 t      1 others
ORIGIN
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  Query Match             24.7%;  Score 603;  DB 14;  Length 612;
  Best Local Similarity   99.0%;  Pred. No. 2e-93;
  Matches  606;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       1798 CCCTGTGGACCTCCTGTTTTGTTTTGTTTTTTTCTGGAGAGGAAGTCTTGGAGGAGCAGG 1857
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCCTGTGGACCTCCTGTTTTGTTTTGTTTTTTTCTGGAGAGGAAGTCTTGGAGGAGCAGG 60

Qy       1858 CACGATCTGGCAGCCACTGACCTGGTGCTACTCACTCAGTGTACATAGCTTTTCTCAGCT 1917
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACGATCTGGCAGCCACTGACCTGGTGCTACTCACTCAGTGTACATAGCTTTTCTCAGCT 120

Qy       1918 GCCTGAGTGTGTGTCTGTGTGTAGTGTGTGTCTGCGTGCAGTGCGTGTGTTTGTGTCTCT 1977
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCTGAGTGTGTGTCTGTGTGTAGTGTGTGTCTGCGTGCAGTGCGTGTGTTTGTGTCTCT 180

Qy       1978 GTATGTGCGTCTGTGTGATGTGGAGTGTGTGTACTCGTGAGAGAGGCCGAGTGTGCCCGG 2037
              || ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        181 GTGTGTGCGTCTGTGTGATGTGGAGTGTGTGTACTCGTGAGATAGGCCGAGTGTGCCCGG 240

Qy       2038 AGCCCAAGGCAGTGGTTGCGAAGATGAGGGGCGCCCTGCCTTATTGCCTGTTTTTTGGGC 2097
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGCCCAAGGCAGCGGTTGCGAAGATGAGGGGCGCCCTGCCTTATTGCCTGTTTTTTGGGC 300

Qy       2098 TTGGAGAACTCAGCAAGGCGACTTGGGGAACCTACGTCGGTCCCTGAGCCGGTTTCGCAG 2157
              |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTGGAGAACTCATCAAGGCGACTTGGGGAACCTACGTCGGTCCCTGAGCCGGTTTCGCAG 360

Qy       2158 TAGATAAGCCATCTTTGTATCCACTCTGCACATCCACTCATCCACTCTGTACACTAATAG 2217
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TAGATAAGCCATCTTTGTATCCACTCTGCACATCCACTCATCCACTCTGTACACTAATAG 420

Qy       2218 AAACTTTGTTGCCCTGCCTGGACCAGCTGAACTGTCCCCAGGCAGCGGGGGAGCACAGAA 2277
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        421 AAACTTTGTTGCCCTGCCTGGACCATCTGAACTGTCCCCAGGCAGCGGGGGAGCACAGAA 480

Qy       2278 AAATGGGGCCTCCCAAGGGAGCTAGCTGTTCAGTTCAGTTCAGTCGCTCAGTCGTGTCCG 2337
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AAATGGGGCCTCCCAAGGGAGCTAGCTGTTCAGTTCAGTTCAGTCGCTCAGTCGTGTCCG 540

Qy       2338 ACTCTTTGCGACCCTGTGAATCGCAGGGACTTCTGTAAATACACTAAAATCTTCCAATTA 2397
              ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db        541 ACTCTTTGCGACCCTGTGAATCGCANGGACTTCTGTAAATACACTAAAATCTTCCAATTA 600

Qy       2398 AAGCTCTGCCCT 2409
              ||||||||||||
Db        601 AAGCTCTGCCCT 612
```

RESULT 9
CB437215

```
LOCUS       CB437215                591 bp    mRNA    linear   EST 25-MAR-2003
DEFINITION  684659 MARC 6BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION   CB437215
VERSION     CB437215.1  GI:29220001
KEYWORDS    EST.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 591)
  AUTHORS   Smith,T.P.L., Roberts,A.J., Echternkamp,S.E., Chitko-McKown,C.G.,
            Wray,J.E. and Keele,J.W.
  TITLE     A second set of bovine ESTs from pooled-tissue normalized libraries
  JOURNAL   Unpublished
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
```

```
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called with phred v0.020425.c and
            trimmed with the aid of the trim_alt option. Vector identified with
            cross_match v0.990329.
            Plate: FQY8039  row: F  column: 18
            Seq primer: GTAATACGACTCACTATAGGG.
FEATURES              Location/Qualifiers
     source           1. .591
                      /organism="Bos taurus"
                      /mol_type="mRNA"
                      /db_xref="taxon:9913"
                      /tissue_type="pooled"
                      /lab_host="DH10B"
                      /clone_lib="MARC 6BOV"
                      /note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: NotI;
                      Library made with RNA pooled from multiple tissues
                      including liver, lung, hypothalamus, pituitary, and
                      placenta/endometrium."
BASE COUNT       80 a    168 c    211 g    132 t
ORIGIN

  Query Match             24.0%;  Score 584.6;  DB 14;  Length 591;
  Best Local Similarity   99.3%;  Pred. No. 2.8e-90;
  Matches  587;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1426 TGGTGGACGGCGTGCCCCCGTCGCGCTGGAAGGAGTTGGTGCGGCGGCTGGGACTGAGCG 1485
             ||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db             1 TGGTGGACGGCGTGCCCCCGTCGCGCTGGAAGGAATTGGTGCGGCGGCTGGGACTGAGCG 60

Qy       1486 AGCACGAGATCGAGCGGCTGGAGCTGGAGAACGGGCGCCACCTGCGCGAGGCGCAGTACA 1545
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            61 AGCACGAGATCGAGCGGCTGGAGCTGGAGAACGGGCGCCACCTGCGCGAGGCGCAGTACA 120

Qy       1546 GCATGCTGGCGGCCTGGCGGCGGCGCACGCCGCGCCGCGAGGCCACGCTGGAGCTGCTGG 1605
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           121 GCATGCTGGCGGCCTGGCGGCGGCGCACGCCGCGCCGCGAGGCCACGCTGGAGCTGCTGG 180

Qy       1606 GCCGCGTGCTCAGGGACATGGACCTGCTGGGTTGCCTGGAAAACATAGAGGAGGCGCTGG 1665
             |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db           181 GCCGCGTGCTCAAGGACATGGACCTGCTGGGTTGCCTGGAAAACATAGAGGAGGCGCTGG 240

Qy       1666 GTGGCGCCGCCCGCCTCGCGTCCGAGCCCCGCCTTCTCTGGTGAAGCCCCGCCCCTCCGA 1725
             ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db           241 GTGGCGCCGCCCGCCTCGCGTCCGAGCCCCGCCTTCTCCGGTGAAGCCCCGCCCCTCCGA 300

Qy       1726 CTGCGGGCCTCCCCGCCCTGCAGACGGCTGCTTCCTTCCTGTGCCAGGCAGCCCGGAAGG 1785
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           301 CTGCGGGCCTCCCCGCCCTGCAGACGGCTGCTTCCTTCCTGTGCCAGGCAGCCCGGAAGG 360

Qy       1786 ATCTGCGAGATGCCCTGTGGACCTCCTGTTTTGTTTTGTTTTTTTCTGGAGAGGAAGTCT 1845
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           361 ATCTGCGAGATGCCCTGTGGACCTCCTGTTTTGTTTTGTTTTTTTCTGGAGAGGAAGTCT 420

Qy       1846 TGGAGGAGCAGGCACGATCTGGCAGCCACTGACCTGGTGCTACTCACTCAGTGTACATAG 1905
             |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db           421 TGGAGGAGCAAGCACGATCTGGCAGCCACTGACCTGGTGCTACTCACTCAGTGTACATAG 480

Qy       1906 CTTTTCTCAGCTGCCTGAGTGTGTGTCTGTGTGTAGTGTGTGTCTGCGTGCAGTGCGTGT 1965
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           481 CTTTTCTCAGCTGCCTGAGTGTGTGTCTGTGTGTAGTGTGTGTCTGCGTGCAGTGCGTGT 540

Qy       1966 GTTTGTGTCTCTGTATGTGCGTCTGTGTGATGTGGAGTGTGTGTACTCGTG 2016
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           541 GTTTGTGTCTCTGTATGTGCGTCTGTGTGATGTGGAGTGTGTGTACTCGTG 591


RESULT 10
CB431220/c
LOCUS       CB431220                586 bp    mRNA    linear   EST 25-MAR-2003
DEFINITION  607179 MARC 6BOV Bos taurus cDNA 3', mRNA sequence.
ACCESSION   CB431220
VERSION     CB431220.1  GI:29208041
KEYWORDS    EST.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 586)
  AUTHORS   Smith,T.P.L., Roberts,A.J., Echternkamp,S.E., Chitko-McKown,C.G.,
            Wray,J.E. and Keele,J.W.
  TITLE     A second set of bovine ESTs from pooled-tissue normalized libraries
  JOURNAL   Unpublished
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called with phred v0.020425.c and
            trimmed with the aid of the trim_alt option. Vector identified with
            cross_match v0.990329.
            Plate: FQY8024  row: F  column: 24
            Seq primer: TAGAAGGCACAGTCGAGG.
FEATURES              Location/Qualifiers
     source           1. .586
                      /organism="Bos taurus"
                      /mol_type="mRNA"
                      /db_xref="taxon:9913"
                      /tissue_type="pooled"
                      /lab_host="DH10B"
                      /clone_lib="MARC 6BOV"
                      /note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: NotI;
                      Library made with RNA pooled from multiple tissues
                      including liver, lung, hypothalamus, pituitary, and
                      placenta/endometrium."
BASE COUNT      156 a    169 c    138 g    122 t      1 others
ORIGIN

  Query Match             22.9%;  Score 559.2;  DB 14;  Length 586;
  Best Local Similarity   97.6%;  Pred. No. 6.4e-86;
  Matches  567;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy       1837 AGGAAGTCTTGGAGGAGCAGGCACGATCTGGCAGCCACTGACCTGGTGCTACTCACTCAG 1896
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            586 AGGAAGTCTTGGAGGAGCAGGCACGATCTGGCAGCCACTGACCTGGTGCTACTCACTCAG 527

Qy       1897 TGTACATAGCTTTTCTCAGCTGCCTGAGTGTGTGTCTGTGTGTAGTGTGTGTCTGCGTGC 1956
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            526 TGTACATAGCTTTTCTCAGCTGCCTGAGTGTGTGTCTGTGTGTAGTGTGTGTCTGCGTGC 467

Qy       1957 AGTGCGTGTGTTTGTGTCTCTGTATGTGCGTCTGTGTGATGTGGAGTGTGTGTACTCGTG 2016
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            466 AGTGCGTGTGTTTGTGTCTCTGTATGTGCGTCTGTGTGATGTGGAGTGTGTGTACTCGTG 407

Qy       2017 AGAGAGGCCGAGTGTGCCCGGAGCCCAAGGCAGTGGTTGCGAAGATGAGGGGCGCCCTGC 2076
             |||||||||||||||||||||||||||||||| |||||||||||||||||||| |||||||
Db            406 AGAGAGGCCGAGTGTGCCCGGAGCCCAAGGCAGCGGTTGCGAAGATGAGGGGCGCCATGC 347

Qy       2077 CTTATTGCCTGTTTTTTGGGCTTGGAGAACTCAGCAAGGCGACTTGGGGAACCTACGTCG 2136
             ||||||| ||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db            346 TTTATTGCATGTTTTTTGGGCTTGGAGAACTCAGCAAGGCGACTTGGGGAACTTACGTCG 287

Qy       2137 GTCCCTGAGCCGGTTTCGCAGTAGATAAGCCATCTTTGTATCCACTCTGCACATCCACTC 2196
             |||| ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db            286 GTCCATGAGCCGGTTTCGCAGTAGATAAGCCATCTTTGTATCCACTNTGCACATCCACTC 227

Qy       2197 ATCCACTCTGTACACTAATAGAAACTTTGTTGCCCTGCCTGGACCAGCTGAACTGTCCCC 2256
             |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db            226 ATCCACTCTGTACACTAATAGAAACTTTGTTGCCCTGCCTGGACCAGCTGCACTGTCCCC 167

Qy       2257 AGGCAGCGGGGGAGCACAGAAAAATGGGGCCTCCCAAGGGAGCTAGCTGTTCAGTTCAGT 2316
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        166 AGGCAGCGGGGGAGCACAGAAAAATGGGGCCTCCCAAGGGAGCTAGCTGTTCAGTTCAGT 107

Qy       2317 TCAGTCGCTCAGTCGTGTCCGACTCTTTGCGACCCTGTGAATCGCAGGGACTTCTGTAAA 2376
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        106 TCAGTCGCTCAGTCGTGTCCGACTCTTTGCGACCCTGTGAATCGCAGGGACTTCTGTAAA 47

Qy       2377 TACACTAAAATCTTCCAATTAAAGCTCTGCCCTGGAGGGAC 2417
              |||||||||||||||||||||||||||||||     || ||
Db         46 TACACTAAAATCTTCCAATTAAAGCTCTGCCTGTAGGGAAC 6


RESULT 11
AL559050
LOCUS       AL559050               1042 bp    mRNA    linear   EST 31-MAY-2003
DEFINITION  AL559050 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED
            Homo sapiens cDNA clone CS0DJ010YB05 5-PRIME, mRNA sequence.
ACCESSION   AL559050
VERSION     AL559050.2  GI:31283183
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1042)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
COMMENT     On Feb 15, 2001 this sequence version replaced gi:12904166.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen. This sequence belongs to sequence cluster
            6595.r For more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DJ010CA03QP1&cluster=6595.r. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DJ010CA03QP1.
FEATURES             Location/Qualifiers
     source          1. .1042
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DJ010YB05"
                     /cell_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
                     /cell_line="JURKAT"
                     /clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE) COT
                     10-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT      247 a    278 c    277 g    236 t      4 others
ORIGIN

  Query Match           21.4%;  Score 522;  DB 9;  Length 1042;
  Best Local Similarity  72.9%;  Pred. No. 1e-79;
  Matches  726;  Conservative    1;  Mismatches  261;  Indels    8;  Gaps    4;

Qy         82 CGGAGCTCTCCGGGCTCTGGGCCGCAGGGCTGGCCTTCCGGGTTTGAGGTCCTCCGGATT 141
              ||||  || | ||      ||| ||| ||||||||  |||||  || ||     |||
Db         43 CGGAATTCCCGGGATCTGAGGCTCCAGTTCTGGCCTTTGGGGTTCAAGATCACTGGGACC 102

Qy        142 GGGCTGTG---TCCCCGCCCCAGTCTCAACCCTCCACTCCCCGACCCGAGGCCCGGGCTC 198
               ||| |||    ||   |||| |||||||||||||| ||| |   ||   |  | ||  |
Db        103 AGGCCGTGATCTCTATGCCCGAGTCTCAACCCTCAACTGTCACCCCAAGGCACTTGGGAC 162

Qy        199 CACTGGGCATACGCGAGGACCGTGTTGCTGTCACTGTCGCGGGCCGCCACTGCCCC-AGC 257
              |  ||       ||||  ||| |  ||      |  |  ||   |  |||||||  |||
Db        163 GTCCTGGACAGACCGAGTCCCGGGAAGCCCCAGCACTGCCGCTGCCACACTGCCCTGAGC 222

Qy        258 CCTGATGGGGGATTGAGAGGCCACAGCTGGCCGGACATGGGCCTCCCCACCGTGCCTGGC 317
              ||  |||||||| |||||||||| |||||  |.|| ||||||||||  |||||||||||  |
Db        223 CCAAATGGGGGAGTGAGAGGCCATAGCTGTCTGG-CATGGGCCTCTCCACCGTGCCTGAC 281

Qy        318 CTGCTGCTGCCACTGGTGCTTCCAGCTCTGTTGGCAGATGTGTACCCCGCAGGGGTTCAG 377
              |||||||||||||||||| |  |  |||||||  |   | ||||||  ||||||||
Db        282 CTGCTGCTGCCACTGGTGCTCCTGGAGCTGTTGGTGGGAATATACCCCTCAGGGGTTATT 341

Qy        378 GGGCTGGTCCCTCACCCCGGGGACCTGGAGAAGAGAGAGAGTCCCTGTCCCCAAGGAAAA 437
              || ||||||||||||| ||||||  |||||||||||| |||   |||||||||||||||
Db        342 GGACTGGTCCCTCACCTAGGGGACAGGGAGAAGAGAGATAGTGTGTGTCCCCAAGGAAAA 401

Qy        438 TATAACCACCCGCAAAATAGCACCATTTGCTGCACCAAGTGCCACAAAGGTACCTATCTG 497
              |||| |||||| |||||||    | ||||||| |||||||||||||||||| |||||  ||
Db        402 TATATCCACCCTCAAAATAATTCGATTTGCTGTACCAAGTGCCACAAAGGAACCTACTTG 461

Qy        498 TACAATGACTGTCCGGGTCCAGGGCGAGACACGGACTGCAGGGTGTGTGCCCCTGGCACC 557
              |||||||||||||| || || |||| || |||||||||||||| |||||      ||| ||
Db        462 TACAATGACTGTCCAGGCCCGGGGCAGGATACGGACTGCAGGGAGTGTGAGAGCGGCTCC 521

Qy        558 TACACTGCCTTGGAGAACCATCTCAGACGATGCCTGAGCTGCTCCAGGTGCCGGGACGAA 617
              | ||| || |  || ||||| |||||||  ||||| ||||||||||  |||||  | |||
Db        522 TTCACCGCTTCAGAAAACCACCTCAGACACTGCCTCAGCTGCTCCAAATGCCGAAAGGAA 581

Qy        618 ATGTTCCAGGTGGAGATTTCGCCTTGTGTAGTGGACCGGGACACTGTGTGCGGCTGCAGG 677
              |||    |||||||||| || ||||  |||||||||||||||| |||||  |||||||||
Db        582 ATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGACCGGGACACCGTGTGTGGCTGCAGG 641

Qy        678 AAGAACCAGTACCGGGAATACTGGGGTGAAACTGGCTTCCGGTGTCTGAACTGCAGCCTC 737
              |||||||||||||| | || ||| ||||||     |||| |||  | || |||||||||
Db        642 AAGAACCAGTACCGGCATTATTGGAGTGAAAACCTTTTCCAGTGCTTCAATTGCAGCCTC 701

Qy        738 TGTCCCAATGGCACAGTGAATATCCCCTGCCAGGAGAGACAGGACACCATCTGCCACTGC 797
              || | |||||| || ||| |  || |||||||||||| |||| ||||| | |||  ||||
Db        702 TGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAGAAACAGAACACCGTGTGCACCTGC 761

Qy        798 CATATGGGCTTCTTTCTTAAAGGCGCCAAGTGCATCTCCTGTCATGATTGTAAGAA---C 854
              |||    || |||||||| | ||    | |||| ||||||||  | | |||||||    |
Db        762 CATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTCTCCTGTAGTAACTGTAAGAAAAGC 821

Qy        855 AAGGAGTGCGAGAAGTTATGTCCAACCCGACCTTCAACTGGTAAAGACTCTCAGGACCCA 914
              |||||||  |||||| || | | |||     |  | || ||| | | || ||||| ||
Db        822 CTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAGAATGTTAAGGGCACTGAGGACTCA 881

Qy        915 GGCACTACAGTACTATTACCCCTGGTGATTGTCTTCGGGCTTTGCCTGGCATCCTTCGCC 974
              ||||| ||||| || || |||||||| ||| |||| || ||||||||   |||| ||  |
Db        882 GGCACCACAGTGCTGTTGCCCCTGGTCATTTTCTTTGGTCTTTGCCTTTTATCCCTCCTC 941

Qy        975 TCTGTCGTCTTAGCATGTCGCTACCAGCGGTGGAAGCCCAAGCTCTACTCCATCATTTGC 1034
              |  | |  |||   | |||||||||| |||||||||||||||||||||||||  ||||
Db        942 TTCATTGGTTTAATGTATCGCTACCAACGGTGGAAGTCCAAGCTCTACTCCATTGTTTGT 1001

Qy       1035 GGGCAGTCGACTCTGGTAAAAGAGGGGGAGCCAGAA 1070
              ||| | ||||| |  | ||||:|||||||||  |||
Db       1002 GGGRAATCGACACCTGAAAAARAGGGGGAGCTTGAA 1037


RESULT 12
CB536686/c
LOCUS       CB536686               519 bp    mRNA    linear   EST 16-MAY-2003
DEFINITION  771726 MARC 6BOV Bos taurus cDNA 3', mRNA sequence.
ACCESSION   CB536686
VERSION     CB536686.1  GI:29404642
KEYWORDS    EST.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 519)
  AUTHORS   Smith,T.P.L., Roberts,A.J., Echternkamp,S.E., Chitko-McKown,C.G.,
            Wray,J.E. and Keele,J.W.
  TITLE     A second set of bovine ESTs from pooled-tissue normalized libraries
```

```
  JOURNAL   Unpublished
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called with phred v0.020425.c and
            trimmed with the aid of the trim_alt option. Vector identified with
            cross_match v0.990329.
            Plate: LAM8024  row: B  column: 16
            Seq primer: TAGAAGGCACAGTCGAGG.
FEATURES             Location/Qualifiers
     source          1. .519
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9913"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /clone_lib="MARC 6BOV"
                     /note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: NotI;
                     Library made with RNA pooled from multiple tissues
                     including liver, lung, hypothalamus, pituitary, and
                     placenta/endometrium."
BASE COUNT      117 a    127 c    158 g    117 t
ORIGIN

  Query Match             21.1%;  Score 514.2;  DB 14;  Length 519;
  Best Local Similarity   99.4%;  Pred. No. 3.5e-78;
  Matches  516;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        643 GTGTAGTGGACCGGGACACTGTGTGCGGCTGCAGGAAGAACCAGTACCGGGAATACTGGG 702
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        519 GTGTAGTGGACCGGGACACTGTGTGCGGCTGCAGGAAGAACCAGTACCGGGAATACTGGG 460

Qy        703 GTGAAACTGGCTTCCGGTGTCTGAACTGCAGCCTCTGTCCCAATGGCACAGTGAATATCC 762
              ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        459 GTGAAACTGGCTTCCGGTGTCTGAACTGCAGCATCTGTCCCAATGGCACAGTGAATATCC 400

Qy        763 CCTGCCAGGAGAGACAGGACACCATCTGCCACTGCCATATGGGCTTCTTTCTTAAAGGCG 822
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        399 CCTGCCAGGAGAGACAGGACACCATCTGCCACTGCCATATGGGCTTCTTTCTTAAAGGCG 340

Qy        823 CCAAGTGCATCTCCTGTCATGATTGTAAGAACAAGGAGTGCGAGAAGTTATGTCCAACCC 882
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        339 CCAAGTGCATCTCCTGTCATGATTGTAAGAACAAGGAGTGCGAGAAGTTATGTCCAACCC 280

Qy        883 GACCTTCAACTGGTAAAGACTCTCAGGACCCAGGCACTACAGTACTATTACCCCTGGTGA 942
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        279 GACCTTCAACTGGTAAAGACTCTCAGGACCCAGGCACTACAGTACTATTACCCCTGGTGA 220

Qy        943 TTGTCTTCGGGCTTTGCCTGGCATCCTTCGCCTCTGTCGTCTTAGCATGTCGCTACCAGC 1002
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        219 TTGTCTTCGGGCTTTGCCTGGCATCCTTCGCCTCTGTCGTCTTAGCATGTCGCTACCAGC 160

Qy       1003 GGTGGAAGCCCAAGCTCTACTCCATCATTTGCGGGCAGTCGACTCTGGTAAAAGAGGGGG 1062
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        159 GGTGGAAGCCCAAGCTCTACTCCATCATTTGCGGGCAGTCGACTCTGGTAAAAGAGGGGG 100

Qy       1063 AGCCAGAACTCCTGGTCCCGGCCCCAGGCTTCAACCCCACCACCACCATCTGCTTCAGCT 1122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         99 AGCCAGAACTCCTGGTCCCGGCCCCAGGCTTCAACCCCACCACCACCATCTGCTTCAGCT 40

Qy       1123 CCACCCCAAGTTCCAGTCCTGTCTCCATTCCCCCTTACA 1161
              |||||||||||||||||||||||||||||||||| | |
Db          39 CCACCCCAAGTTCCAGTCCTGTCTCCATTCCCCCTAAAA 1


RESULT 13
CD288290
LOCUS       CD288290                545 bp    mRNA    linear   EST 27-MAY-2003
DEFINITION  3_P15.abd POE14_(Day_14_pregnant_ovine_endometrium) Ovis aries cDNA
            , mRNA sequence.
ACCESSION   CD288290
VERSION     CD288290.1  GI:31086333
KEYWORDS    EST.
SOURCE      Ovis aries (sheep)
  ORGANISM  Ovis aries
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Caprinae; Ovis.
REFERENCE   1  (bases 1 to 545)
  AUTHORS   Gray,C.A., Adelson,D.L. and Spencer,T.E.
  TITLE     Ovine ESTs
  JOURNAL   Unpublished
COMMENT     Contact: Thomas E. Spencer
            Center for Animal Biotechnology and Genomics
            Texas A&M University
            Animal Science Dept., TAMU-2471, College Station, TX 77843-2471,
            USA
            Tel: 9798454896
            Fax: 9798622662
            Email: tspencer@ansc.tamu.edu.
FEATURES             Location/Qualifiers
     source          1. .545
                     /organism="Ovis aries"
                     /mol_type="mRNA"
                     /db_xref="taxon:9940"
                     /sex="Female"
                     /tissue_type="endometrium"
                     /dev_stage="Day 14 pregnant"
                     /clone_lib="POE14_(Day_14_pregnant_ovine_endometrium)"
                     /note="Organ: uterus; Vector: TriplEx2; Site_1: EcoRI;
                     Site_2: XhoI; Non-normalized library, sequenced 5' with
                     Triplex2 primer (CTCCGAGATCTGGACGAGC). Library constructed
                     by Clontech with total RNA extracted using the Trizol
                     method and pooled from 5 females."
BASE COUNT      109 a    165 c    167 g    104 t
ORIGIN

  Query Match             21.0%;  Score 513;  DB 14;  Length 545;
  Best Local Similarity   96.3%;  Pred. No. 5.4e-78;
  Matches  525;  Conservative    0;  Mismatches   20;  Indels    0;  Gaps    0;

Qy        187 AGGCCCGGGCTCCACTGGGCATACGCGAGGACCGTGTTGCTGTCACTGTCGCGGGCCGCC 246
              | | |||||||||||||||| |||| | ||||| |||| |||| ||||||||||||||||||
Db          1 ACGGCCGGGCTCCACTGGGGATACACAAGGACTGTGTCGCTGCCACTGTCGCGGGCCGCC 60

Qy        247 ACTGCCCCAGCCCTGATGGGGGATTGAGAGGCCACAGCTGGCCGGACATGGGCCTCCCCA 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACTGCCCCAGCCCTGATGGGGGATTGAGAGGCCACAGCTGGCCGGACATGGGCCTCCCCA 120

Qy        307 CCGTGCCTGGCCTGCTGCTGCCACTGGTGCTTCCAGCTCTGTTGGCAGATGTGTACCCCG 366
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        121 CCGTGCCTGGCCTGCTGCTGCCACTGGTGCTTCCGGCTCTGTTGGCAGATGTGTACCCCG 180

Qy        367 CAGGGGTTCAGGGGCTGGTCCCTCACCCCGGGGACCTGGAGAAGAGAGAGAGTCCCTGTC 426
              ||||||||| |||||||||||||||||||||||||||||||||||||| | ||||||
Db        181 CAGGGGTTCATGGGCTGGTCCCTCACCCCGGGGACCTGGAGAAGAGAGAGACTTCCTGTC 240

Qy        427 CCCAAGGAAAATATAACCACCCGCAAAATAGCACCATTTGCTGCACCAAGTGCCACAAAG 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CCCAAGGAAAATATAACCACCCGCAAAATAGCACCATTTGCTGCACCAAGTGCCACAAAG 300

Qy        487 GTACCTATCTGTACAATGACTGTCCGGGTCCAGGGCGAGACACGGACTGCAGGGTGTGTG 546
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        301 GTACCTATCTGTACAATGACTGTCCGGCTCCAGGGCGAGACACGGACTGCAGGGTGTGTG 360

Qy        547 CCCCTGGCACCTACACTGCCTTGGAGAACCATCTCAGACGATGCCTGAGCTGCTCCAGGT 606
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        361 CCCCTGGCACCTACACTGCCTTGGAGAACCATCTCCGACGATGCCTGAGCTGCTCCAGGT 420

Qy        607 GCCGGGACGAAATGTTCCAGGTGGAGATTTCGCCTTGTGTAGTGGACCGGGACACTGTGT 666
              |||||||||||||||||||||||||||||| |||||| ||||||||||||||||||||||
Db        421 GCCGGGATGAAATGTTCCAGGTGGAGATTTCCCCTTGTACAGTGGACCGGGACACTGTGT 480
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```
Qy        667 GCGGCTGCAGGAAGAACCAGTACCGGGAATACTGGGGTGAAACTGGCTTCCGGTGTCTGA 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGCTGCAGGAAGAACCAGTACCGGGAATACTGGGGCGAAACTGGCTTCCGGTGTCTGA 540

Qy        727 ACTGC 731
              |||||
Db        541 ACTGC 545


RESULT 14
BX377601
LOCUS       BX377601                1096 bp    mRNA    linear   EST 08-MAY-2003
DEFINITION  BX377601 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI008YP21 5-PRIME, mRNA sequence.
ACCESSION   BX377601
VERSION     BX377601.1  GI:30435085
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1096)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 6595.r For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DI008CH11QP1&cluster=6595.r. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DI008CH11QP1.
FEATURES             Location/Qualifiers
     source          1. .1096
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI008YP21"
                     /tissue_type="PLACENTA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT      258 a    303 c    284 g    248 t      3 others
ORIGIN

  Query Match             21.0%;  Score 511.8;  DB 13;  Length 1096;
  Best Local Similarity   73.2%;  Pred. No. 5.6e-78;
  Matches  708;  Conservative    2;  Mismatches  249;  Indels    8;  Gaps    4;

Qy        111 CTGGCCTTCCGGGTTTGAGGTCCTCCGGATTGGGCTGTG---TCCCCGCCCCAGTCTCAA 167
              ||||||||  |||||  ||  ||    |||   ||| |||   ||  |||| ||||||||
Db         55 CTGGCCTTTGGGGTTCAAGATCACTGGGACCAGGCCGTGATCTCTATGCCCGAGTCTCAA 114

Qy        168 CCCTCCACTCCCCGACCCGAGGCCCGGGCTCCACTGGGCATACGCGAGGACCGTGTTGCT 227
              |||||  |||  |   ||   |  |  ||  |  |  ||       ||||  |||  |  ||
Db        115 CCCTCAACTGTCACCCCAAGGCACTTGGGACGTCCTGGACAGACCGAGTCCCGGGAAGCC 174

Qy        228 GTCACTGTCGCGGGCCGCCACTGCCC-CAGCCCTGATGGGGGATTGAGAGGCCACAGCTG 286
              |  |  ||   |  |||||||| |||||  |||||||| |||||||||| |||||
Db        175 CCAGCACTGCCGCTGCCACACTGCCCTGAGCCCAAATGGGGGAGTGAGAGGCCATAGCTG 234

Qy        287 GCCGGACATGGGCCTCCCCACCGTGCCTGGCCTGCTGCTGCCACTGGTGCTTCCAGCTCT 346
              | ||  |||||||||| |||||||||||  |||||||||||||||||||||  |  ||
Db        235 TCTGG-CATGGGCCTCTCCACCGTGCCTGACCTGCTGCTGCCACTGGTGCTCCTGGAGCT 293

Qy        347 GTTGGCAGATGTGTACCCCGCAGGGGTTCAGGGGCTGGTCCCTCACCCCGGGGACCTGGA 406
              |||||  |   | ||||||  |||||||   || ||||||||||||  ||||||  |||
Db        294 GTTGGTGGGAATATACCCCTCAGGGGTTATTGGACTGGTCCCTCACCTAGGGGACAGGGA 353

Qy        407 GAAGAGAGAGAGTCCCTGTCCCCAAGGAAAATATAACCACCCGCAAAATAGCACCATTTG 466
              |||||||||  |||  |||||||||||||||||||  ||||||  |||||||   |  |||||
Db        354 GAAGAGAGATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTG 413

Qy        467 CTGCACCAAGTGCCACAAAGGTACCTATCTGTACAATGACTGTCCGGGTCCAGGGCGAGA 526
              |||  ||||||||||||||||||  |  |::||||||||||||  ||  ||  ||||  ||
Db        414 CTGTACCAAGTGCCACAAAGGAACCTACTTTTWYAATGACTGTCCAGGCCCGGGGCAGGA 473

Qy        527 CACGGACTGCAGGGTGTGTGCCCCTGGCACCTACACTGCCTTGGAGAACCATCTCAGACG 586
              |||||||||||||  |||||      |||  |||  |||  ||  |  ||  |||||  |||||||
Db        474 TACGGACTGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACA 533

Qy        587 ATGCCTGAGCTGCTCCAGGTGCCGGGACGAAATGTTCCAGGTGGAGATTTCGCCTTGTGT 646
              |||||  ||||||||||  |||||  |  ||||||   ||||||||||  ||  ||||
Db        534 CTGCCTCAGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCAC 593

Qy        647 AGTGGACCGGGACACTGTGTGCGGCTGCAGGAAGAACCAGTACCGGGAATACTGGGGTGA 706
              ||||||||||||||  |||||  ||||||||||||||||||||||||  |  ||  ||||
Db        594 AGTGGACCGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGA 653

Qy        707 AACTGGCTTCCGGTGTCTGAACTGCAGCCTCTGTCCCAATGGCACAGTGAATATCCCCTG 766
              ||      |||| |||   | ||  ||||||||||| | ||||||  ||  |||  |  || ||||
Db        654 AAACCTTTTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTG 713

Qy        767 CCAGGAGAGACAGGACACCATCTGCCACTGCCATATGGGCTTCTTTCTTAAAGGCGCCAA 826
              ||||||||  |||| |||||  |  |||  |||||||   |  |||||||| | ||    | |
Db        714 CCAGGAGAAACAGAACACCGTGTGCACCTGCCATGCAGTTTTCTTTCTAAGAGAAAACGA 773

Qy        827 GTGCATCTCCTGTCATGATTGTAAGAA---CAAGGAGTGCGAGAAGTTATGTCCAACCCG 883
              |||  ||||||||  | |  ||||||||   |  |||||||  ||||||  || |  | |||
Db        774 GTGTGTCTCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCA 833

Qy        884 ACCTTCAACTGGTAAAGACTCTCAGGACCCAGGCACTACAGTACTATTACCCCTGGTGAT 943
              |    | || |||  |  | ||  |||||  |||||||  |||||  ||  ||  |||||||| ||
Db        834 GATTGAGAATGTTAAGGGCACTGAGGACTCAGGCACCACAGTGCTGTTGCCCCTGGTCAT 893

Qy        944 TGTCTTCGGGCTTTGCCTGGCATCCTTCGCCTCTGTCGTCTTAGCATGTCGCTACCAGCG 1003
              | ||||  ||  ||||||||    ||||  ||  ||    |  |  |||    | |||||||| ||
Db        894 TTTCTTTGGTCTTTGCCTTTTATCCCTCCTCTTCATTGGTTTAATGTATCGCTACCAACG 953

Qy       1004 GTGGAAGCCCAAGCTCTACTCCATCATTTGCGGGCAGTCGACTCTGGTAAAAGAGGGGGA 1063
              |||||||  |||||||||||||||||  ||||  |||  |  |||||  |   | ||||||||||||
Db        954 GTGGAAGTCCAAGCTCTACTCCATTGTTTGTGGGAAATCGACACCTGAAAAAGAGGGGGA 1013

Qy       1064 GCCAGAA 1070
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Db       1014 GCTTGAA 1020


RESULT 15
BI898540
LOCUS       BI898540                502 bp    mRNA    linear   EST 17-OCT-2001
DEFINITION  479493 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION   BI898540
VERSION     BI898540.1  GI:16203989
KEYWORDS    EST.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 502)
  AUTHORS   Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
            Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett
            ,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G.,
            Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
            Keele,J.W.
  TITLE     Sequence evaluation of four pooled-tissue normalized bovine cDNA
            libraries and construction of a gene index for cattle
  JOURNAL   Genome Res. 11 (4), 626-630 (2001)
```

```
  MEDLINE   21180013
   PUBMED   11282978
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and alt_trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -minmatch 12 options.
            PCR PRimers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTTCCCAGTCACGACG
            Plate: 105  row: B  column: 10
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .502
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9913"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /clone_lib="MARC 2BOV"
                     /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
                     Library made from pooled tissue from testis, thymus,
                     semitendonosus muscle, longissimus muscle, pancreas,
                     adrenal, and endometrium."
BASE COUNT       96 a    123 c    149 g    134 t
ORIGIN

  Query Match             20.5%;  Score 500.4;  DB 12;  Length 502;
  Best Local Similarity   99.8%;  Pred. No. 8.2e-76;
  Matches  501;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1914 AGCTGCCTGAGTGTGTGTCTGTGTGTAGTGTGTGTCTGCGTGCAGTGCGTGTGTTTGTGT 1973
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGCTGCCTGAGTGTGTGTCTGTGTGTAGTGTGTGTCTGCGTGCAGTGCGTGTGTTTGTGT 60

Qy       1974 CTCTGTATGTGCGTCTGTGTGATGTGGAGTGTGTGTACTCGTGAGAGAGGCCGAGTGTGC 2033
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTCTGTATGTGCGTCTGTGTGATGTGGAGTGTGTGTACTCGTGAGAGAGGCCGAGTGTGC 120

Qy       2034 CCGGAGCCCAAGGCAGTGGTTGCGAAGATGAGGGGCGCCCTGCCTTATTGCCTGTTTTTT 2093
             |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCGGAGCCCAAGGCAGCGGTTGCGAAGATGAGGGGCGCCCTGCCTTATTGCCTGTTTTTT 180

Qy       2094 GGGCTTGGAGAACTCAGCAAGGCGACTTGGGGAACCTACGTCGGTCCCTGAGCCGGTTTC 2153
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GGGCTTGGAGAACTCAGCAAGGCGACTTGGGGAACCTACGTCGGTCCCTGAGCCGGTTTC 240

Qy       2154 GCAGTAGATAAGCCATCTTTGTATCCACTCTGCACATCCACTCATCCACTCTGTACACTA 2213
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCAGTAGATAAGCCATCTTTGTATCCACTCTGCACATCCACTCATCCACTCTGTACACTA 300

Qy       2214 ATAGAAACTTTGTTGCCCTGCCTGGACCAGCTGAACTGTCCCCAGGCAGCGGGGGAGCAC 2273
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATAGAAACTTTGTTGCCCTGCCTGGACCAGCTGAACTGTCCCCAGGCAGCGGGGGAGCAC 360

Qy       2274 AGAAAAATGGGGCCTCCCAAGGGAGCTAGCTGTTCAGTTCAGTTCAGTCGCTCAGTCGTG 2333
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AGAAAAATGGGGCCTCCCAAGGGAGCTAGCTGTTCAGTTCAGTTCAGTCGCTCAGTCGTG 420

Qy       2334 TCCGACTCTTTGCGACCCTGTGAATCGCAGGGACTTCTGTAAATACACTAAAATCTTCCA 2393
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCCGACTCTTTGCGACCCTGTGAATCGCAGGGACTTCTGTAAATACACTAAAATCTTCCA 480

Qy       2394 ATTAAAGCTCTGCCCTGGAGGG 2415
             |||||||||||||||||||||||
Db        481 ATTAAAGCTCTGCCCTGGAGGG 502

Search completed: September 15, 2003, 07:49:33

Job time : 3439 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 13, 2003, 06:55:24 ; Search time 47 Seconds
(without alignments)
1590.643 Million cell updates/sec

Title: US-09-970-532-2
Perfect score: 2603
Sequence: 1 MGLPTVPGLLLPLVLPALLA.....NIEEALGGAARLASEPRLLW 471

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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9: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:*
10: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*
11: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:*
12: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
13: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*
14: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:*
15: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:*
16: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:*
17: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:*
18: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:*
19: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:*
20: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*
21: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*
22: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
23: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2603	100.0	471	23	AAE25816	Bovine tumour necr
2	2603	100.0	471	23	ABB98169	Bovine tumour necr
3	1517	58.3	455	11	ABG74751	Human TNF receptor
4	1517	58.3	455	11	ABG74755	Human TNF-R protei
5	1517	58.3	455	12	AAR10986	30kD TNF inhibitor
6	1517	58.3	455	14	AAR42059	Lambda derived TNF
7	1517	58.3	455	16	AAR75084	p55 TNF-R. Homo s
8	1517	58.3	455	20	AAY30934	Human tumour necro
9	1517	58.3	455	21	AAB36266	Human tumour necro
10	1517	58.3	455	21	AAB37800	Human tumour necro
11	1517	58.3	455	21	AAB26984	Human TNFR 1. Hom
12	1517	58.3	455	21	AAB23446	Human tumour necro
13	1517	58.3	455	21	AAB01336	TNF-R1 death recep
14	1517	58.3	455	22	AAB86817	Human TNFBP-associ
15	1517	58.3	455	22	AAB36697	Human tumour necro
16	1517	58.3	455	22	AAB37677	Human 30 kDa TNF i
17	1517	58.3	455	23	ABP54799	Human COPD-related
18	1517	58.3	455	23	AAO22286	TNFR1 expression m
19	1517	58.3	455	23	ABB81649	Human tumour necro
20	1517	58.3	455	23	AAU75064	Human tumour necro
21	1514	58.2	455	12	AAR11082	Human 55kD TNF-bin
22	1511	58.0	455	13	AAR20787	TNF-alpha binding
23	1508	57.9	455	11	AAR07451	Human Tumour Necro
24	1508	57.9	455	14	AAR42197	p55 Tumour necrosi
25	1505	57.8	455	14	AAR51034	Mutant p55 tumour
26	1500.5	57.6	909	19	AAW64485	Human Fas protein.
27	1496	57.5	453	22	AAB50895	Human TNFR 1. Hom
28	1494	57.4	455	12	AAR12550	Type I TNF recepto
29	1492	57.3	455	13	AAR24000	TNF-alpha 55kD rec
30	1491	57.3	443	14	AAR51033	Mutant p55 tumour
31	1456	55.9	433	14	AAR51032	Mutant p55 tumour
32	1325.5	50.9	461	11	ABG74754	Rat TNF-R protein
33	1319.5	50.7	461	11	AAR07450	Rat Tumour Necrosi
34	1319	50.7	454	23	AAO22289	TNFR1 expression m
35	1178	45.3	371	11	ABG74753	Human TNF-BP prote
36	1178	45.3	371	11	AAR07449	Tumour Necrosis Fa
37	1072	41.2	181	23	AAE25817	Bovine tumour necr
38	1072	41.2	181	23	ABB98170	Soluble bovine tum
39	1019	39.1	280	22	AAB66979	Tnfr1 protein. Un
40	834.5	32.1	213	24	ABB99540	Amino acid sequenc
41	833	32.0	444	24	ABJ37098	Concatameric immun
42	832.5	32.0	211	20	AAW89225	Tumour necrosis fa
43	832.5	32.0	311	20	AAW89229	Tumour necrosis fa
44	832.5	32.0	366	20	AAW89228	Tumour necrosis fa
45	832.5	32.0	397	20	AAW89227	Tumour necrosis fa

ALIGNMENTS

RESULT 1
AAE25816
ID AAE25816 standard; Protein; 471 AA.
XX
AC AAE25816;
XX
DT 15-NOV-2002 (first entry)
XX
DE Bovine tumour necrosis factor receptor-I (TNF-RI).
XX
KW Bovine; cattle; coliform mastitis; inflammatory disease; receptor;
KW tumour necrosis factor receptor-I; TNF-RI; antiinflammatory.
XX
OS Bos taurus.
XX
FH Key Location/Qualifiers
FT Peptide 1..29
FT /label= Signal_peptide
FT Protein 30..471
FT /note= "Mature bovine TNF-RI"
FT Domain 30..210
FT /note= "Extracellular domain"
FT Modified-site 54..56
FT /note= "N-linked glycosylation site"
FT Modified-site 145..147
FT /note= "N-linked glycosylation site"
FT Modified-site 151..153
FT /note= "N-linked glycosylation site"
FT Domain 211..235
FT /note= "Transmembrane domain"
XX
PN US6406907-B1.

XX
PD 18-JUN-2002.
XX
PF 25-FEB-2000; 2000US-0513007.
XX
PR 26-FEB-1999; 99US-122156P.
XX
PA (IOWA) UNIV IOWA STATE RES FOUND INC.
PA (U9DA) US SEC OF AGRIC.
XX
PI Taylor MJ, Kehrli ME, Lee E;
XX
DR WPI; 2002-588816/63.
DR N-PSDB; AAD42477.
XX
PT Novel nucleic acid molecule encoding bovine tumor necrosis factor
PT receptor-1 which is a potent inhibitor of tumor necrosis factor-alpha
PT useful for treating coliform mastitis or other inflammatory disease in
PT cattle -
XX
PS Claim 8; Column 17-20; 16pp; English.
XX
CC The invention relates to an isolated nucleic acid encoding a polypeptide
CC that binds bovine tumour necrosis factor (TNF). The invention is useful
CC for expressing bovine TNF-RI or soluble bovine TNF-RI which is useful as
CC an inhibitor of TNF in cattle suffering from coliform mastitis or other
CC inflammatory disease. The nucleic acids and polypeptide or their
CC fragments are useful for treating mastitis. The present sequence is
CC bovine tumour necrosis factor receptor-I (TNF-RI).
XX
SQ Sequence 471 AA;

Query Match 100.0%; Score 2603; DB 23; Length 471;
Best Local Similarity 100.0%; Pred. No. 8.9e-170;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MGLPTVPGLLLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGLPTVPGLLLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCT 60

Qy         61 KCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCLSCSRCRDEMFQVEISPCVVD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCLSCSRCRDEMFQVEISPCVVD 120

Qy        121 RDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQERQDTICHCHMGFFLKGAKCI 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQERQDTICHCHMGFFLKGAKCI 180

Qy        181 SCHDCKNKECEKLCPTRPSTGKDSQDPGTTVLLPLVIVFGLCLASFASVVLACRYQRWKP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SCHDCKNKECEKLCPTRPSTGKDSQDPGTTVLLPLVIVFGLCLASFASVVLACRYQRWKP 240

Qy        241 KLYSIICGQSTLVKEGEPELLVPAPGFNPTTTICFSSTPSSSPVSIPPYISCDRSNFGAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 KLYSIICGQSTLVKEGEPELLVPAPGFNPTTTICFSSTPSSSPVSIPPYISCDRSNFGAV 300

Qy        301 ASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLCTPVQKWEASA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLCTPVQKWEASA 360

Qy        361 PSAPDQLADADPATLYAVVDGVPPSRWKELVRRLGLSEHEIERLELENGRHLREAQYSML 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 PSAPDQLADADPATLYAVVDGVPPSRWKELVRRLGLSEHEIERLELENGRHLREAQYSML 420

Qy        421 AAWRRRTPRREATLELLGRVLRDMDLLGCLENIEEALGGAARLASEPRLLW 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AAWRRRTPRREATLELLGRVLRDMDLLGCLENIEEALGGAARLASEPRLLW 471
```

RESULT 2
ABB98169
ID ABB98169 standard; Protein; 471 AA.
XX
AC ABB98169;
XX
DT 05-NOV-2002 (first entry)
XX
DE Bovine tumour necrosis factor receptor-I.
XX
KW Bovine; tumour necrosis factor receptor-I; TNF-RI; antiinflammatory;
KW TNF cytotoxicity; mastitis; tumour necrosis factor-alpha; TNF-alpha;
KW monoclonal antibody BC9; TNF-beta.
XX
OS Bos taurus.
XX
PN US2002076765-A1.
XX
PD 20-JUN-2002.
XX
PF 03-OCT-2001; 2001US-0970532.
XX
PR 26-FEB-1999; 99US-122156P.
PR 25-FEB-2000; 2000US-0513007.
XX
PA (IOWA) UNIV IOWA STATE RES FOUND INC.
XX
PI Taylor MJ, Kehrli ME, Lee E, Mwangi S;
XX
DR WPI; 2002-557247/59.
DR N-PSDB; ABQ79378.
XX
PT New isolated, soluble, bovine tumour necrosis factor receptor I, useful
PT for inhibiting tumour necrosis factor cytotoxicity for treating
PT mastitis, is a better inhibitor of tumour necrosis factor compared to
PT monoclonal antibody BC9 -
XX
PS Claim 8; Fig 1; 17pp; English.
XX
CC The invention relates to an isolated nucleic acid encoding bovine tumour
CC necrosis factor receptor-I (TNF-RI). The activity of polynucleotides of
CC the invention may be described as antiinflammatory. Polypeptides of the
CC invention are useful for inhibiting TNF cytotoxicity in a bovine. This is
CC useful for treating mastitis and other inflammatory disease. Soluble
CC bovine TNF-RI is a better inhibitor of bovine TNF-alpha than monoclonal
CC antibody BC9 (an antibody directed towards TNF-alpha), and can bind both
CC TNF-alpha and TNF-beta. The current sequence represents bovine tumour
CC necrosis factor receptor-I.
XX
SQ Sequence 471 AA;

Query Match 100.0%; Score 2603; DB 23; Length 471;
Best Local Similarity 100.0%; Pred. No. 8.9e-170;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MGLPTVPGLLLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGLPTVPGLLLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCT 60

Qy         61 KCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCLSCSRCRDEMFQVEISPCVVD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCLSCSRCRDEMFQVEISPCVVD 120

Qy        121 RDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQERQDTICHCHMGFFLKGAKCI 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQERQDTICHCHMGFFLKGAKCI 180

Qy        181 SCHDCKNKECEKLCPTRPSTGKDSQDPGTTVLLPLVIVFGLCLASFASVVLACRYQRWKP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SCHDCKNKECEKLCPTRPSTGKDSQDPGTTVLLPLVIVFGLCLASFASVVLACRYQRWKP 240

Qy        241 KLYSIICGQSTLVKEGEPELLVPAPGFNPTTTICFSSTPSSSPVSIPPYISCDRSNFGAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 KLYSIICGQSTLVKEGEPELLVPAPGFNPTTTICFSSTPSSSPVSIPPYISCDRSNFGAV 300

Qy        301 ASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLCTPVQKWEASA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db        301 ASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLCTPVQKWEASA 360

Qy        361 PSAPDQLADADPATLYAVVDGVPPSRWKELVRRLGLSEHEIERLELENGRHLREAQYSML 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 PSAPDQLADADPATLYAVVDGVPPSRWKELVRRLGLSEHEIERLELENGRHLREAQYSML 420

Qy        421 AAWRRRTPRREATLELLGRVLRDMDLLGCLENIEEALGGAARLASEPRLLW 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AAWRRRTPRREATLELLGRVLRDMDLLGCLENIEEALGGAARLASEPRLLW 471


RESULT 3
ABG74751
ID   ABG74751 standard; Protein; 455 AA.
XX
AC   ABG74751;
XX
DT   14-MAY-2003  (first entry)
XX
DE   Human TNF receptor protein.
XX
KW   TNF; human; tumour necrosis factor; tumour necrosis factor receptor;
KW   TNF-R; tumour necrosis factor binding protein; TNF-BP; tumour.
XX
OS   Homo sapiens.
XX
PN   EP393438-A.
XX
PD   24-OCT-1990.
XX
PF   06-APR-1990;   90EP-0106624.
XX
PR   21-APR-1989;   89DE-3913101.
PR   21-JUN-1989;   89DE-3920282.
XX
PA   (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
PA   (SYND ) SYNERGEN INC.
XX
PI   Hauptmann R,  Himmler A,  Maurer-Fogy I,  Stratowa C;
XX
DR   WPI; 1990-321987/43.
XX
PT   DNA encoding TNF binding protein and TNF- receptor - used in tumour
PT   treatment and to understand mechanisms to TNF action
XX
PS   Claim 22; Page 34; 51pp; German.
XX
CC   This invention describes novel polynucleotide sequences encoding tumour
CC   necrosis factor (TNF) receptor (TNF-R) or TNF binding protein (TNF-BP).
CC   The products of the invention are useful in pharmaceutical compositions
CC   for prophylaxis or treatment of human tumours and to understand the
CC   mechanisms of TNF action. This sequence represents the TNF receptor
CC   described in the disclosure of the invention.
XX
SQ   Sequence   455 AA;

  Query Match             58.3%;  Score 1517;  DB 11;  Length 455;
  Best Local Similarity   62.9%;  Pred. No. 1.4e-95;
  Matches  302;  Conservative   38;  Mismatches  104;  Indels   36;  Gaps    7;

Qy          1 MGLPTVPGLLLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCT 60
              ||| ||| |||||||  ||  :||:|| ||||| || |||:| |||||| ||||::||||
Db          1 MGLSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCT 60

Qy         61 KCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCLSCSRCRDEMFQVEISPCVVD 120
              ||||||||||||||||:||||| |  |::|| ||||| |||||:|| || ||||| | ||
Db         61 KCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVD 120

Qy        121 RDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQERQDTICHCHMGFFLKGAKCI 180
              |||||||||||||  ||  |  |:| ||||| ||||:: |||:|:|:|  || ||||:  :|:
Db        121 RDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECV 180

Qy        181 SCHDCKNK-ECEKLCPTRPSTGKDSQDPGTTVLLPLVIVFGLCLASFASVVLACRYQRWK 239
              ||| :||  || |||  :.  | ::| |||||||||| ||||| |   : |  ||||||
Db        181 SCSNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPLVIFFGLCLLSLLFIGLMYRYQRWK 240

Qy        240 PKLYSIICGQSTLVKEGEPE-----LLVPAPGFNP----TTTICFSSTPSSSPVSIPPYI 290
              |||||:||:||  |||| |       | | | |:|    | |: ||  |||:  |  |
Db        241 SKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPTPGFTPTLGFSPVPSSTFTSSSTYT 300

Qy        291 SCDRSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLC 350
              |  ||   |:|  | |||:  | |||                 :| |      ||  :
Db        301 PGDCPNF---AAPRREVAPPYQGADPIL---------------ATAL------ASDPIP 335

Qy        351 TPVQKWEASAPSAPDQLADADPATLYAVVDGVPPSRWKELVRRLGLSEHEIERLELENGR 410
              |:|||| ||   |  |  |||||||||: ||| |||| |||||||:|||:|||:|||
Db        336 NPLQKWEDSA-HKPQSLDTDDPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLELQNGR 394

Qy        411 HLREAQYSMLAAWRRRTPRREATLELLGRVLRDMDLLGCLENIEEALGGAARLASEPRLL 470
              |||||||||| ||||||||||||||||||||||||||:|||| | | |   | ||
Db        395 CLREAQYSMLATWRRRTPRREATLELLGRVLRDMDLLGCLEDIEEALCGPAALPPAPSLL 454


RESULT 4
ABG74755
ID   ABG74755 standard; Protein; 455 AA.
XX
AC   ABG74755;
XX
DT   14-MAY-2003  (first entry)
XX
DE   Human TNF-R protein huTNF-R.
XX
KW   TNF; human; tumour necrosis factor; tumour necrosis factor receptor;
KW   TNF-R; tumour necrosis factor binding protein; TNF-BP; tumour.
XX
OS   Homo sapiens.
XX
PN   EP393438-A.
XX
PD   24-OCT-1990.
XX
PF   06-APR-1990;   90EP-0106624.
XX
PR   21-APR-1989;   89DE-3913101.
PR   21-JUN-1989;   89DE-3920282.
XX
PA   (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
PA   (SYND ) SYNERGEN INC.
XX
PI   Hauptmann R,  Himmler A,  Maurer-Fogy I,  Stratowa C;
XX
DR   WPI; 1990-321987/43.
DR   N-PSDB; ABQ77487.
XX
PT   DNA encoding TNF binding protein and TNF- receptor - used in tumour
PT   treatment and to understand mechanisms to TNF action
XX
PS   Example 9; Fig 9; 51pp; German.
XX
CC   This invention describes novel polynucleotide sequences encoding tumour
CC   necrosis factor (TNF) receptor (TNF-R) or TNF binding protein (TNF-BP).
CC   The products of the invention are useful in pharmaceutical compositions
CC   for prophylaxis or treatment of human tumours and to understand the
CC   mechanisms of TNF action. This sequence represents the huma TNF-R,
CC   huTNF-R described in the disclosure of the invention.
XX
SQ   Sequence   455 AA;

  Query Match             58.3%;  Score 1517;  DB 11;  Length 455;
  Best Local Similarity   62.9%;  Pred. No. 1.4e-95;
  Matches  302;  Conservative   38;  Mismatches  104;  Indels   36;  Gaps    7;

Qy          1 MGLPTVPGLLLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCT 60
              ||| ||| |||||||  ||  :||:|| ||||| || |||:| |||||| ||||::||||
Db          1 MGLSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCT 60
```

```
Qy          61 KCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCLSCSRCRDEMFQVEISPCVVD 120
               ||||||||||||||||:|||||  |  |::|| |||||  |||||:|| || |||||  | ||
Db          61 KCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVD 120

Qy         121 RDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQERQDTICHCHMGFFLKGAKCI 180
               |||||||||||||| ||  |  |:| |||||  ||||:: |||:|:|:| || ||||:  :|:
Db         121 RDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECV 180

Qy         181 SCHDCKNK-ECEKLCPTRPSTGKDSQDPGTTVLLPLVIVFGLCLASFASVVLACRYQRWK 239
               || :||  || |||  :    | ::| ||||||||||  |||||  |   :  |  ||||||
Db         181 SCSNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPLVIFFGLCLLSLLFIGLMYRYQRWK 240

Qy         240 PKLYSIICGQSTLVKEGEPE-----LLVPAPGFNP----TTTICFSSTPSSSPVSIPPYI 290
               |||||:||:||  |||| |     | | | |:|    | |: ||  |||:  |   |
Db         241 SKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPTPGFTPTLGFSPVPSSTFTSSSTYT 300

Qy         291 SCDRSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLC 350
                 |  ||   |:|  | |||:  | |||                :| |      ||  :
Db         301 PGDCPNF---AAPRREVAPPYQGADPIL---------------ATAL------ASDPIP 335

Qy         351 TPVQKWEASAPSAPDQLADADPATLYAVVDGVPPSRWKELVRRLGLSEHEIERLELENGR 410
               |:|||| ||   |  |   ||||||||||: ||| |||| ||||||:|||:||||:|||
Db         336 NPLQKWEDSA-HKPQSLDTDDPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLELQNGR 394

Qy         411 HLREAQYSMLAAWRRRTPRREATLELLGRVLRDMDLLGCLENIEEALGGAARLASEPRLL 470
               |||||||||| ||||||||||||||||||||||||||||:|||| | | |   | ||
Db         395 CLREAQYSMLATWRRRTPRREATLELLGRVLRDMDLLGCLEDIEEALCGPAALPPAPSLL 454
```

RESULT 5
AAR10986
ID AAR10986 standard; Protein; 455 AA.
XX
AC AAR10986;
XX
DT 25-MAR-2003 (updated)
DT 13-MAY-1991 (first entry)
XX
DE 30kD TNF inhibitor precursor.
XX
KW Tumour necrosis factor; inhibitor.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT Cleavage-site   40..41
FT   note=" cleavage gives active protein "
XX
PN AU9058976-A.
XX
PD 24-JAN-1991.
XX
PF 16-JUL-1990; 90AU-0058976.
XX
PR 07-FEB-1990; 90US-0479661.
PR 18-JUL-1989; 89US-0381080.
PR 11-DEC-1989; 89US-0450329.
XX
PA (SYND) SYNERGEN INC.
XX
DR WPI; 1991-073847/11.
DR N-PSDB; AAQ10883.
XX
PT Tumour necrosis factor inhibitor - for suppression of TNF-alpha
PT and -beta, useful as therapeutic agent.
XX
PS Disclosure; Fig 21; 142pp; English.
XX
CC The sequence comprises the entire 30 kD TNF inhibitor. The clone
CC from which the sequence was deduced was isolated from a cDNA
CC library prepd. from RNA form U937 cells treated with PMA/PHA.
CC The whole gene can be inserted into expression vectors for prepn.
CC of TNF inhibitor for use in the treatment of inflammatory and
CC degenerative diseases. The active protein is claimed (Claim 8).
CC See also AAR10984 and AAR11001.
CC (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 455 AA;

```
  Query Match             58.3%;  Score 1517;  DB 12;  Length 455;
  Best Local Similarity   62.9%;  Pred. No. 1.4e-95;
  Matches  302;  Conservative   38;  Mismatches  104;  Indels   36;  Gaps    7;

Qy           1 MGLPTVPGLLLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCT 60
               ||| ||| |||||||  ||  :||:|| ||||| || |||:| |||||| ||||::||||
Db           1 MGLSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCT 60

Qy          61 KCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCLSCSRCRDEMFQVEISPCVVD 120
               |||||||||||||||:|||||  |  |::|| |||||  |||||:|| || |||||  | ||
Db          61 KCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVD 120

Qy         121 RDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQERQDTICHCHMGFFLKGAKCI 180
               |||||||||||||| ||  |  |:| |||||  ||||:: |||:|:|:| || ||||:  :|:
Db         121 RDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECV 180

Qy         181 SCHDCKNK-ECEKLCPTRPSTGKDSQDPGTTVLLPLVIVFGLCLASFASVVLACRYQRWK 239
               || :||  || |||  :    | ::| ||||||||||  |||||  |   :  |  ||||||
Db         181 SCSNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPLVIFFGLCLLSLLFIGLMYRYQRWK 240

Qy         240 PKLYSIICGQSTLVKEGEPE-----LLVPAPGFNP----TTTICFSSTPSSSPVSIPPYI 290
               |||||:||:||  |||| |     | | | |:|    | |: ||  |||:  |   |
Db         241 SKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPTPGFTPTLGFSPVPSSTFTSSSTYT 300

Qy         291 SCDRSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLC 350
                 |  ||   |:|  | |||:  | |||                :| |      ||  :
Db         301 PGDCPNF---AAPRREVAPPYQGADPIL---------------ATAL------ASDPIP 335

Qy         351 TPVQKWEASAPSAPDQLADADPATLYAVVDGVPPSRWKELVRRLGLSEHEIERLELENGR 410
               |:|||| ||   |  |   ||||||||||: ||| |||| ||||||:|||:||||:|||
Db         336 NPLQKWEDSA-HKPQSLDTDDPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLELQNGR 394

Qy         411 HLREAQYSMLAAWRRRTPRREATLELLGRVLRDMDLLGCLENIEEALGGAARLASEPRLL 470
               |||||||||| ||||||||||||||||||||||||||||:|||| | | |   | ||
Db         395 CLREAQYSMLATWRRRTPRREATLELLGRVLRDMDLLGCLEDIEEALCGPAALPPAPSLL 454
```

RESULT 6
AAR42059
ID AAR42059 standard; Protein; 455 AA.
XX
AC AAR42059;
XX
DT 25-MAR-2003 (updated)
DT 29-APR-1994 (first entry)
XX
DE Lambda derived TNF-R.
XX
KW Human; tumour necrosis factor receptor; TNF-R; interleukin-1 receptor;
KW IL-1R; fusion protein; linker; TNF; IL-1; cachexia; cerebral malaria;
KW rheumatoid arthritis; diabetes; multiple sclerosis; septic shock;
KW pulmonary fibrosis; silicosis; allograft; xenograft; rejection;
KW graft verses host disease; sepsis; inflammation; allergy;
KW autoimmune dysfunction.
XX
OS Homo sapiens.
OS Lambda-gt10-7ctnfbp.
XX
FH Key   Location/Qualifiers.
FT Peptide   1..40
FT   /note= "Signal peptide"
FT Protein   41..455
FT   /note= "Mature hTNF-R"
XX
PN WO9319777-A1.
XX

PD 14-OCT-1993.
XX
PF 26-MAR-1993; 93WO-US02938.
XX
PR 30-MAR-1992; 92US-0860710.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Smith CA;
XX
DR WPI; 1993-336592/42.
DR N-PSDB; AAQ49932.
XX
PT New fusion protein tumour necrosis factor and human interleukin-1
PT receptor - useful in therapy, diagnosis and assays of e.g.
PT rheumatoid arthritis, diabetes, cerebral malaria, sepsis, etc.
XX
PS Disclosure; Page 57-59; 85pp; English.
XX
CC The sequences given in AAR42058-59 represent human tumour necrosis
CC factor receptor (TNF-R) and the sequences in AAR42060-61 represent
CC human interleukin-1 receptor (IL-1R). These sequences were used in
CC the production of a fusion protein which conformed to one of the
CC formulae:
CC TNF-R-linker-TNF-R-linker-IL-1R
CC IL-1R-linker-TNF-R-linker-TNF-R or
CC TNF-R-linker-TNF-R
CC The linker may comprise 5-100 amino acids selected from Gly, Asp,
CC Ser, Thr and Ala. These linkers separate the individual moeities
CC by such a distance that each component of the fusion protien is
CC capable of folding into the secondary or tertiary structure required
CC for its biological activity. These fusion proteins may be used in
CC therapy, diagnosis and assays for conditions mediated by TNF or IL-1,
CC particularly in conditions in which both TNF and IL-1 play a causitive
CC role. They may be used to treat cachexia, rheumatoid arthritis,
CC diabetes, multiple sclerosis, pulmonary fibrosis and silicosis,
CC cerebral malaria, allograft and xenograft rejection in graft verses
CC host disease, sepsis, septic shock, inflammation, allergies and
CC autoimmune dysfunctions.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 455 AA;

Query Match 58.3%; Score 1517; DB 14; Length 455;
Best Local Similarity 62.9%; Pred. No. 1.4e-95;
Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

```
Qy          1 MGLPTVPGLLLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCT 60
              ||| ||| |||||||  ||  :||:|| ||||| || |||:| |||||| ||||::||||
Db          1 MGLSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCT 60

Qy         61 KCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCLSCSRCRDEMFQVEISPCVVD 120
              |||||||||||||||:||||| |  |::|| ||||| |||||:|| || ||||| | ||
Db         61 KCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVD 120

Qy        121 RDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQERQDTICHCHMGFFLKGAKCI 180
              |||||||||||||| || |  |:| ||||| |||:: |||:|:|:| || ||||:  :|:
Db        121 RDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECV 180

Qy        181 SCHDCKNK-ECEKLCPTRPSTGKDSQDPGTTVLLPLVIVFGLCLASFASVVLACRYQRWK 239
              || :||   || |||  :    | ::| |||||||||| ||||| |   : |  ||||||
Db        181 SCSNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPLVIFFGLCLLSLLFIGLMYRYQRWK 240

Qy        240 PKLYSIICGQSTLVKEGEPE-----LLVPAPGFNP----TTTICFSSTPSSSPVSIPPYI 290
              |||||:||:||  |||| |      | | | |:|    | |: ||  |||:  |   |
Db        241 SKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPTPGFTPTLGFSPVPSSTFTSSSTYT 300

Qy        291 SCDRSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLC 350
                |  ||   |:|  | |||:  | |||                :| |      ||  :
Db        301 PGDCPNF---AAPRREVAPPYQGADPIL----------------ATAL------ASDPIP 335

Qy        351 TPVQKWEASAPSAPDQLADADPATLYAVVDGVPPSRWKELVRRLGLSEHEIERLELENGR 410
              |:|||| ||   |  |   |||||||||: ||| |||| |||||||:|||:||||:|||
```

Db 336 NPLQKWEDSA-HKPQSLDTDDPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLELQNGR 394

Qy 411 HLREAQYSMLAAWRRRTPRREATLELLGRVLRDMDLLGCLENIEEALGGAARLASEPRLL 470
|||||||||| |||||||||||||||||||||||||||||:|||| | | | | ||
Db 395 CLREAQYSMLATWRRRTPRREATLELLGRVLRDMDLLGCLEDIEEALCGPAALPPAPSLL 454

RESULT 7
AAR75084
ID AAR75084 standard; Protein; 455 AA.
XX
AC AAR75084;
XX
DT 19-JAN-1996 (first entry)
XX
DE p55 TNF-R.
XX
KW p55; tumour necrosis factor receptor; TNF-R; human; murine; chimera;
KW epidermal growth factor receptor; EGF-R; protease; inhibitor;
KW phorbol myristate acetate; PMA.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
FT	Peptide	41..53
FT		/note= "N terminus of soluble p55 TNF-R"
FT	Modified-site	54..56
FT		/note= "glycosylation site"
FT	Modified-site	145..147
FT		/note= "glycosylation site"
FT	Modified-site	161..163
FT		/note= "glycosylation site"
FT	Peptide	193..210
FT		/note= "peptide used in creation of chimeras"
FT	Region	198..210
FT		/note= "spacer region"
FT	Misc-difference	201
FT		/note= "major C terminus for soluble p55 TNF-R"
FT	Misc-difference	202
FT		/note= "essential for shedding reaction"
FT	Misc-difference	203
FT		/note= "minor C terminus for soluble p55 TNF-R"
FT	Region	212..234
FT		/note= "transmembrane region"

XX
PN AU9475742-A.
XX
PD 04-MAY-1995.
XX
PF 11-OCT-1994; 94AU-0075742.
XX
PR 12-OCT-1993; 93IL-0107268.
XX
PA (YEDA) YEDA RES & DEV CO LTD.
XX
PI Batkin M, Brakebusch C, Varfolomeev E, Wallach D;
XX
DR WPI; 1995-194342/26.
DR N-PSDB; AAQ90513.
XX
PT New protease capable of cleaving soluble tumour necrosis factor
PT (TNF) receptor - from cell-bound TNF- receptor, useful for
PT antagonising deleterious effects of TNF.
XX
PS Disclosure; Fig 1; 40pp; English.
XX
CC This sequence represents human p55 tumour necrosis factor (TNF-R).
CC Expression of this receptor is regulated by shedding of the
CC extracellular receptor fragment. The p55 TNF-R can be shed in response
CC to different inducing agents, e.g. phorbol myristate acetate (PMA),
CC depending on cell type. The only region of the receptor whose structure
CC affects the shedding response is the spacer region (see AAR75012) in the
CC extracellular domain. This region is located close to a site of cleavage

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CC   of the molecule, and links the Cys rich module to the transmembrane
CC   domain.  The spacer region of the encoded protein was used to create the
CC   chimeras between human p55 TNF-R and murine epidermal growth factor
CC   receptor (EGF-R) that are represented by AAR75007-11.  This spacer region
CC   was subjected to deletion mutations (AAR75013-25) and substitutions
CC   (AAR75026-47).  Of the spacer region, the most important residues are
CC   Asn 172, Val 173, Lys 174 and Gly 175, with Val 173 being the most
CC   important of these.  The shedding of the receptor is independent of the
CC   side chain identity of these residues, with the exception of a limited
CC   dependence on the identity of Val 173.  Mutations which alter the
CC   conformation of the protein adversely effect the shedding process.
CC   The mutations shown in AAR75013-47 were introduced in order to create an
CC   inhibitor of a protease that is capable of cleaving the soluble TNF-R
CC   from the cell bound TNF-R.  Fragments of these inhibitors can be seen in
CC   AAR75017-9, AAR75025, AAR75033-5 and AAR75042-3.  These protease
CC   inhibitors can be used for enhancing TNF function.
XX
SQ   Sequence   455 AA;

  Query Match             58.3%;  Score 1517;  DB 16;  Length 455;
  Best Local Similarity   62.9%;  Pred. No. 1.4e-95;
  Matches  302;  Conservative   38;  Mismatches  104;  Indels   36;  Gaps    7;

Qy          1 MGLPTVPGLLLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCT 60
              ||| ||| |||||||  ||  :||:|| ||||| || |||:| |||||| ||||::||||
Db          1 MGLSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCT 60

Qy         61 KCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCLSCSRCRDEMFQVEISPCVVD 120
              ||||||||||||||||:|||||  |   |::|| ||||| |||||:|| || ||||| | ||
Db         61 KCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVD 120

Qy        121 RDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQERQDTICHCHMGFFLKGAKCI 180
              |||||||||||||| || |  |:| ||||| ||||:: |||:|:|:| || ||||:  :|:
Db        121 RDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECV 180

Qy        181 SCHDCKNK-ECEKLCPTRPSTGKDSQDPGTTVLLPLVIVFGLCLASFASVVLACRYQRWK 239
              || :||   || |||  :    | ::| ||||||||| ||||| |   : |  ||||||
Db        181 SCSNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPLVIFFGLCLLSLLFIGLMYRYQRWK 240

Qy        240 PKLYSIICGQSTLVKEGEPE-----LLVPAPGFNP----TTTICFSSTPSSSPVSIPPYI 290
              |||||:||:||  |||| |       | | | |:|    | |: ||  |||:  |   |
Db        241 SKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPTPGFTPTLGFSPVPSSTFTSSSTYT 300

Qy        291 SCDRSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLC 350
              |  ||   |:|  | |||:  | |||                  :| |      ||  :
Db        301 PGDCPNF---AAPRREVAPPYQGADPIL----------------ATAL------ASDPIP 335

Qy        351 TPVQKWEASAPSAPDQLADADPATLYAVVDGVPPSRWKELVRRLGLSEHEIERLELENGR 410
              |:|||| ||   |  |  |||||||||: ||| |||| ||||||:|||:||||:|||
Db        336 NPLQKWEDSA-HKPQSLDTDDPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLELQNGR 394

Qy        411 HLREAQYSMLAAWRRRTPRREATLELLGRVLRDMDLLGCLENIEEALGGAARLASEPRLL 470
              |||||||||| |||||||||||||||||||||||||||||:|||| | | |   | ||
Db        395 CLREAQYSMLATWRRRTPRREATLELLGRVLRDMDLLGCLEDIEEALCGPAALPPAPSLL 454


RESULT 8
AAY30934
ID   AAY30934 standard; Protein; 455 AA.
XX
AC   AAY30934;
XX
DT   20-MAR-2003  (updated)
DT   18-OCT-1999  (first entry)
XX
DE   Human tumour necrosis factor binding protein.
XX
KW   Tumour necrosis factor binding protein; TNF; insoluble protein; agonist;
KW   anti-inflammatory; antimalarial; treatment; septic shock; inflammation;
KW   autoimmune glomerulonephritis; cerebral malaria; immune response;
KW   antagonist; diagnosis.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..29
FT                   /label= signal_peptide
FT   Protein         30..455
FT   Modified-site   34
FT                   /note= "hypothetical glycosylation site"
FT   Modified-site   125
FT                   /note= "hypothetical glycosylation site"
FT   Modified-site   131
FT                   /note= "hypothetical glycosylation site"
FT   Region          212..230
FT                   /note= "transmembrane region"
FT   Modified-site   250
FT                   /note= "hypothetical glycosylation site"
XX
PN   EP939121-A2.
XX
PD   01-SEP-1999.
XX
PF   31-AUG-1990;   99EP-0100703.
XX
PR   12-SEP-1989;   89CH-0003319.
PR   08-MAR-1990;   90CH-0000746.
PR   20-APR-1990;   90CH-0001347.
PR   31-AUG-1990;   90EP-0116707.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
PI   Brockhaus M,  Dembic Z,  Gentz R,  Lesslauer W,  Loetscher H;
PI   Schlaeger E;
XX
DR   WPI; 1999-480840/41.
DR   N-PSDB; AAZ09170.
XX
PT   New insoluble proteins, and fragments, that bind to tumor necrosis
PT   factor, used to treat e.g. septic shock or cerebral malaria
XX
PS   Claim 4a; Fig 1; 25pp; German.
XX
CC   This invention describes novel homogeneous insoluble proteins (I),
CC   their (in)soluble fragments (Ia) and their salts that can bind tumour
CC   necrosis factor (TNF). The products of the invention have
CC   anti-inflammatory and antimalarial activity. (I) and (Ia) are used (i)
CC   to treat diseases in which TNF is involved (e.g. septic shock, autoimmune
CC   glomerulonephritis, cerebral malaria, immune responses and inflammation),
CC   (ii) to purify TNF, (iii) to identify TNF (ant)agonists and (iv) for
CC   diagnostic determination of TNF in body fluids. Antibodies raised against
CC   (I) are used for affinity purification of (I). This sequence represents
CC   a tumour necrosis factor binding protein described in the method of
CC   the invention.
CC   (Updated on 20-MAR-2003 to correct PF field.)
CC   (Updated on 20-MAR-2003 to correct PR field.)
XX
SQ   Sequence   455 AA;

  Query Match             58.3%;  Score 1517;  DB 20;  Length 455;
  Best Local Similarity   62.9%;  Pred. No. 1.4e-95;
  Matches  302;  Conservative   38;  Mismatches  104;  Indels   36;  Gaps    7;

Qy          1 MGLPTVPGLLLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCT 60
              ||| ||| |||||||  ||  :||:|| ||||| || |||:| |||||| ||||::||||
Db          1 MGLSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCT 60

Qy         61 KCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCLSCSRCRDEMFQVEISPCVVD 120
              ||||||||||||||||:|||||  |   |::|| ||||| |||||:|| || ||||| | ||
Db         61 KCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVD 120

Qy        121 RDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQERQDTICHCHMGFFLKGAKCI 180
              |||||||||||||| || |  |:| ||||| ||||:: |||:|:|:| || ||||:  :|:
Db        121 RDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECV 180

Qy        181 SCHDCKNK-ECEKLCPTRPSTGKDSQDPGTTVLLPLVIVFGLCLASFASVVLACRYQRWK 239
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Db        181 SCSNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPLVIFFGLCLLSLLFIGLMYRYQRWK 240

Qy        240 PKLYSIICGQSTLVKEGEPE-----LLVPAPGFNP----TTTICFSSTPSSSPVSIPPYI 290

Db        241 SKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPTPGFTPTLGFSPVPSSTFTSSSTYT 300

Qy        291 SCDRSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLC 350

Db        301 PGDCPNF---AAPRREVAPPYQGADPIL----------------ATAL------ASDPIP 335

Qy        351 TPVQKWEASAPSAPDQLADADPATLYAVVDGVPPSRWKELVRRLGLSEHEIERLELENGR 410

Db        336 NPLQKWEDSA-HKPQSLDTDDPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLELQNGR 394

Qy        411 HLREAQYSMLAAWRRRTPRREATLELLGRVLRDMDLLGCLENIEEALGGAARLASEPRLL 470

Db        395 CLREAQYSMLATWRRRTPRREATLELLGRVLRDMDLLGCLEDIEEALCGPAALPPAPSLL 454
```

RESULT 9
AAB36266
ID AAB36266 standard; Protein; 455 AA.
XX
AC AAB36266;
XX
DT 20-FEB-2001 (first entry)
XX
DE Human tumour necrosis factor receptor 1.
XX
KW Human; death domain containing receptor; DR3-V1; cancer;
KW autoimmune disorder; inflammation; cardiovascular disorder; infection;
KW neurodegenerative disease; angiogenesis.
XX
OS Homo sapiens.
XX
PN WO200064465-A1.
XX
PD 02-NOV-2000.
XX
PF 21-APR-2000; 2000WO-US10741.
XX
PR 22-APR-1999; 99US-0130488.
PR 28-MAY-1999; 99US-0136741.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (UNMI) UNIV MICHIGAN.
PA (YUGG/) YU G.
PA (NIJJ/) NI J.
PA (GENT/) GENTZ R L.
PA (DILL/) DILLON P J.
PA (DIXI/) DIXIT V M.
XX
PI Yu G, Ni J, Gentz RL, Dillon PJ, Dixit VM;
XX
DR WPI; 2000-687263/67.
XX
PT Treating graft-versus-host disease, cancer, immunodeficiency or an
PT autoimmune disease comprising administering an antibody to Death Domain
PT Containing Receptor proteins and a second therapeutic agent -
XX
PS Disclosure; Fig 3; 273pp; English.
XX
CC The present invention provides the protein and coding sequences for two
CC death domain containing receptors, designated DR3 and DR3-V1. These
CC receptors are involved in apoptosis, and the sequences given can be used
CC in the treatment of cancers, infections, cardiovascular disorders such as
CC arrhythmias, ischaemia, aneurysms, arterial occlusive diseases, embolisms
CC and congenital heart defects, neurodegenerative diseases including
CC Alzheimer's and Parkinson's diseases, autoimmune disease such as multiple
CC sclerosis, arthritis, diabetes, Graves' disease, asthma and psoriasis,
CC and to promote angiogenesis and wound healing.
XX

SQ Sequence 455 AA;

Query Match 58.3%; Score 1517; DB 21; Length 455;
Best Local Similarity 62.9%; Pred. No. 1.4e-95;
Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

```
Qy          1 MGLPTVPGLLLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCT 60

Db          1 MGLSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCT 60

Qy         61 KCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCLSCSRCRDEMFQVEISPCVVD 120

Db         61 KCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVD 120

Qy        121 RDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQERQDTICHCHMGFFLKGAKCI 180

Db        121 RDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECV 180

Qy        181 SCHDCKNK-ECEKLCPTRPSTGKDSQDPGTTVLLPLVIVFGLCLASFASVVLACRYQRWK 239

Db        181 SCSNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPLVIFFGLCLLSLLFIGLMYRYQRWK 240

Qy        240 PKLYSIICGQSTLVKEGEPE-----LLVPAPGFNP----TTTICFSSTPSSSPVSIPPYI 290

Db        241 SKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPTPGFTPTLGFSPVPSSTFTSSSTYT 300

Qy        291 SCDRSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLC 350

Db        301 PGDCPNF---AAPRREVAPPYQGADPIL----------------ATAL------ASDPIP 335

Qy        351 TPVQKWEASAPSAPDQLADADPATLYAVVDGVPPSRWKELVRRLGLSEHEIERLELENGR 410

Db        336 NPLQKWEDSA-HKPQSLDTDDPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLELQNGR 394

Qy        411 HLREAQYSMLAAWRRRTPRREATLELLGRVLRDMDLLGCLENIEEALGGAARLASEPRLL 470

Db        395 CLREAQYSMLATWRRRTPRREATLELLGRVLRDMDLLGCLEDIEEALCGPAALPPAPSLL 454
```

RESULT 10
AAB37800
ID AAB37800 standard; Protein; 455 AA.
XX
AC AAB37800;
XX
DT 23-FEB-2001 (first entry)
XX
DE Human tumour necrosis factor p55 receptor.
XX
KW Human; tumour necrosis factor; TNF; TNF-alpha; TNF-beta; p55 receptor;
KW p75 receptor; antiinflammatory; haemostatic; antibacterial; sepsis;
KW immunosuppressive; immunomodulator; cardiant; cytostatic; cachexia;
KW neuroprotective; respiratory; inflammation; infection; Crohn's disease;
KW multiple sclerosis; autoimmune disorder; cardiovascular disorder;
KW chronic myelogenous leukaemia; inflammatory bowel disease.
XX
OS Homo sapiens.
XX
PN WO200064479-A1.
XX
PD 02-NOV-2000.
XX
PF 26-APR-2000; 2000WO-US11700.
XX
PR 27-APR-1999; 99US-0301274.
XX
PA (ANTI-) ANTIBODY SYSTEMS INC.
XX
PI Fredeking TM, Ignatyev GM;
XX
DR WPI; 2000-679646/66.
XX
PT Novel compositions comprising tetracycline or tetracycline-like

PT compounds for the treatment and/or prevention of acute inflammatory
PT responses and diseases, e.g. septic shock and immune complex-induced
PT colitis -
XX
PS Disclosure; Page 167-169; 183pp; English.
XX
CC The present sequence is given in a specification relating to novel
CC compositions and methods containing tetracycline or tetracycline-like
CC compounds for treating and/or preventing acute inflammatory responses and
CC diseases. Such diseases include acute inflammatory conditions associated
CC with viral haemorrhagic diseases (including diseases caused by
CC Bunyaviridea, Filoviridae, Flaviviridae or Arenaviridae viruses),
CC parasitic diseases, bacterial infections, sepsis, cachexia, autoimmune
CC disorders, acute cardiovascular events, chronic myelogenous leukaemia and
CC transplanted bone marrow-induced graft-versus-host disease, septic shock,
CC immune complex-induced colitis, cerebrospinal fluid inflammation,
CC multiple sclerosis, inflammatory responses associated with trauma,
CC systemic inflammatory response syndrome (SIRS), adult respiratory
CC distress syndrome (ARDS), acute liver failure, inflammatory bowel disease
CC and Crohn's disease.
XX
SQ Sequence 455 AA;

Query Match 58.3%; Score 1517; DB 21; Length 455;
Best Local Similarity 62.9%; Pred. No. 1.4e-95;
Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

```
Qy          1 MGLPTVPGLLLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCT 60
              ||| ||| ||||||| || :||:|| ||||| || |||:| |||||| ||||::||||
Db          1 MGLSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCT 60

Qy         61 KCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCLSCSRCRDEMFQVEISPCVVD 120
              ||||||||||||||:|||| |  |::|| ||||| |||||:|| || ||||| | ||
Db         61 KCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVD 120

Qy        121 RDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQERQDTICHCHMGFFLKGAKCI 180
              |||||||||||| || |  |:| ||||| |||:: |||:|:|:| || ||||:  :|:
Db        121 RDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECV 180

Qy        181 SCHDCKNK-ECEKLCPTRPSTGKDSQDPGTTVLLPLVIVFGLCLASFASVVLACRYQRWK 239
              || :||   || |||  :    | ::| |||||||||| ||||| |   : |  ||||||
Db        181 SCSNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPLVIFFGLCLLSLLFIGLMYRYQRWK 240

Qy        240 PKLYSIICGQSTLVKEGEPE-----LLVPAPGFNP----TTTICFSSTPSSSPVSIPPYI 290
              |||||:||:||  |||| |      | | | |:|    | |: ||  |||:  |   |
Db        241 SKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPTPGFTPTLGFSPVPSSTFTSSSTYT 300

Qy        291 SCDRSNPGAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLC 350
              |  ||   |:|  | |||:  | |||                :| |      ||  :
Db        301 PGDCPNP---AAPRREVAPPYQGADPIL---------------ATAL------ASDPIP 335

Qy        351 TPVQKWEASAPSAPDQLADADPATLYAVVDGVPPSRWKELVRRLGLSEHEIERLELENGR 410
              |:|||| ||   |  |||||||||: ||| |||| |||||||:|||:||||:|||
Db        336 NPLQKWEDSA-HKPQSLDTDDPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLELQNGR 394

Qy        411 HLREAQYSMLAAWRRRTPRREATLELLGRVLRDMDLLGCLENIEEALGGAARLASEPRLL 470
              |||||||||| |||||||||||||||||||||||||||||:|||| | | |   | ||
Db        395 CLREAQYSMLATWRRRTPRREATLELLGRVLRDMDLLGCLEDIEEALCGPAALPPAPSLL 454
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RESULT 11
AAB26984
ID AAB26984 standard; Protein; 455 AA.
XX
AC AAB26984;
XX
DT 02-FEB-2001 (first entry)
XX
DE Human TNFR 1.
XX
KW Human; TNFR 1; tumour necrosis factor; TR9 receptor; immunosuppressive;
KW antiinflammatory; cardiant; antiasthmatic; antidiabetic; antiallergic;
KW antiathritic; antirheumatic; anti-HIV; anticonvulsant; cytostatic;
KW neuroprotective; gene therapy; Death Domain Containing Receptor 6;
KW common variable immunodeficiency; X-linked agammaglobulinaemia;
KW severe combined immunodeficiency; Wiskott-Aldrich syndrome;
KW autoimmune disease; rheumatoid arthritis; allergic encephalomyelitis;
KW multiple sclerosis; diabetes mellitus; asthma; epilepsy; cancer;
KW cardiovascular disease; neurological disease; protein coordinate data.
XX
OS Homo sapiens.
XX
PN WO200056862-A1.
XX
PD 28-SEP-2000.
XX
PF 16-MAR-2000; 2000WO-US06831.
XX
PR 24-MAR-1999; 99US-0126019.
PR 14-MAY-1999; 99US-0134220.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ni J, Gentz RL, Yu G, Fan P;
XX
DR WPI; 2000-594575/56.
XX
PT Nucleic acid molecule encoding a human tumor necrosis factor receptor,
PT known as TR9, useful for treating, preventing and diagnosing severe
PT combined immunodeficiency, autoimmune diseases, HIV infection, epilepsy
PT and cancer -
XX
PS Disclosure; Fig 2; 220pp; English.
XX
CC The present sequence is TNFR 1, a member of the tumour necrosis factor
CC receptor family. A novel human tumour necrosis factor receptor,
CC designated TR9, has been isolated. The TR9 receptor is also known as
CC Death Domain Containing Receptor 6. TR9 polypeptides, polynucleotides or
CC agonists are useful for treating, preventing or diagnosing common
CC variable immunodeficiency, X-linked agammaglobulinaemia, severe combined
CC immunodeficiency and Wiskott-Aldrich syndrome, autoimmune diseases (such
CC as rheumatoid arthritis, allergic encephalomyelitis, multiple sclerosis,
CC diabetes mellitus and asthma), HIV infection, epilepsy, cancer,
CC cardiovascular diseases and other neurological diseases.
XX
SQ Sequence 455 AA;

Query Match 58.3%; Score 1517; DB 21; Length 455;
Best Local Similarity 62.9%; Pred. No. 1.4e-95;
Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

```
Qy          1 MGLPTVPGLLLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCT 60
              ||| ||| ||||||| || :||:|| ||||| || |||:| |||||| ||||::||||
Db          1 MGLSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCT 60

Qy         61 KCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCLSCSRCRDEMFQVEISPCVVD 120
              ||||||||||||||:|||| |  |::|| ||||| |||||:|| || ||||| | ||
Db         61 KCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVD 120

Qy        121 RDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQERQDTICHCHMGFFLKGAKCI 180
              |||||||||||| || |  |:| ||||| |||:: |||:|:|:| || ||||:  :|:
Db        121 RDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECV 180

Qy        181 SCHDCKNK-ECEKLCPTRPSTGKDSQDPGTTVLLPLVIVFGLCLASFASVVLACRYQRWK 239
              || :||   || |||  :    | ::| |||||||||| ||||| |   : |  ||||||
Db        181 SCSNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPLVIFFGLCLLSLLFIGLMYRYQRWK 240

Qy        240 PKLYSIICGQSTLVKEGEPE-----LLVPAPGFNP----TTTICFSSTPSSSPVSIPPYI 290
              |||||:||:||  |||| |      | | | |:|    | |: ||  |||:  |   |
Db        241 SKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPTPGFTPTLGFSPVPSSTFTSSSTYT 300

Qy        291 SCDRSNPGAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLC 350
              |  ||   |:|  | |||:  | |||                :| |      ||  :
Db        301 PGDCPNF---AAPRREVAPPYQGADPIL---------------ATAL------ASDPIP 335

Qy        351 TPVQKWEASAPSAPDQLADADPATLYAVVDGVPPSRWKELVRRLGLSEHEIERLELENGR 410
```

```
              |:|||| ||   | | |  |||||||||: ||| |||| |||||||:|||:||||:|||
Db        336 NPLQKWEDSA-HKPQSLDTDDPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLELQNGR 394

Qy        411 HLREAQYSMLAAWRRRTPRREATLELLGRVLRDMDLLGCLENIEEALGGAARLASEPRLL 470
              |||||||||| |||||||||||||||||||||||||||||:|||| | | |   | ||
Db        395 CLREAQYSMLATWRRRTPRREATLELLGRVLRDMDLLGCLEDIEEALCGPAALPPAPSLL 454


RESULT 12
AAB23446
ID   AAB23446 standard; Protein; 455 AA.
XX
AC   AAB23446;
XX
DT   12-JAN-2001  (first entry)
XX
DE   Human tumour necrosis factor receptor 1 protein.
XX
KW   TNFR1; tumour necrosis factor receptor; polymorphism; human;
KW   tumour; cancer; apoptosis; bacterial infection.
XX
OS   Homo sapiens.
XX
PN   WO200050436-A1.
XX
PD   31-AUG-2000.
XX
PF   23-FEB-2000; 2000WO-US04606.
XX
PR   23-FEB-1999;   99US-0121314.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
PA   (NAND/) NANDABALAN K.
PA   (SCHU/) SCHULZ V P.
PA   (STEP/) STEPHENS J C.
PA   (CHEW/) CHEW A.
XX
PI   Nandabalan K,  Schulz VP,  Stephens JC,  Chew A;
XX
DR   WPI; 2000-543909/49.
DR   N-PSDB; AAA95105.
XX
PT   Polynucleotides comprising polymorphic variants of a reference sequence
PT   for tumour necrosis factor receptor 1 (TNFR1), useful for studying the
PT   biological function of TNFR1 and identifying drugs targeting the
PT   protein for treating disorders -
XX
PS   Claim 10; Fig 5; 79pp; English.
XX
CC   The present invention relates to polymorphic variants of the tumour
CC   necrosis factor receptor 1 (TNFR1) gene. The present sequence is
CC   the TNFR1 protein. The sequence of the whole gene is given in AAA95102,
CC   AAA95103 and AAA95104. The polymorphisms were identified by amplifying
CC   and sequencing regions of the gene. Twelve polymorphic loci
CC   were discovered. Of these twelve polymorphisms, four can cause a
CC   change in the TNFR1 protein.  The TNFR1 polymorphisms may be useful
CC   for studying the biological function of TNFR1 as well as for
CC   identifying drugs targeting the protein for treatment of disorders
CC   related to its abnormal expression or function such as tumours,
CC   apoptosis related disorders and bacterial infection.
XX
SQ   Sequence   455 AA;

  Query Match             58.3%;  Score 1517;  DB 21;  Length 455;
  Best Local Similarity   62.9%;  Pred. No. 1.4e-95;
  Matches  302;  Conservative   38;  Mismatches  104;  Indels   36;  Gaps    7;

Qy          1 MGLPTVPGLLLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCT 60
              ||| ||| |||||||  ||  :||:|| ||||| || |||:| |||||| ||||::|||
Db          1 MGLSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCT 60

Qy         61 KCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCLSCSRCRDEMFQVEISPCVVD 120
              ||||||||||||||||:||||| |  |::|| ||||| ||||||:|| || ||||| | ||
Db         61 KCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVD 120

Qy        121 RDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQERQDTICHCHMGFFLKGAKCI 180
              |||||||||||||| || |  |:| ||||| ||||:: |||:|:|:| || ||||:  :|:
Db        121 RDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECV 180

Qy        181 SCHDCKNK-ECEKLCPTRPSTGKDSQDPGTTVLLPLVIVFGLCLASFASVVLACRYQRWK 239
              || :||   || |||  :    | ::| |||||||||| ||||| |   : |  ||||||
Db        181 SCSNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPLVIFFGLCLLSLLFIGLMYRYQRWK 240

Qy        240 PKLYSIICGQSTLVKEGEPE-----LLVPAPGFNP----TTTICFSSTPSSSPVSIPPYI 290
              |||||:||:||  |||| |      | | | |:|    | |: ||  |||:  |   |
Db        241 SKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPTPGFTPTLGFSPVPSSTFTSSSTYT 300

Qy        291 SCDRSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLC 350
              |  ||   |:|  | |||:  | |||           :| |     ||  :
Db        301 PGDCPNF---AAPRREVAPPYQGADPIL---------------ATAL------ASDPIP 335

Qy        351 TPVQKWEASAPSAPDQLADADPATLYAVVDGVPPSRWKELVRRLGLSEHEIERLELENGR 410
              |:|||| ||   |  |  |||||||||: ||| |||| |||||||:|||:||||:|||
Db        336 NPLQKWEDSA-HKPQSLDTDDPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLELQNGR 394

Qy        411 HLREAQYSMLAAWRRRTPRREATLELLGRVLRDMDLLGCLENIEEALGGAARLASEPRLL 470
              |||||||||| |||||||||||||||||||||||||||||:|||| | | |   | ||
Db        395 CLREAQYSMLATWRRRTPRREATLELLGRVLRDMDLLGCLEDIEEALCGPAALPPAPSLL 454


RESULT 13
AAB01336
ID   AAB01336 standard; Protein; 455 AA.
XX
AC   AAB01336;
XX
DT   25-SEP-2000  (first entry)
XX
DE   TNF-R1 death receptor.
XX
KW   UL144; death receptor; apoptosis; programmed cell death; FAS;
KW   TNF-R1; TRAMP; DR-6; TRAIL; modulation; treatment; cancer; virus;
KW   human.
XX
OS   Homo sapiens.
XX
PN   WO200034335-A2.
XX
PD   15-JUN-2000.
XX
PF   03-DEC-1999;   99WO-US26035.
XX
PR   04-DEC-1998;   98US-0205018.
XX
PA   (SCHE ) SCHERING CORP.
XX
PI   Leong C,  Phillips JH;
XX
DR   WPI; 2000-423383/36.
XX
PT   Purified or recombinant polypeptide for modulating apoptosis comprises
PT   a sequence which binds to an antibody specific for UL144 or its
PT   fragments
XX
PS   Disclosure; Page 65-67; 76pp; English.
XX
CC   A pure or recombinant polypeptide which binds to a polyclonal antibody
CC   specific for the mature UL144 is useful for screening molecules which
CC   block induction of apoptosis or interfere with antiapoptotic activity.
CC   The polypeptide is also useful for modulating apoptosis and useful in
CC   treatment of conditions associated with abnormal physiology or
CC   development, such as cancer or degenerative conditions and for
CC   regulation of viral infection and replication. At least five
CC   different death receptors are known, which include the CD95
CC   (Fas/APO-1), the TNF receptor-1, TNF receptor apoptosis-mediated
CC   protein (TRAMP), death receptor-6 (DR-6), and TNF-related
```

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CC   apoptosis-inducing ligand (TRAIL) receptors 1, 2 and 4.
XX
SQ   Sequence   455 AA;

  Query Match           58.3%;  Score 1517;  DB 21;  Length 455;
  Best Local Similarity   62.9%;  Pred. No. 1.4e-95;
  Matches  302;  Conservative   38;  Mismatches  104;  Indels   36;  Gaps    7;

Qy          1 MGLPTVPGLLLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCT 60
              ||| ||| |||||||  ||  :||:|| ||||| || |||:| |||||| ||||::||||
Db          1 MGLSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCT 60

Qy         61 KCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCLSCSRCRDEMFQVEISPCVVD 120
              |||||||||||||||:|||||  |  |::|| ||||| |||||:|| || ||||| | ||
Db         61 KCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVD 120

Qy        121 RDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQERQDTICHCHMGFFLKGAKCI 180
              |||||||||||||  ||  |  |:| ||||| ||||:: |||:|:|:|  || ||||:  :|:
Db        121 RDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECV 180

Qy        181 SCHDCKNK-ECEKLCPTRPSTGKDSQDPGTTVLLPLVIVFGLCLASFASVVLACRYQRWK 239
              || :||   || |||  :    | ::| |||||||||| ||||| |   : |  ||||||
Db        181 SCSNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPLVIFFGLCLLSLLFIGLMYRYQRWK 240

Qy        240 PKLYSIICGQSTLVKEGEPE-----LLVPAPGFNP----TTTICFSSTPSSSPVSIPPYI 290
              |||||:||:||  |||| |       | | | |:|    | |: ||  |||:  |   |
Db        241 SKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPTPGFTPTLGFSPVPSSTFTSSSTYT 300

Qy        291 SCDRSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLC 350
              |  ||   |:|  | |||:  | |||                :| |      ||  :
Db        301 PGDCPNF---AAPRREVAPPYQGADPIL---------------ATAL------ASDPIP 335

Qy        351 TPVQKWEASAPSAPDQLADADPATLYAVVDGVPPSRWKELVRRLGLSEHEIERLELENGR 410
              |:|||| ||   |  |  |||||||||: ||| |||| |||||||:|||:||||:|||
Db        336 NPLQKWEDSA-HKPQSLDTDDPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLELQNGR 394

Qy        411 HLREAQYSMLAAWRRRTPRREATLELLGRVLRDMDLLGCLENIEEALGGAARLASEPRLL 470
              |||||||||| ||||||||||||||||||||||||||||:||||| | | |   | ||
Db        395 CLREAQYSMLATWRRRTPRREATLELLGRVLRDMDLLGCLEDIEEALCGPAALPPAPSLL 454


RESULT 14
AAB86817
ID   AAB86817 standard; Protein; 455 AA.
XX
AC   AAB86817;
XX
DT   12-NOV-2001  (first entry)
XX
DE   Human TNFBP-associated protein #1.
XX
KW   TNF; tumor necrosis factor binding protein; TNFBP; treatment;
KW   insoluble protein; antiinflammatory; immunosuppressive; antibacterial;
KW   antiprotozoal; treatment; meningococcal sepsis; cerebral malaria;
KW   autoimmune glomerulonephritis.
XX
OS   Homo sapiens.
XX
PN   EP1132471-A2.
XX
PD   12-SEP-2001.
XX
PF   31-AUG-1990; 2001EP-0108117.
XX
PR   12-SEP-1989;   89CH-0003319.
PR   08-MAR-1990;   90CH-0000746.
PR   20-APR-1990;   90CH-0001347.
PR   31-AUG-1990;   90EP-0116707.
PR   31-AUG-1990;   99EP-0100703.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
PI   Brockhaus M,  Dembic Z,  Gentz R,  Lesslauer W,  Loetscher H;
PI   Schlaeger E;
XX
DR   WPI; 2001-559312/63.
DR   N-PSDB; AAH48859.
XX
PT   New homogeneous, insoluble proteins that bind tumor necrosis factor
PT   (TNF), useful for treating TNF-mediated disorders, e.g. inflammation -
XX
PS   Claim 4a; Fig 1; 26pp; German.
XX
CC   This invention describes novel insoluble proteins (I), also their
CC   (in)soluble fragments and pharmaceutically acceptable salts, able to bind
CC   tumor necrosis factor (TNF) and in homogeneous form. The products of the
CC   invention have antiinflammatory, immunosuppressive, antibacterial,
CC   antiprotozoal activity. (I), and related recombinant proteins, are used
CC   to treat diseases mediated by TNF, e.g. shock in cases of meningococcal
CC   sepsis; development of autoimmune glomerulonephritis and cerebral
CC   malaria. Also (I), or antibodies specific for them, are used for
CC   diagnostic determination of TNF in body fluids, for affinity purification
CC   of TNF and for identifying (ant)agonists of TNF. This sequence represents
CC   a human TNF binding protein described in the method of the invention.
XX
SQ   Sequence   455 AA;

  Query Match           58.3%;  Score 1517;  DB 22;  Length 455;
  Best Local Similarity   62.9%;  Pred. No. 1.4e-95;
  Matches  302;  Conservative   38;  Mismatches  104;  Indels   36;  Gaps    7;

Qy          1 MGLPTVPGLLLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCT 60
              ||| ||| |||||||  ||  :||:|| ||||| || |||:| |||||| ||||::||||
Db          1 MGLSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCT 60

Qy         61 KCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCLSCSRCRDEMFQVEISPCVVD 120
              |||||||||||||||:|||||  |  |::|| ||||| |||||:|| || ||||| | ||
Db         61 KCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVD 120

Qy        121 RDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQERQDTICHCHMGFFLKGAKCI 180
              |||||||||||||  ||  |  |:| ||||| ||||:: |||:|:|:|  || ||||:  :|:
Db        121 RDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECV 180

Qy        181 SCHDCKNK-ECEKLCPTRPSTGKDSQDPGTTVLLPLVIVFGLCLASFASVVLACRYQRWK 239
              || :||   || |||  :    | ::| |||||||||| ||||| |   : |  ||||||
Db        181 SCSNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPLVIFFGLCLLSLLFIGLMYRYQRWK 240

Qy        240 PKLYSIICGQSTLVKEGEPE-----LLVPAPGFNP----TTTICFSSTPSSSPVSIPPYI 290
              |||||:||:||  |||| |       | | | |:|    | |: ||  |||:  |   |
Db        241 SKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPTPGFTPTLGFSPVPSSTFTSSSTYT 300

Qy        291 SCDRSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLC 350
              |  ||   |:|  | |||:  | |||                :| |      ||  :
Db        301 PGDCPNF---AAPRREVAPPYQGADPIL---------------ATAL------ASDPIP 335

Qy        351 TPVQKWEASAPSAPDQLADADPATLYAVVDGVPPSRWKELVRRLGLSEHEIERLELENGR 410
              |:|||| ||   |  |  |||||||||: ||| |||| |||||||:|||:||||:|||
Db        336 NPLQKWEDSA-HKPQSLDTDDPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLELQNGR 394

Qy        411 HLREAQYSMLAAWRRRTPRREATLELLGRVLRDMDLLGCLENIEEALGGAARLASEPRLL 470
              |||||||||| ||||||||||||||||||||||||||||:||||| | | |   | ||
Db        395 CLREAQYSMLATWRRRTPRREATLELLGRVLRDMDLLGCLEDIEEALCGPAALPPAPSLL 454


RESULT 15
AAB36697
ID   AAB36697 standard; Protein; 455 AA.
XX
AC   AAB36697;
XX
DT   15-MAR-2001  (first entry)
XX
DE   Human tumour necrosis factor receptor TNFR1 protein SEQ ID NO:3.
XX
KW   Human; tumour necrosis factor receptor 5; TRID; TNFR-5; TR5; nootropic;
KW   TRAIL receptor without intracellular domain; diagnosis; cytostatic;
```

KW tumour necrosis factor related apoptosis inducing ligand; vasotropic;
KW immunosuppressive; neuroprotective; antiviral; antiinflammatory;
KW anticonvulsant; antiparasitic; cardiant; anti-HIV; antiparkinsonian;
KW gene therapy; restenosis; graft versus host disease; tumour; cancer;
KW apoptotic cell death related disease; autoimmune disorder;
KW cardiovascular disorder; viral infection.
XX
OS Homo sapiens.
XX
PN WO200071150-A1.
XX
PD 30-NOV-2000.
XX
PF 18-MAY-2000; 2000WO-US13515.
XX
PR 20-MAY-1999; 99US-0135164.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Wei Y, Ruben SM, Gentz RL, Ni J;
XX
DR WPI; 2001-041051/05.
XX
PT Nucleic acid encoding a TRID polypeptide, also referred to as tumor
PT necrosis factor receptor 5, useful in the diagnosis, treatment or
PT prevention of cancer, autoimmune disorders and viral infection -
XX
PS Disclosure; Fig 2; 285pp; English.
XX
CC The present invention describes the human TRID protein (tumour necrosis
CC factor (TNF) related apoptosis inducing ligand (TRAIL) receptor without
CC intracellular domain, also referred to as tumour necrosis factor
CC receptor 5 (TNFR-5 or TR5)). TRID has cytostatic, immunosuppressive,
CC nootropic, neuroprotective, antiviral, antiinflammatory, anticonvulsant,
CC antiparasitic, cardiant, anti-HIV, antiparkinsonian and vasotropic
CC activities, and can be used in gene therapy. The TRID polynucleotides
CC are useful for detecting complementary polynucleotides. TRID proteins and
CC polynucleotides are useful in the treatment of tumours, resistance to
CC parasite, bacteria and viruses, restenosis and graft versus host disease.
CC They are also useful for inducing proliferation of T-cells, endothelial
CC cells and certain haematopoietic cells, to regulate antiviral responses
CC and to prevent certain autoimmune diseases after stimulation of TRID by
CC an agonist or TRAIL binding facilitator. The antibodies which bind TRID
CC polypeptides are useful for treating and/or preventing diseases
CC associated with increased or decreased apoptotic cell death. The TRID
CC polynucleotides, proteins, antibodies, agonists and antagonists are
CC useful in the diagnosis, treatment or prevention of: (a) cancer;
CC (b) autoimmune disorders; (c) diseases associated with increased
CC apoptosis; (d) cardiovascular disorders; and (e) viral infection. The
CC present sequence represents a tumour necrosis factor receptor used in
CC comparison with TRID in the exemplification of the present invention.
XX
SQ Sequence 455 AA;

Query Match 58.3%; Score 1517; DB 22; Length 455;
Best Local Similarity 62.9%; Pred. No. 1.4e-95;
Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

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Qy          1 MGLPTVPGLLLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCT 60
              ||| ||| ||||||| ||  :||:|| ||||| || |||:| |||||| ||||::||||
Db          1 MGLSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCT 60

Qy         61 KCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCLSCSRCRDEMFQVEISPCVVD 120
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Db         61 KCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVD 120

Qy        121 RDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQERQDTICHCHMGFFLKGAKCI 180
              |||||||||||| || |  |:| ||||| ||||:: |||:|:|:| || ||||:  :|:
Db        121 RDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECV 180

Qy        181 SCHDCKNK-ECEKLCPTRPSTGKDSQDPGTTVLLPLVIVFGLCLASFASVVLACRYQRWK 239
              || :||   || |||  :    | ::| |||||||||| ||||| |   : |  ||||||
Db        181 SCSNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPLVIFFGLCLLSLLFIGLMYRYQRWK 240

Qy        240 PKLYSIICGQSTLVKEGEPE-----LLVPAPGFNP----TTTICFSSTPSSSPVSIPPYI 290
              |||||:||:||  |||| |      | | | |:|    | |: ||  |||:  |   |
Db        241 SKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPTPGFTPTLGFSPVPSSTFTSSSTYT 300

Qy        291 SCDRSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLC 350
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Qy        351 TPVQKWEASAPSAPDQLADADPATLYAVVDGVPPSRWKELVRRLGLSEHEIERLELENGR 410
              |:|||| ||   |  |||||||||: ||| |||| |||||||:|||:||||:|||
Db        336 NPLQKWEDSA-HKPQSLDTDDPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLELQNGR 394

Qy        411 HLREAQYSMLAAWRRRTPRREATLELLGRVLRDMDLLGCLENIEEALGGAARLASEPRLL 470
              |||||||||| ||||||||||||||||||||||||||||:||||| | | |   | ||
Db        395 CLREAQYSMLATWRRRTPRREATLELLGRVLRDMDLLGCLEDIEEALCGPAALPPAPSLL 454
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Search completed: September 13, 2003, 07:04:10
Job time : 48 secs

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OM protein - protein search, using sw model

Run on: September 13, 2003, 07:03:14 ; Search time 21 Seconds
(without alignments)
948.972 Million cell updates/sec

Title: US-09-970-532-2
Perfect score: 2603
Sequence: 1 MGLPTVPGLLLPLVLPALLA.....NIEEALGGAARLASEPRLLW 471

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2603	100.0	471	4	US-09-513-007-2	Sequence 2, Appli
2	1519	58.4	455	4	US-08-406-824A-4	Sequence 4, Appli
3	1517	58.3	455	1	US-08-321-668-2	Sequence 2, Appli
4	1517	58.3	455	1	US-08-837-941-2	Sequence 2, Appli
5	1517	58.3	455	2	US-08-126-016-2	Sequence 2, Appli
6	1517	58.3	455	3	US-08-815-469-5	Sequence 5, Appli
7	1517	58.3	455	3	US-09-006-353A-3	Sequence 3, Appli
8	1517	58.3	455	4	US-09-527-236A-5	Sequence 5, Appli
9	1517	58.3	455	4	US-08-054-970-2	Sequence 2, Appli
10	1517	58.3	455	4	US-09-565-918-4	Sequence 4, Appli
11	1517	58.3	455	4	US-09-573-986-3	Sequence 3, Appli
12	1517	58.3	455	4	US-09-027-287-3	Sequence 3, Appli
13	1517	58.3	455	4	US-09-252-656B-3	Sequence 3, Appli
14	1512	58.1	455	1	US-08-050-319B-25	Sequence 25, Appl
15	1512	58.1	455	2	US-08-465-982-25	Sequence 25, Appl
16	1500.5	57.6	909	4	US-09-013-895A-4	Sequence 4, Appli
17	1500.5	57.6	909	4	US-09-448-868-4	Sequence 4, Appli
18	1496	57.5	453	3	US-09-086-483A-5	Sequence 5, Appli
19	1496	57.5	453	4	US-09-580-212-5	Sequence 5, Appli
20	1423	54.7	426	4	US-08-747-562-37	Sequence 37, Appl
21	1072	41.2	181	4	US-09-513-007-4	Sequence 4, Appli
22	1019	39.1	280	3	US-08-974-022-46	Sequence 46, Appl
23	1019	39.1	280	3	US-08-795-445A-46	Sequence 46, Appl
24	1019	39.1	280	3	US-08-795-447A-46	Sequence 46, Appl
25	1019	39.1	280	3	US-08-974-186-46	Sequence 46, Appl
26	1019	39.1	280	3	US-08-795-446B-46	Sequence 46, Appl
27	1019	39.1	280	4	US-08-706-945D-132	Sequence 132, App
28	813.5	31.3	197	4	US-08-828-683A-21	Sequence 21, Appl
29	807.5	31.0	199	1	US-08-050-319B-48	Sequence 48, Appl
30	807.5	31.0	199	2	US-08-465-982-48	Sequence 48, Appl
31	727.5	27.9	336	3	US-08-804-166-8	Sequence 8, Appli
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33	719	27.6	167	1	US-08-050-319B-2	Sequence 2, Appli
34	719	27.6	167	1	US-08-050-319B-57	Sequence 57, Appl
35	719	27.6	167	2	US-08-465-982-2	Sequence 2, Appli
36	719	27.6	167	2	US-08-465-982-57	Sequence 57, Appl
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39	679	26.1	307	3	US-08-804-166-4	Sequence 4, Appli
40	679	26.1	307	3	US-08-910-991-4	Sequence 4, Appli
41	674.5	25.9	161	4	US-09-326-394-2	Sequence 2, Appli
42	670.5	25.8	153	2	US-08-219-237B-4	Sequence 4, Appli
43	670.5	25.8	153	3	US-08-477-347-12	Sequence 12, Appl
44	670.5	25.8	153	3	US-08-476-862-3	Sequence 3, Appli
45	670.5	25.8	153	3	US-08-468-560C-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-09-513-007-2
; Sequence 2, Application US/09513007
; Patent No. 6406907
; GENERAL INFORMATION:
; APPLICANT: Taylor, J. Michael
; APPLICANT: Kehrli, Jr., Marcus
; APPLICANT: Lee, Eun-Kyung
; APPLICANT: Mwangi, Simon
; TITLE OF INVENTION: BOVINE TUMOR NECROSIS FACTOR RECEPTOR-1
; TITLE OF INVENTION: AND METHODS OF USE
; FILE REFERENCE: 08411-018001
; CURRENT APPLICATION NUMBER: US/09/513,007
; CURRENT FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 60/122,156
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 471
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-513-007-2

Query Match 100.0%; Score 2603; DB 4; Length 471;
Best Local Similarity 100.0%; Pred. No. 5.6e-197;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MGLPTVPGLLLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGLPTVPGLLLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCT 60

Qy         61 KCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCLSCSRCRDEMFQVEISPCVVD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCLSCSRCRDEMFQVEISPCVVD 120

Qy        121 RDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQERQDTICHCHMGFFLKGAKCI 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQERQDTICHCHMGFFLKGAKCI 180

Qy        181 SCHDCKNKECEKLCPTRPSTGKDSQDPGTTVLLPLVIVFGLCLASFASVVLACRYQRWKP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SCHDCKNKECEKLCPTRPSTGKDSQDPGTTVLLPLVIVFGLCLASFASVVLACRYQRWKP 240

Qy        241 KLYSIICGQSTLVKEGEPELLVPAPGFNPTTTICPSSTPSSSPVSIPPYISCDRSNFGAV 300
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Qy        301 ASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLCTPVQKWEASA 360
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RESULT 2
US-08-406-824A-4
; Sequence 4, Application US/08406824A
; Patent No. 6541610
; GENERAL INFORMATION:
;  APPLICANT: SMITH, Craig A.
;  TITLE OF INVENTION: TUMOR NECROSIS FACTOR-ALPHA AND BETA-RECEPTORS
;  FILE REFERENCE: A-71592
;  CURRENT APPLICATION NUMBER: US/08/406,824A
;  CURRENT FILING DATE:  1995-03-20
;  PRIOR APPLICATION NUMBER: US 08/255,849
;  PRIOR FILING DATE: 1994-06-08
;  PRIOR APPLICATION NUMBER: US 07/860,710
;  PRIOR FILING DATE: 1992-03-30
;  PRIOR APPLICATION NUMBER: US  07/523,635
;  PRIOR FILING DATE: 1990-05-10
;  PRIOR APPLICATION NUMBER: US 07/421,417
;  PRIOR FILING DATE: 1989-10-13
;  PRIOR APPLICATION NUMBER: US 07/405,370
;  PRIOR FILING DATE: 1989-09-11
;  PRIOR APPLICATION NUMBER: US 07/403,241
;  PRIOR FILING DATE: 1989-09-05
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 455
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-08-406-824A-4

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  Best Local Similarity   62.9%;  Pred. No. 1e-111;
  Matches  302;  Conservative   39;  Mismatches  103;  Indels   36;  Gaps    7;

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Db          1 MGLSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCT 60

Qy         61 KCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCLSCSRCRDEMFQVEISPCVVD 120
              ||||||||||||||:||||| |  |::|| ||||| ||||||:|| || ||||| | ||
Db         61 KCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVD 120

Qy        121 RDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQERQDTICHCHMGFFLKGAKCI 180
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Db        121 RDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECV 180

Qy        181 SCHDCKNK-ECEKLCPTRPSTGKDSQDPGTTVLLPLVIVFGLCLASFASVVLACRYQRWK 239
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Db        181 SCSNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPLVIFFGLCLLSLLFIGLSYRYQRWK 240

Qy        240 PKLYSIICGQSTLVKEGEPE-----LLVPAPGFNP----TTTICFSSTPSSSPVSIPPYI 290
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Db        241 SKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPTPGFTPTLGFSPVPSSTFTSSSTYT 300

Qy        291 SCDRSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLC 350
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Qy        411 HLREAQYSMLAAWRRRTPRREATLELLGRVLRDMDLLGCLENIEEALGGAARLASEPRLL 470
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Db        395 CLREAQYSMLATWRRRTPRREATLELLGRVLRDMDLLGCLEDIEEALCGPAALPPAPSLL 454


RESULT 3
US-08-321-668-2
; Sequence 2, Application US/08321668
; Patent No. 5665859
;  GENERAL INFORMATION:
;    APPLICANT:  WALLACH, David
;    APPLICANT:  BRAKEBUSCH, Cord
;    APPLICANT:  VARFOLOMEEV, Eugene
;    APPLICANT:  BATKIN, Michael
;    TITLE OF INVENTION:  MOLECULES INFLUENCING THE SHEDDING OF
;    TITLE OF INVENTION:  THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE
;    NUMBER OF SEQUENCES:  42
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/321,668
;      FILING DATE:  12-OCT-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  IL 107268
;      FILING DATE:  12-OCT-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  WALLACH=13
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;      TELEX:  248633
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  455 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-321-668-2

  Query Match           58.3%;  Score 1517;  DB 1;  Length 455;
  Best Local Similarity   62.9%;  Pred. No. 1.5e-111;
  Matches  302;  Conservative   38;  Mismatches  104;  Indels   36;  Gaps    7;

Qy          1 MGLPTVPGLLLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCT 60
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Db          1 MGLSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCT 60

Qy         61 KCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCLSCSRCRDEMFQVEISPCVVD 120
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Db         61 KCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVD 120

Qy        121 RDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQERQDTICHCHMGFFLKGAKCI 180
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Db        121 RDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECV 180

Qy        181 SCHDCKNK-ECEKLCPTRPSTGKDSQDPGTTVLLPLVIVFGLCLASFASVVLACRYQRWK 239
              || :||   || |||  :    | ::| |||||||||| ||||| |   : |  ||||||
Db        181 SCSNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPLVIFFGLCLLSLLFIGLMYRYQRWK 240

Qy        240 PKLYSIICGQSTLVKEGEPE-----LLVPAPGFNP----TTTICFSSTPSSSPVSIPPYI 290
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Db        241 SKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPTPGFTPTLGFSPVPSSTFTSSSTYT 300

Qy        291 SCDRSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLC 350
              .|  ||   |:|  | |||:  | |||                :| |       ||  :
Db        301 PGDCPNF---AAPRREVAPPYQGADPIL---------------ATAL------ASDPIP 335

Qy        351 TPVQKWEASAPSAPDQLADADPATLYAVVDGVPPSRWKELVRRLGLSEHEIERLELENGR 410
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Db        336 NPLQKWEDSA-HKPQSLDTDDPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLELQNGR 394

Qy        411 HLREAQYSMLAAWRRRTPRREATLELLGRVLRDMDLLGCLENIEEALGGAARLASEPRLL 470
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Db        395 CLREAQYSMLATWRRRTPRREATLELLGRVLRDMDLLGCLEDIEEALCGPAALPPAPSLL 454


RESULT 4
US-08-837-941-2
; Sequence 2, Application US/08837941
; Patent No. 5766917
;  GENERAL INFORMATION:
;    APPLICANT:  WALLACH, David
;    APPLICANT:  BRAKEBUSCH, Cord
;    APPLICANT:  VARFOLOMEEV, Eugene
;    APPLICANT:  BATKIN, Michael
;    TITLE OF INVENTION:  MOLECULES INFLUENCING THE SHEDDING OF
;    TITLE OF INVENTION:  THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE
;    NUMBER OF SEQUENCES:  42
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/837,941
;      FILING DATE:  28-APR-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/321,668
;      FILING DATE:  12-OCT-1994
;      APPLICATION NUMBER:  IL 107268
;      FILING DATE:  12-OCT-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  WALLACH=13
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;      TELEX:  248633
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  455 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-837-941-2

  Query Match           58.3%;  Score 1517;  DB 1;  Length 455;
  Best Local Similarity   62.9%;  Pred. No. 1.5e-111;
  Matches  302;  Conservative   38;  Mismatches  104;  Indels   36;  Gaps    7;

Qy          1 MGLPTVPGLLLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCT 60
              ||| ||| ||||||| ||  :||:|| ||||| || |||:| |||||| ||||::||||
Db          1 MGLSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCT 60

Qy         61 KCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCLSCSRCRDEMFQVEISPCVVD 120
              |||||||||||||||:|||||  |  |:|| ||||| |||||:|| || ||||| | ||
Db         61 KCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVD 120

Qy        121 RDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQERQDTICHCHMGFFLKGAKCI 180
              |||||||||||| || |  |:| ||||| ||||:: |||:|:|:| || ||||:  :|:
Db        121 RDTVCGCRKNQYRHYWSENLPQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECV 180

Qy        181 SCHDCKNK-ECEKLCPTRPSTGKDSQDPGTTVLLPLVIVFGLCLASFASVVLACRYQRWK 239
              || :||   || |||  :   | ::| |||||||||| ||||| |   : |  ||||||
Db        181 SCSNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPLVIFFGLCLLSLLFIGLMYRYQRWK 240

Qy        240 PKLYSIICGQSTLVKEGEPE-----LLVPAPGFNP----TTTICFSSTPSSSPVSIPPYI 290
              |||||:||:||  |||| |      | | | |:|    | |: ||  |||:  |   |
Db        241 SKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPTPGFTPTLGFSPVPSSTFTSSSTYT 300

Qy        291 SCDRSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLC 350
              |  ||   |:|  | |||:  | |||                :| |       ||  :
Db        301 PGDCPNF---AAPRREVAPPYQGADPIL---------------ATAL------ASDPIP 335

Qy        351 TPVQKWEASAPSAPDQLADADPATLYAVVDGVPPSRWKELVRRLGLSEHEIERLELENGR 410
              |:|||| ||   |  |   |||||||||: ||| |||| ||||||:|||:||||:|||
Db        336 NPLQKWEDSA-HKPQSLDTDDPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLELQNGR 394

Qy        411 HLREAQYSMLAAWRRRTPRREATLELLGRVLRDMDLLGCLENIEEALGGAARLASEPRLL 470
              |||||||||| ||||||||||||||||||||||||||||:||||| | | |    | ||
Db        395 CLREAQYSMLATWRRRTPRREATLELLGRVLRDMDLLGCLEDIEEALCGPAALPPAPSLL 454


RESULT 5
US-08-126-016-2
; Sequence 2, Application US/08126016
; Patent No. 5811261
;  GENERAL INFORMATION:
;    APPLICANT:  WALLACH, DAVID
;    APPLICANT:  NOPHAR, YARON
;    APPLICANT:  KEMPER, OLIVER
;    APPLICANT:  ENGELMANN, HARTMUT
;    APPLICANT:  BRAKEBUSCH, CORD
;    APPLICANT:  ADERKA, DAN
;    TITLE OF INVENTION:  EXPRESSION OF THE RECOMBINANT TUMOR
;    TITLE OF INVENTION:  NECROSIS FACTOR BINDING PROTEIN I (TBP-I)
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Browdy and Neimark
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/126,016
;      FILING DATE:  24-SEP-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/625668
;      FILING DATE:  13-DEC-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, ROGER L
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  WALLACH4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;      TELEX:  248633
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  455 amino acids
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;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-126-016-2

  Query Match             58.3%;  Score 1517;  DB 2;  Length 455;
  Best Local Similarity   62.9%;  Pred. No. 1.5e-111;
  Matches  302;  Conservative   38;  Mismatches  104;  Indels   36;  Gaps    7;

Qy          1 MGLPTVPGLLLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCT 60
              ||| ||| |||||||  ||  :||:|| ||||| || |||:| |||||| ||||::||||
Db          1 MGLSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCT 60

Qy         61 KCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCLSCSRCRDEMFQVEISPCVVD 120
              ||||||||||||||||:|||||  |  |::|| ||||| |||||:|| || ||||| | ||
Db         61 KCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVD 120

Qy        121 RDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQERQDTICHCHMGFFLKGAKCI 180
              |||||||||||||| || |  |:| ||||| ||||:: |||:|:|:| || ||||:  :|:
Db        121 RDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECV 180

Qy        181 SCHDCKNK-ECEKLCPTRPSTGKDSQDPGTTVLLPLVIVFGLCLASFASVVLACRYQRWK 239
              || :||   || |||  :    | ::| |||||||||| ||||| |   : |  ||||||
Db        181 SCSNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPLVIFFGLCLLSLLFIGLMYRYQRWK 240

Qy        240 PKLYSIICGQSTLVKEGEPE-----LLVPAPGFNP----TTTICFSSTPSSSPVSIPPYI 290
              |||||:||:||  |||| |      | | | |:|    | |: ||  |||:  |   |
Db        241 SKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPTPGFTPTLGFSPVPSSTFTSSSTYT 300

Qy        291 SCDRSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLC 350
              |  ||   |:|  | |||:  | |||                :| |      ||  :
Db        301 PGDCPNF---AAPRREVAPPYQGADPIL---------------ATAL------ASDPIP 335

Qy        351 TPVQKWEASAPSAPDQLADADPATLYAVVDGVPPSRWKELVRRLGLSEHEIERLELENGR 410
              |:|||| ||   |  |  |||||||||: ||| |||| |||||||:|||:||||:|||
Db        336 NPLQKWEDSA-HKPQSLDTDDPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLELQNGR 394

Qy        411 HLREAQYSMLAAWRRRTPRREATLELLGRVLRDMDLLGCLENIEEALGGAARLASEPRLL 470
              |||||||||| ||||||||||||||||||||||||||||:|||| | | |   | ||
Db        395 CLREAQYSMLATWRRRTPRREATLELLGRVLRDMDLLGCLEDIEEALCGPAALPPAPSLL 454


RESULT 6
US-08-815-469-5
; Sequence 5, Application US/08815469
; Patent No. 6153402
;  GENERAL INFORMATION:
;    APPLICANT:  Yu, Guo-Liang
;    APPLICANT:  Ni, Jian
;    APPLICANT:  Dixit, Vishva
;    APPLICANT:  Gentz, Reiner L.
;    APPLICANT:  Dillon, Patrick J.
;    TITLE OF INVENTION:  Death Domain Containing Receptors
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox, P.L.L.C.
;      STREET:  1100 New York Ave., NW, Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/815,469
;      FILING DATE:  HEREWITH
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  No. 6153402 Yet Assigned
;      FILING DATE:  06-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/028,711
;      FILING DATE:  17-OCT-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/013,285
;      FILING DATE:  12-MAR-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Steffe, Eric K.
;      REGISTRATION NUMBER:  36,688
;      REFERENCE/DOCKET NUMBER:  1488.0310003/EKS/KRM
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  455 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  protein
US-08-815-469-5

  Query Match             58.3%;  Score 1517;  DB 3;  Length 455;
  Best Local Similarity   62.9%;  Pred. No. 1.5e-111;
  Matches  302;  Conservative   38;  Mismatches  104;  Indels   36;  Gaps    7;

Qy          1 MGLPTVPGLLLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCT 60
              ||| ||| |||||||  ||  :||:|| ||||| || |||:| |||||| ||||::||||
Db          1 MGLSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCT 60

Qy         61 KCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCLSCSRCRDEMFQVEISPCVVD 120
              ||||||||||||||||:|||||  |  |::|| ||||| |||||:|| || ||||| | ||
Db         61 KCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVD 120

Qy        121 RDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQERQDTICHCHMGFFLKGAKCI 180
              |||||||||||||| || |  |:| ||||| ||||:: |||:|:|:| || ||||:  :|:
Db        121 RDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECV 180

Qy        181 SCHDCKNK-ECEKLCPTRPSTGKDSQDPGTTVLLPLVIVFGLCLASFASVVLACRYQRWK 239
              || :||   || |||  :    | ::| |||||||||| ||||| |   : |  ||||||
Db        181 SCSNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPLVIFFGLCLLSLLFIGLMYRYQRWK 240

Qy        240 PKLYSIICGQSTLVKEGEPE-----LLVPAPGFNP----TTTICFSSTPSSSPVSIPPYI 290
              |||||:||:||  |||| |      | | | |:|    | |: ||  |||:  |   |
Db        241 SKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPTPGFTPTLGFSPVPSSTFTSSSTYT 300

Qy        291 SCDRSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLC 350
              |  ||   |:|  | |||:  | |||                :| |      ||  :
Db        301 PGDCPNF---AAPRREVAPPYQGADPIL---------------ATAL------ASDPIP 335

Qy        351 TPVQKWEASAPSAPDQLADADPATLYAVVDGVPPSRWKELVRRLGLSEHEIERLELENGR 410
              |:|||| ||   |  |  |||||||||: ||| |||| |||||||:|||:||||:|||
Db        336 NPLQKWEDSA-HKPQSLDTDDPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLELQNGR 394

Qy        411 HLREAQYSMLAAWRRRTPRREATLELLGRVLRDMDLLGCLENIEEALGGAARLASEPRLL 470
              |||||||||| ||||||||||||||||||||||||||||:|||| | | |   | ||
Db        395 CLREAQYSMLATWRRRTPRREATLELLGRVLRDMDLLGCLEDIEEALCGPAALPPAPSLL 454


RESULT 7
US-09-006-353A-3
; Sequence 3, Application US/09006353A
; Patent No. 6261801
;  GENERAL INFORMATION:
;    APPLICANT:  WEI, YING-FEI
;    APPLICANT:  YU, GUO-LIANG
;    APPLICANT:  GENTZ, REINER
;    APPLICANT:  RUBEN, STEVEN
;    TITLE OF INVENTION:  TUMOR NECROSIS FACTOR RECEPTOR 5
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  HUMAN GENOME SCIENCES, INC.
;      STREET:  9410 KEY WEST AVENUE
```

```
;       CITY:  ROCKVILLE
;       STATE:  MD
;       COUNTRY:  US
;       ZIP:  20850
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/006,353A
;       FILING DATE:
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  BROOKES, ANDERS A
;       REGISTRATION NUMBER:  36,373
;       REFERENCE/DOCKET NUMBER:  PF341
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (301) 309-8504
;       TELEFAX:  (301) 309-8512
;   INFORMATION FOR SEQ ID NO:  3:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  455 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-09-006-353A-3

  Query Match             58.3%;  Score 1517;  DB 3;  Length 455;
  Best Local Similarity   62.9%;  Pred. No. 1.5e-111;
  Matches  302;  Conservative   38;  Mismatches  104;  Indels   36;  Gaps    7;

Qy          1 MGLPTVPGLLLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCT 60
              ||| ||| |||||||  ||  :||:|| ||||| || |||:| ||||||  |||| ::||||
Db          1 MGLSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCT 60

Qy         61 KCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCLSCSRCRDEMFQVEISPCVVD 120
              |||||||||||||||:|||||  |  |::|| ||||| |||||:|| || ||||| | ||
Db         61 KCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVD 120

Qy        121 RDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQERQDTICHCHMGFFLKGAKCI 180
              |||||||||||||  || |  |:| ||||| ||||:: |||:|:|:| || ||||:  :|:
Db        121 RDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECV 180

Qy        181 SCHDCKNK-ECEKLCPTRPSTGKDSQDPGTTVLLPLVIVFGLCLASFASVVLACRYQRWK 239
              || :||   || |||  :    | ::| |||||||||| ||||| |   : |  ||||||
Db        181 SCSNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPLVIFFGLCLLSLLFIGLMYRYQRWK 240

Qy        240 PKLYSIICGQSTLVKEGEPE-----LLVPAPGFNP----TTTICFSSTPSSSPVSIPPYI 290
              |||||:||:||  |||| |       | | | |:|    | |: ||  |||:  |   |
Db        241 SKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPTPGFTPTLGFSPVPSSTFTSSSTYT 300

Qy        291 SCDRSNPGAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLC 350
                |  ||   |:|  | |||:  | |||                :| |      || :
Db        301 PGDCPNF---AAPRREVAPPYQGADPIL---------------ATAL------ASDPIP 335

Qy        351 TPVQKWEASAPSAPDQLADADPATLYAVVDGVPPSRWKELVRRLGLSEHEIERLELENGR 410
              |:|||| ||   |  |  |||||||||: ||| |||| |||||||:|||:||||:|||
Db        336 NPLQKWEDSA-HKPQSLDTDDPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLELQNGR 394

Qy        411 HLREAQYSMLAAWRRRTPRREATLELLGRVLRDMDLLGCLENIEEALGGAARLASEPRLL 470
              |||||||||| |||||||||||||||||||||||||||||:|||||  | | |   | ||
Db        395 CLREAQYSMLATWRRRTPRREATLELLGRVLRDMDLLGCLEDIEEALCGPAALPPAPSLL 454


RESULT 8
US-09-527-236A-5
; Sequence 5, Application US/09527236A
; Patent No. 6358508
; GENERAL INFORMATION:
;  APPLICANT: Ni, Jian
;  APPLICANT:  Yu, Guo-Liang
;  APPLICANT:  Fan, Ping
;  APPLICANT:  Gentz, Reiner L.
;  TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
;  FILE REFERENCE: PF375P1
;  CURRENT APPLICATION NUMBER: US/09/527,236A
;  CURRENT FILING DATE:  2000-03-16
;  PRIOR APPLICATION NUMBER: 60/052,991
;  PRIOR FILING DATE: 1997-06-11
;  PRIOR APPLICATION NUMBER: 09/095,094
;  PRIOR FILING DATE: 1998-06-10
;  PRIOR APPLICATION NUMBER: 60/126,019
;  PRIOR FILING DATE: 1999-03-24
;  PRIOR APPLICATION NUMBER: 60/134,220
;  PRIOR FILING DATE: 1999-05-14
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 455
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-527-236A-5

  Query Match             58.3%;  Score 1517;  DB 4;  Length 455;
  Best Local Similarity   62.9%;  Pred. No. 1.5e-111;
  Matches  302;  Conservative   38;  Mismatches  104;  Indels   36;  Gaps    7;

Qy          1 MGLPTVPGLLLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCT 60
              ||| ||| |||||||  ||  :||:|| ||||| || |||:| ||||||  |||| ::||||
Db          1 MGLSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCT 60

Qy         61 KCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCLSCSRCRDEMFQVEISPCVVD 120
              |||||||||||||||:|||||  |  |::|| ||||| |||||:|| || ||||| | ||
Db         61 KCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVD 120

Qy        121 RDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQERQDTICHCHMGFFLKGAKCI 180
              |||||||||||||  || |  |:| ||||| ||||:: |||:|:|:| || ||||:  :|:
Db        121 RDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECV 180

Qy        181 SCHDCKNK-ECEKLCPTRPSTGKDSQDPGTTVLLPLVIVFGLCLASFASVVLACRYQRWK 239
              || :||   || |||  :    | ::| |||||||||| ||||| |   : |  ||||||
Db        181 SCSNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPLVIFFGLCLLSLLFIGLMYRYQRWK 240

Qy        240 PKLYSIICGQSTLVKEGEPE-----LLVPAPGFNP----TTTICFSSTPSSSPVSIPPYI 290
              |||||:||:||  |||| |       | | | |:|    | |: ||  |||:  |   |
Db        241 SKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPTPGFTPTLGFSPVPSSTFTSSSTYT 300

Qy        291 SCDRSNPGAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLC 350
                |  ||   |:|  | |||:  | |||                :| |      || :
Db        301 PGDCPNF---AAPRREVAPPYQGADPIL---------------ATAL------ASDPIP 335

Qy        351 TPVQKWEASAPSAPDQLADADPATLYAVVDGVPPSRWKELVRRLGLSEHEIERLELENGR 410
              |:|||| ||   |  |  |||||||||: ||| |||| |||||||:|||:||||:|||
Db        336 NPLQKWEDSA-HKPQSLDTDDPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLELQNGR 394

Qy        411 HLREAQYSMLAAWRRRTPRREATLELLGRVLRDMDLLGCLENIEEALGGAARLASEPRLL 470
              |||||||||| |||||||||||||||||||||||||||||:|||||  | | |   | ||
Db        395 CLREAQYSMLATWRRRTPRREATLELLGRVLRDMDLLGCLEDIEEALCGPAALPPAPSLL 454


RESULT 9
US-08-054-970-2
; Sequence 2, Application US/08054970
; Patent No. 6395267
;  GENERAL INFORMATION:
;    APPLICANT:  WALLACH, David
;    APPLICANT:  BRAKEBUSCH, Cord
;    TITLE OF INVENTION:  TNF RECEPTOR ACTION MODULATION
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
```

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;       COUNTRY:  USA
;       ZIP:  20004
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/054,970
;       FILING DATE:  03-MAY-1993
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Townsend, Kevin G.
;       REGISTRATION NUMBER:  34,033
;       REFERENCE/DOCKET NUMBER:  WALLACH=9
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  202-628-5197
;       TELEFAX:  202-737-3528
;       TELEX:  248633
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  455 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-054-970-2

  Query Match             58.3%;  Score 1517;  DB 4;  Length 455;
  Best Local Similarity   62.9%;  Pred. No. 1.5e-111;
  Matches  302;  Conservative   38;  Mismatches  104;  Indels   36;  Gaps    7;

Qy          1 MGLPTVPGLLLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCT 60
              ||| ||| ||||||| || :||:|| ||||| || |||:| |||||| ||||::||||
Db          1 MGLSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCT 60

Qy         61 KCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCLSCSRCRDEMFQVEISPCVVD 120
              |||||||||||||||:||||| |  |::|| ||||| |||||:|| || ||||| | ||
Db         61 KCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVD 120

Qy        121 RDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQERQDTICHCHMGFFLKGAKCI 180
              |||||||||||| || |  |:| ||||| ||||:: |||:|:|:| || ||||:  :|:
Db        121 RDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECV 180

Qy        181 SCHDCKNK-ECEKLCPTRPSTGKDSQDPGTTVLLPLVIVFGLCLASFASVVLACRYQRWK 239
              || :||   || |||  :    | ::| |||||||||| ||||| |   : |  ||||||
Db        181 SCSNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPLVIFFGLCLLSLLFIGLMYRYQRWK 240

Qy        240 PKLYSIICGQSTLVKEGEPE-----LLVPAPGFNP----TTTICFSSTPSSSPVSIPPYI 290
              |||||:||:||  |||| |       | | | |:|    | |: ||  |||:  |   |
Db        241 SKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPTPGFTPTLGFSPVPSSTFTSSSTYT 300

Qy        291 SCDRSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLC 350
              |  ||   |:|  | |||:  | |||                :| |      || :
Db        301 PGDCPNF---AAPRREVAPPYQGADPIL---------------ATAL------ASDPIP 335

Qy        351 TPVQKWEASAPSAPDQLADADPATLYAVVDGVPPSRWKELVRRLGLSEHEIERLELENGR 410
              |:|||| ||   |  |  |||||||||: ||| |||| |||||||:|||:||||:|||
Db        336 NPLQKWEDSA-HKPQSLDTDDPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLELQNGR 394

Qy        411 HLREAQYSMLAAWRRRTPRREATLELLGRVLRDMDLLGCLENIEEALGGAARLASEPRLL 470
              |||||||||| |||||||||||||||||||||||||||||:||||| | | |   | ||
Db        395 CLREAQYSMLATWRRRTPRREATLELLGRVLRDMDLLGCLEDIEEALCGPAALPPAPSLL 454


RESULT 10
US-09-565-918-4
; Sequence 4, Application US/09565918
; Patent No. 6433147
; GENERAL INFORMATION:
;  APPLICANT:  Ni, Jian
;  APPLICANT:  Rosen, Craig A.
;  APPLICANT:  Pan, James G.
;  APPLICANT:  Gentz, Reiner L.
;  APPLICANT:  Dixit, Vishva M.
;  TITLE OF INVENTION:  Death Domain Containing Receptor 4
;  FILE REFERENCE:  1488.1300005
;  CURRENT APPLICATION NUMBER: US/09/565,918
;  CURRENT FILING DATE:  2000-05-05
;  PRIOR APPLICATION NUMBER:  US 60/132,922
;  PRIOR FILING DATE:  1999-05-06
;  PRIOR APPLICATION NUMBER:  US 09/013,895
;  PRIOR FILING DATE:  1998-01-27
;  PRIOR APPLICATION NUMBER:  US 60/037,829
;  PRIOR FILING DATE:  1997-02-05
;  PRIOR APPLICATION NUMBER:  US 60/035,722
;  PRIOR FILING DATE:  1997-01-28
;  NUMBER OF SEQ ID NOS:  13
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 455
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-565-918-4

  Query Match             58.3%;  Score 1517;  DB 4;  Length 455;
  Best Local Similarity   62.9%;  Pred. No. 1.5e-111;
  Matches  302;  Conservative   38;  Mismatches  104;  Indels   36;  Gaps    7;

Qy          1 MGLPTVPGLLLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCT 60
              ||| ||| ||||||| || :||:|| ||||| || |||:| |||||| ||||::||||
Db          1 MGLSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCT 60

Qy         61 KCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCLSCSRCRDEMFQVEISPCVVD 120
              |||||||||||||||:||||| |  |::|| ||||| |||||:|| || ||||| | ||
Db         61 KCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVD 120

Qy        121 RDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQERQDTICHCHMGFFLKGAKCI 180
              |||||||||||| || |  |:| ||||| ||||:: |||:|:|:| || ||||:  :|:
Db        121 RDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECV 180

Qy        181 SCHDCKNK-ECEKLCPTRPSTGKDSQDPGTTVLLPLVIVFGLCLASFASVVLACRYQRWK 239
              || :||   || |||  :    | ::| |||||||||| ||||| |   : |  ||||||
Db        181 SCSNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPLVIFFGLCLLSLLFIGLMYRYQRWK 240

Qy        240 PKLYSIICGQSTLVKEGEPE-----LLVPAPGFNP----TTTICFSSTPSSSPVSIPPYI 290
              |||||:||:||  |||| |       | | | |:|    | |: ||  |||:  |   |
Db        241 SKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPTPGFTPTLGFSPVPSSTFTSSSTYT 300

Qy        291 SCDRSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLC 350
              |  ||   |:|  | |||:  | |||                :| |      || :
Db        301 PGDCPNF---AAPRREVAPPYQGADPIL---------------ATAL------ASDPIP 335

Qy        351 TPVQKWEASAPSAPDQLADADPATLYAVVDGVPPSRWKELVRRLGLSEHEIERLELENGR 410
              |:|||| ||   |  |  |||||||||: ||| |||| |||||||:|||:||||:|||
Db        336 NPLQKWEDSA-HKPQSLDTDDPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLELQNGR 394

Qy        411 HLREAQYSMLAAWRRRTPRREATLELLGRVLRDMDLLGCLENIEEALGGAARLASEPRLL 470
              |||||||||| |||||||||||||||||||||||||||||:||||| | | |   | ||
Db        395 CLREAQYSMLATWRRRTPRREATLELLGRVLRDMDLLGCLEDIEEALCGPAALPPAPSLL 454


RESULT 11
US-09-573-986-3
; Sequence 3, Application US/09573986
; Patent No. 6455040
; GENERAL INFORMATION:
;  APPLICANT:  Wei, Ying-Fei
;  APPLICANT:  Ni, Jian
;  APPLICANT:  Gentz, Reiner
;  APPLICANT:  Ruben, Steven
;  TITLE OF INVENTION:  Tumor Necrosis Factor Receptor 5
;  FILE REFERENCE:  1488.1280004
;  CURRENT APPLICATION NUMBER: US/09/573,986
;  CURRENT FILING DATE:  2000-05-18
;  NUMBER OF SEQ ID NOS:  27
;  SOFTWARE:  PatentIn Ver. 2.1
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; SEQ ID NO 3
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-573-986-3

Query Match 58.3%; Score 1517; DB 4; Length 455;
Best Local Similarity 62.9%; Pred. No. 1.5e-111;
Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

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Qy          1 MGLPTVPGLLLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCT 60
              ||| ||| ||||||| ||  :||:|| ||||| || |||:| |||||| ||||::||||
Db          1 MGLSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCT 60

Qy         61 KCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCLSCSRCRDEMFQVEISPCVVD 120
              |||||||||||||||:||||| |  |::|| ||||| |||||:|| || ||||| | ||
Db         61 KCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVD 120

Qy        121 RDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQERQDTICHCHMGFFLKGAKCI 180
              |||||||||||| || |  |:| ||||| |||:: |||:|:|:| || ||||:  :|:
Db        121 RDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECV 180

Qy        181 SCHDCKNK-ECEKLCPTRPSTGKDSQDPGTTVLLPLVIVFGLCLASFASVVLACRYQRWK 239
              || :||  || |||  :   | ::| |||||||||| ||||| |  : |  ||||||
Db        181 SCSNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPLVIFFGLCLLSLLFIGLMYRYQRWK 240

Qy        240 PKLYSIICGQSTLVKEGEPE-----LLVPAPGFNP----TTTICFSSTPSSSPVSIPPYI 290
              |||||:||:||  |||| |      | | | |:|    | |: ||  |||:  |   |
Db        241 SKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPTPGFTPTLGFSPVPSSTFTSSSTYT 300

Qy        291 SCDRSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLC 350
              |  ||   |:|  | |||:  | |||          :| |       || :
Db        301 PGDCPNF---AAPRREVAPPYQGADPIL---------------ATAL------ASDPIP 335

Qy        351 TPVQKWEASAPSAPDQLADADPATLYAVVDGVPPSRWKELVRRLGLSEHEIERLELENGR 410
              |:|||| ||   |  |   |||||||||: ||| |||| |||||||:|||:||||:|||
Db        336 NPLQKWEDSA-HKPQSLDTDDPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLELQNGR 394

Qy        411 HLREAQYSMLAAWRRRTPRREATLELLGRVLRDMDLLGCLENIEEALGGAARLASEPRLL 470
              |||||||||| |||||||||||||||||||||||||||||:||||| | | |   | ||
Db        395 CLREAQYSMLATWRRRTPRREATLELLGRVLRDMDLLGCLEDIEEALCGPAALPPAPSLL 454
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RESULT 12
US-09-027-287-3
; Sequence 3, Application US/09027287A
; Patent No. 6479254
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ruben, Steven M.
; APPLICANT: Ullrich, Stephen
; TITLE OF INVENTION: Apoptosis Inducing Molecule II
; FILE REFERENCE: 1488.0650004
; CURRENT APPLICATION NUMBER: US/09/027,287A
; CURRENT FILING DATE: 1998-02-20
; EARLIER APPLICATION NUMBER: US 09/003,886
; EARLIER FILING DATE: 1998-01-07
; EARLIER APPLICATION NUMBER: US 08/822,953
; EARLIER FILING DATE: 1997-03-21
; EARLIER APPLICATION NUMBER: US 60/030,157
; EARLIER FILING DATE: 1996-10-31
; EARLIER APPLICATION NUMBER: US 60/013,923
; EARLIER FILING DATE: 1996-03-22
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-027-287-3

Query Match 58.3%; Score 1517; DB 4; Length 455;
Best Local Similarity 62.9%; Pred. No. 1.5e-111;
Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

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Qy          1 MGLPTVPGLLLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCT 60
              ||| ||| ||||||| ||  :||:|| ||||| || |||:| |||||| ||||::||||
Db          1 MGLSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCT 60

Qy         61 KCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCLSCSRCRDEMFQVEISPCVVD 120
              |||||||||||||||:||||| |  |::|| ||||| |||||:|| || ||||| | ||
Db         61 KCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVD 120

Qy        121 RDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQERQDTICHCHMGFFLKGAKCI 180
              |||||||||||| || |  |:| ||||| |||:: |||:|:|:| || ||||:  :|:
Db        121 RDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECV 180

Qy        181 SCHDCKNK-ECEKLCPTRPSTGKDSQDPGTTVLLPLVIVFGLCLASFASVVLACRYQRWK 239
              || :||  || |||  :   | ::| |||||||||| ||||| |  : |  ||||||
Db        181 SCSNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPLVIFFGLCLLSLLFIGLMYRYQRWK 240

Qy        240 PKLYSIICGQSTLVKEGEPE-----LLVPAPGFNP----TTTICFSSTPSSSPVSIPPYI 290
              |||||:||:||  |||| |      | | | |:|    | |: ||  |||:  |   |
Db        241 SKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPTPGFTPTLGFSPVPSSTFTSSSTYT 300

Qy        291 SCDRSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLC 350
              |  ||   |:|  | |||:  | |||          :| |       || :
Db        301 PGDCPNF---AAPRREVAPPYQGADPIL---------------ATAL------ASDPIP 335

Qy        351 TPVQKWEASAPSAPDQLADADPATLYAVVDGVPPSRWKELVRRLGLSEHEIERLELENGR 410
              |:|||| ||   |  |   |||||||||: ||| |||| |||||||:|||:||||:|||
Db        336 NPLQKWEDSA-HKPQSLDTDDPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLELQNGR 394

Qy        411 HLREAQYSMLAAWRRRTPRREATLELLGRVLRDMDLLGCLENIEEALGGAARLASEPRLL 470
              |||||||||| |||||||||||||||||||||||||||||:||||| | | |   | ||
Db        395 CLREAQYSMLATWRRRTPRREATLELLGRVLRDMDLLGCLEDIEEALCGPAALPPAPSLL 454
```

RESULT 13
US-09-252-656B-3
; Sequence 3, Application US/09252656B
; Patent No. 6495520
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ruben, Steven M.
; APPLICANT: Zhang, Jun
; APPLICANT: Ullrich, Stephen
; APPLICANT: Zhai, Yifan
; TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use
; FILE REFERENCE: 1488.0650006
; CURRENT APPLICATION NUMBER: US/09/252,656B
; CURRENT FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: US 60/075,409
; PRIOR FILING DATE: 1998-02-20
; PRIOR APPLICATION NUMBER: US 09/027,287
; PRIOR FILING DATE: 1998-02-20
; PRIOR APPLICATION NUMBER: US 09/003,886
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: US 08/822,953
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/013,923
; PRIOR FILING DATE: 1996-03-22
; PRIOR APPLICATION NUMBER: US 60/030,157
; PRIOR FILING DATE: 1996-10-31
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-252-656B-3

Query Match 58.3%; Score 1517; DB 4; Length 455;
Best Local Similarity 62.9%; Pred. No. 1.5e-111;

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  Matches  302;  Conservative   38;  Mismatches  104;  Indels   36;  Gaps    7;

Qy          1 MGLPTVPGLLLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCT 60
              ||| ||| |||||||  ||  :||:|| ||||| || |||:| |||||| ||||::||||
Db          1 MGLSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCT 60

Qy         61 KCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCLSCSRCRDEMFQVEISPCVVD 120
              |||||||||||||||:||||| |   |::|| ||||| |||||:|| || ||||| | ||
Db         61 KCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVD 120

Qy        121 RDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQERQDTICHCHMGFFLKGAKCI 180
              |||||||||||| || |  |:| ||||| ||||:: |||:|:|:| || ||||:  :|:
Db        121 RDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECV 180

Qy        181 SCHDCKNK-ECEKLCPTRPSTGKDSQDPGTTVLLPLVIVFGLCLASFASVVLACRYQRWK 239
              || :||   || |||  :    | ::| |||||||||| ||||| |   : |  ||||||
Db        181 SCSNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPLVIFFGLCLLSLLFIGLMYRYQRWK 240

Qy        240 PKLYSIICGQSTLVKEGEPE-----LLVPAPGFNP----TTTICFSSTPSSSPVSIPPYI 290
              |||||:||:||  |||| |       | | | |:|    | |: ||  |||:  |   |
Db        241 SKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPTPGFTPTLGFSPVPSSTFTSSSTYT 300

Qy        291 SCDRSNPGAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLC 350
              |  ||   |:|  | |||:  | |||                :| |      ||  :
Db        301 PGDCPNF---AAPRREVAPPYQGADPIL---------------ATAL------ASDPIP 335

Qy        351 TPVQKWEASAPSAPDQLADADPATLYAVVDGVPPSRWKELVRRLGLSEHEIERLELENGR 410
              |:|||| ||   |  |  |||||||||: ||| |||| |||||||:|||:||||:|||
Db        336 NPLQKWEDSA-HKPQSLDTDDPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLELQNGR 394

Qy        411 HLREAQYSMLAAWRRRTPRREATLELLGRVLRDMDLLGCLENIEEALGGAARLASEPRLL 470
              |||||||||| |||||||||||||||||||||||||||||:||||| | | |   | ||
Db        395 CLREAQYSMLATWRRRTPRREATLELLGRVLRDMDLLGCLEDIEEALCGPAALPPAPSLL 454


RESULT 14
US-08-050-319B-25
; Sequence 25, Application US/08050319B
; Patent No. 5633145
;  GENERAL INFORMATION:
;    APPLICANT:  M.Feldmann, P.W. Gray,
;    APPLICANT:  M.J.C. Turner, F.M Brennan
;    TITLE OF INVENTION:  Modified human TNFalpha (Tumor
;    TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
;    NUMBER OF SEQUENCES:  57
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Reed & Robbins
;      STREET:  635 Bryant Street
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94301
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/050,319B
;      FILING DATE:  10-May-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Robbins, Roberta L.
;      REGISTRATION NUMBER:  33,208
;      REFERENCE/DOCKET NUMBER:  5150-0030
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 617-8999
;      TELEFAX:  (415) 327-3231
;  INFORMATION FOR SEQ ID NO:  25:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  455 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-050-319B-25

  Query Match           58.1%;  Score 1512;  DB 1;  Length 455;
  Best Local Similarity  62.7%;  Pred. No. 3.6e-111;
  Matches  301;  Conservative   38;  Mismatches  105;  Indels   36;  Gaps    7;

Qy          1 MGLPTVPGLLLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCT 60
              ||| ||| |||||||  ||  :||:|| ||||| || |||:| |||||| ||||::||||
Db          1 MGLSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCT 60

Qy         61 KCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCLSCSRCRDEMFQVEISPCVVD 120
              |||||||||||||||:||||| |   |::|| ||||| |||||:|| || ||||| | ||
Db         61 KCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVD 120

Qy        121 RDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQERQDTICHCHMGFFLKGAKCI 180
              |||||||||||| || |  |:| ||||| |||| :: |||:|:|:| || ||||:  :|:
Db        121 RDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECV 180

Qy        181 SCHDCKNK-ECEKLCPTRPSTGKDSQDPGTTVLLPLVIVFGLCLASFASVVLACRYQRWK 239
              || :||   || |||  :    | ::| |||||||||| ||||| |   : |  ||||||
Db        181 SCSNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPLVIFFGLCLLSLLFIGLMYRYQRWK 240

Qy        240 PKLYSIICGQSTLVKEGEPE-----LLVPAPGFNP----TTTICFSSTPSSSPVSIPPYI 290
              |||||:||:||  |||| |       | | | |:|    | |: ||  |||:  |   |
Db        241 SKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPTPGFTPTLGFSPVPSSTFTSSSTYT 300

Qy        291 SCDRSNPGAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLC 350
              |  ||   |:|  | |||:  | |||                :| |      ||  :
Db        301 PGDCPNF---AAPRREVAPPYQGADPIL---------------ATAL------ASDPIP 335

Qy        351 TPVQKWEASAPSAPDQLADADPATLYAVVDGVPPSRWKELVRRLGLSEHEIERLELENGR 410
              |:|||| ||   |  |  |||||||||: ||| |||| |||||||:|||:||||:|||
Db        336 NPLQKWEDSA-HKPQSLDTDDPRTLYAVVENVPPLRWKEFVRRLGLSDHEIDRLELQNGR 394

Qy        411 HLREAQYSMLAAWRRRTPRREATLELLGRVLRDMDLLGCLENIEEALGGAARLASEPRLL 470
              |||||||||| |||||||||||||||||||||||||||||:||||| | | |   | ||
Db        395 CLREAQYSMLATWRRRTPRREATLELLGRVLRDMDLLGCLEDIEEALCGPAALPPAPSLL 454


RESULT 15
US-08-465-982-25
; Sequence 25, Application US/08465982
; Patent No. 5863786
;  GENERAL INFORMATION:
;    APPLICANT:  M.Feldmann, P.W. Gray,
;    APPLICANT:  M.J.C. Turner, F.M Brennan
;    TITLE OF INVENTION:  Modified human TNFalpha (Tumor
;    TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
;    NUMBER OF SEQUENCES:  57
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Reed & Robbins
;      STREET:  635 Bryant Street
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94301
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/465,982
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/050,319
;      FILING DATE:  10-May-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Robbins, Roberta L.
;      REGISTRATION NUMBER:  33,208
;      REFERENCE/DOCKET NUMBER:  5150-0030
```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 617-8999
; TELEFAX: (415) 327-3231
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 455 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-465-982-25

Query Match 58.1%; Score 1512; DB 2; Length 455;
Best Local Similarity 62.7%; Pred. No. 3.6e-111;
Matches 301; Conservative 38; Mismatches 105; Indels 36; Gaps 7;

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Qy    1 MGLPTVPGLLLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCT 60
Db    1 MGLSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCT 60

Qy   61 KCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCLSCSRCRDEMFQVEISPCVVD 120
Db   61 KCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVD 120

Qy  121 RDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQERQDTICHCHMGFFLKGAKCI 180
Db  121 RDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECV 180

Qy  181 SCHDCKNK-ECEKLCPTRPSTGKDSQDPGTTVLLPLVIVFGLCLASFASVVLACRYQRWK 239
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Qy  240 PKLYSIICGQSTLVKEGEPE-----LLVPAPGFNP----TTTICFSSTPSSSPVSIPPYI 290
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Search completed: September 13, 2003, 07:06:40
Job time : 23 secs

OM protein - protein search, using sw model

Run on: September 13, 2003, 07:05:40 ; Search time 26 Seconds
(without alignments)
2643.260 Million cell updates/sec

Title: US-09-970-532-2
Perfect score: 2603
Sequence: 1 MGLPTVPGLLLPLVLPALLA.....NIEEALGGAARLASEPRLLW 471

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 541936 seqs, 145912426 residues

Total number of hits satisfying chosen parameters: 541936

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	1519	58.4	455	15	US-10-252-408-4	Sequence 4, Appli
3	1517	58.3	455	9	US-09-826-212-3	Sequence 3, Appli
4	1517	58.3	455	9	US-09-333-966-5	Sequence 5, Appli
5	1517	58.3	455	9	US-09-027-287-3	Sequence 3, Appli
6	1517	58.3	455	9	US-09-874-138-3	Sequence 3, Appli
7	1517	58.3	455	9	US-09-840-707A-16	Sequence 16, Appl
8	1517	58.3	455	9	US-09-252-656B-3	Sequence 3, Appli
9	1517	58.3	455	9	US-09-899-422-2	Sequence 2, Appli
10	1517	58.3	455	9	US-09-899-422-17	Sequence 17, Appl
11	1517	58.3	455	10	US-09-935-727-5	Sequence 5, Appli
12	1517	58.3	455	10	US-09-898-234-2	Sequence 2, Appli
13	1517	58.3	455	10	US-09-898-234-17	Sequence 17, Appl
14	1517	58.3	455	10	US-09-756-854-5	Sequence 5, Appli
15	1517	58.3	455	10	US-09-899-429A-2	Sequence 2, Appli
16	1517	58.3	455	10	US-09-899-429A-27	Sequence 27, Appl
17	1517	58.3	455	10	US-09-792-356-2	Sequence 2, Appli
18	1517	58.3	455	10	US-09-792-356-17	Sequence 17, Appl
19	1517	58.3	455	11	US-09-314-889-5	Sequence 5, Appli
20	1517	58.3	455	13	US-10-005-842-3	Sequence 3, Appli
21	1517	58.3	455	14	US-10-120-397-2	Sequence 2, Appli
22	1517	58.3	455	14	US-10-041-574-5	Sequence 5, Appli
23	1517	58.3	455	15	US-10-038-557A-16	Sequence 16, Appl
24	1517	58.3	455	15	US-10-175-902-4	Sequence 4, Appli
25	1517	58.3	455	15	US-10-186-643-3	Sequence 3, Appli
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27	1500.5	57.6	909	15	US-10-226-296-4	Sequence 4, Appli
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29	1325.5	50.9	461	9	US-09-899-422-15	Sequence 15, Appl
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33	1178	45.3	371	9	US-09-899-422-12	Sequence 12, Appl
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36	1171	45.0	371	10	US-09-899-429A-22	Sequence 22, Appl
37	1072	41.2	181	9	US-09-970-532-4	Sequence 4, Appli
38	874	33.6	247	15	US-10-193-616-10	Sequence 10, Appl
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41	813.5	31.3	197	14	US-10-112-793-21	Sequence 21, Appl
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44	753	28.9	190	10	US-09-899-429A-18	Sequence 18, Appl
45	738.5	28.4	183	10	US-09-899-429A-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-09-970-532-2
; Sequence 2, Application US/09970532
; Patent No. US20020076765A1
; GENERAL INFORMATION:
; APPLICANT: Taylor, J. Michael
; APPLICANT: Kehrli, Jr., Marcus
; APPLICANT: Lee, Eun-Kyung
; APPLICANT: Mwangi, Simon
; TITLE OF INVENTION: BOVINE TUMOR NECROSIS FACTOR RECEPTOR-1
; TITLE OF INVENTION: AND METHODS OF USE
; FILE REFERENCE: 08411-018001
; CURRENT APPLICATION NUMBER: US/09/970,532
; CURRENT FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 09/513,007
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 471
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-970-532-2

Query Match 100.0%; Score 2603; DB 9; Length 471;
Best Local Similarity 100.0%; Pred. No. 1.1e-178;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 MGLPTVPGLLLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCT 60

Qy         61 KCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCLSCSRCRDEMFQVEISPCVVD 120
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Qy        121 RDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQERQDTICHCHMGFFLKGAKCI 180
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Qy        241 KLYSIICGQSTLVKEGEPELLVPAPGFNPTTTICFSSTPSSSPVSIPPYISCDRSNFGAV 300
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RESULT 2
US-10-252-408-4
; Sequence 4, Application US/10252408
; Publication No. US20030082736A1
; GENERAL INFORMATION:
;  APPLICANT: SMITH, Craig A.
;  TITLE OF INVENTION: TUMOR NECROSIS FACTOR-ALPHA AND BETA-RECEPTORS
;  FILE REFERENCE: A-71592
;  CURRENT APPLICATION NUMBER: US/10/252,408
;  CURRENT FILING DATE:  2002-09-24
;  PRIOR APPLICATION NUMBER: US/08/406,824
;  PRIOR FILING DATE: 1995-03-20
;  PRIOR APPLICATION NUMBER: US 08/255,849
;  PRIOR FILING DATE: 1994-06-08
;  PRIOR APPLICATION NUMBER: US 07/860,710
;  PRIOR FILING DATE: 1992-03-30
;  PRIOR APPLICATION NUMBER: US  07/523,635
;  PRIOR FILING DATE: 1990-05-10
;  PRIOR APPLICATION NUMBER: US 07/421,417
;  PRIOR FILING DATE: 1989-10-13
;  PRIOR APPLICATION NUMBER: US 07/405,370
;  PRIOR FILING DATE: 1989-09-11
;  PRIOR APPLICATION NUMBER: US 07/403,241
;  PRIOR FILING DATE: 1989-09-05
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 455
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-252-408-4

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  Best Local Similarity   62.9%;  Pred. No. 5.1e-101;
  Matches  302;  Conservative   39;  Mismatches  103;  Indels   36;  Gaps    7;

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Qy        121 RDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQERQDTICHCHMGFFLKGAKCI 180
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; Sequence 3, Application US/09826212
; Patent No. US20010021516A1
; GENERAL INFORMATION:
;  APPLICANT: Wei, Ying-Fei
;  APPLICANT:  Gentz, Reiner
;  APPLICANT:  Ruben, Steven
;  APPLICANT:  Ni, Jian
;  TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
;  FILE REFERENCE: 1488.1280006
;  CURRENT APPLICATION NUMBER: US/09/826,212
;  CURRENT FILING DATE:  2001-04-05
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
;   LENGTH: 455
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-826-212-3

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Db        181 SCSNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPLVIFFGLCLLSLLFIGLMYRYQRWK 240

Qy        240 PKLYSIICGQSTLVKEGEPE-----LLVPAPGFNP----TTTICFSSTPSSSPVSIPPYI 290
              |||||:||:||  |||| |       | | | |:|    | |: ||  |||:  |   |
Db        241 SKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPTPGFTPTLGFSPVPSSTFTSSSTYT 300

Qy        291 SCDRSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLC 350
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Qy        411 HLREAQYSMLAAWRRRTPRREATLELLGRVLRDMDLLGCLENIEEALGGAARLASEPRLL 470
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RESULT 4
US-09-333-966-5
; Sequence 5, Application US/09333966
; Patent No. US20020009773A1
;  GENERAL INFORMATION:
;    APPLICANT:  Yu, Guo-Liang
;    APPLICANT:  Ni, Jian
;    APPLICANT:  Dixit, Vishva
;    APPLICANT:  Gentz, Reiner L.
;    APPLICANT:  Dillon, Patrick J.
;    TITLE OF INVENTION:  Death Domain Containing Receptors
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox, P.L.L.C.
;      STREET:  1100 New York Ave., NW, Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/333,966
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/815,469
;      FILING DATE:
;      APPLICATION NUMBER:  No. US20020009773A1 Yet Assigned
;      FILING DATE:  06-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/028,711
;      FILING DATE:  17-OCT-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/013,285
;      FILING DATE:  12-MAR-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Steffe, Eric K.
;      REGISTRATION NUMBER:  36,688
;      REFERENCE/DOCKET NUMBER:  1488.0310003/EKS/KRM
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  455 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  No. US20020009773A1 Relevant
;      TOPOLOGY:  No. US20020009773A1 Relevant
;    MOLECULE TYPE:  protein
US-09-333-966-5

  Query Match             58.3%;  Score 1517;  DB 9;  Length 455;
  Best Local Similarity   62.9%;  Pred. No. 7.1e-101;
  Matches  302;  Conservative   38;  Mismatches  104;  Indels   36;  Gaps    7;

Qy          1 MGLPTVPGLLLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCT 60
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Qy        121 RDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQERQDTICHCHMGFFLKGAKCI 180
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Qy        181 SCHDCKNK-ECEKLCPTRPSTGKDSQDPGTTVLLPLVIVFGLCLASFASVVLACRYQRWK 239
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Db        181 SCSNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPLVIFFGLCLLSLLFIGLMYRYQRWK 240

Qy        240 PKLYSIICGQSTLVKEGEPE-----LLVPAPGFNP----TTTICFSSTPSSSPVSIPPYI 290
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Qy        351 TPVQKWEASAPSAPDQLADADPATLYAVVDGVPPSRWKELVRRLGLSEHEIERLELENGR 410
              |:|||| ||   |  | ||||||||: ||| |||| ||||||:|||:||||:|||
Db        336 NPLQKWEDSA-HKPQSLDTDDPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLELQNGR 394

Qy        411 HLREAQYSMLAAWRRRTPRREATLELLGRVLRDMDLLGCLENIEEALGGAARLASEPRLL 470
              |||||||||| ||||||||||||||||||||||||||||:||||| | | |   | ||
Db        395 CLREAQYSMLATWRRRTPRREATLELLGRVLRDMDLLGCLEDIEEALCGPAALPPAPSLL 454


RESULT 5
US-09-027-287-3
; Sequence 3, Application US/09027287A
; Patent No. US20020064869A1
; GENERAL INFORMATION:
;  APPLICANT: Ebner, Reinhard
;  APPLICANT: Yu, Guo-Liang
;  APPLICANT: Ruben, Steven M.
;  APPLICANT: Ullrich, Stephen
;  TITLE OF INVENTION: Apoptosis Inducing Molecule II
;  FILE REFERENCE: 1488.0650004
;  CURRENT APPLICATION NUMBER: US/09/027,287A
;  CURRENT FILING DATE: 1998-02-20
;  EARLIER APPLICATION NUMBER: US 09/003,886
;  EARLIER FILING DATE: 1998-01-07
;  EARLIER APPLICATION NUMBER: US 08/822,953
;  EARLIER FILING DATE: 1997-03-21
;  EARLIER APPLICATION NUMBER: US 60/030,157
;  EARLIER FILING DATE: 1996-10-31
;  EARLIER APPLICATION NUMBER: US 60/013,923
;  EARLIER FILING DATE: 1996-03-22
;  NUMBER OF SEQ ID NOS: 55
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 455
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-027-287-3

  Query Match             58.3%;  Score 1517;  DB 9;  Length 455;
  Best Local Similarity   62.9%;  Pred. No. 7.1e-101;
  Matches  302;  Conservative   38;  Mismatches  104;  Indels   36;  Gaps    7;

Qy          1 MGLPTVPGLLLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCT 60
              ||| ||| ||||||| ||  :||:|| ||||| || |||:| |||||| ||||::||||
Db          1 MGLSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCT 60

Qy         61 KCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCLSCSRCRDEMFQVEISPCVVD 120
              |||||||||||||||:||||| |  |::|| ||||| |||||:|| || ||||| | ||
Db         61 KCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVD 120

Qy        121 RDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQERQDTICHCHMGFFLKGAKCI 180
              |||||||||||||| || |  |:| ||||| ||||:: |||:|:|:|: || ||||:  :|:
Db        121 RDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECV 180

Qy        181 SCHDCKNK-ECEKLCPTRPSTGKDSQDPGTTVLLPLVIVFGLCLASFASVVLACRYQRWK 239
              || :||   || |||  :    | ::| |||||||||| ||||| |   : |  ||||||
Db        181 SCSNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPLVIFFGLCLLSLLFIGLMYRYQRWK 240

Qy        240 PKLYSIICGQSTLVKEGEPE-----LLVPAPGFNP----TTTICFSSTPSSSPVSIPPYI 290
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Db        241 SKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPTPGFTPTLGFSPVPSSTFTSSSTYT 300

Qy        291 SCDRSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLC 350
              |  ||   |:|  | |||:  | |||                :| |      ||  :
Db        301 PGDCPNF---AAPRREVAPPYQGADPIL---------------ATAL------ASDPIP 335

Qy        351 TPVQKWEASAPSAPDQLADADPATLYAVVDGVPPSRWKELVRRLGLSEHEIERLELENGR 410
              |:|||| ||   | |   |||||||||: ||| |||| |||||||:|||:||||:|||
Db        336 NPLQKWEDSA-HKPQSLDTDDPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLELQNGR 394

Qy        411 HLREAQYSMLAAWRRRTPRREATLELLGRVLRDMDLLGCLENIEEALGGAARLASEPRLL 470
              |||||||||| |||||||||||||||||||||||||||:|||| | | |   | ||
Db        395 CLREAQYSMLATWRRRTPRREATLELLGRVLRDMDLLGCLEDIEEALCGPAALPPAPSLL 454


RESULT 6
US-09-874-138-3
; Sequence 3, Application US/09874138
; Patent No. US20020072091A1
; GENERAL INFORMATION:
;  APPLICANT: Ni, Jian
;  APPLICANT:  Gentz, Reiner L.
;  APPLICANT:  Yu, Guo-liang
;  APPLICANT:  Rosen, Craig A.
;  TITLE OF INVENTION: Death Domain Containing Receptor 5
;  FILE REFERENCE: 1488.1310006
;  CURRENT APPLICATION NUMBER: US/09/874,138
;  CURRENT FILING DATE:  2001-06-06
;  PRIOR APPLICATION NUMBER: 09/565,009
;  PRIOR FILING DATE: 2000-05-04
;  PRIOR APPLICATION NUMBER: 60/148,939
;  PRIOR FILING DATE: 1999-08-13
;  PRIOR APPLICATION NUMBER: 60/133,238
;  PRIOR FILING DATE: 1999-05-07
;  PRIOR APPLICATION NUMBER: 60/132,498
;  PRIOR FILING DATE: 1999-05-04
;  PRIOR APPLICATION NUMBER: 09/042,583
;  PRIOR FILING DATE: 1998-03-17
;  PRIOR APPLICATION NUMBER: 60/054,021
;  PRIOR FILING DATE: 1997-07-29
;  PRIOR APPLICATION NUMBER: 60/040,846
;  PRIOR FILING DATE: 1997-03-17
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 455
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-874-138-3

  Query Match           58.3%;  Score 1517;  DB 9;  Length 455;
  Best Local Similarity  62.9%;  Pred. No. 7.1e-101;
  Matches  302;  Conservative   38;  Mismatches  104;  Indels   36;  Gaps    7;

Qy          1 MGLPTVPGLLLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCT 60
              ||| ||| |||||||  ||  :||:|| ||||| || |||:| |||||| ||||::||||
Db          1 MGLSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCT 60

Qy         61 KCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCLSCSRCRDEMFQVEISPCVVD 120
              ||||||||||||||||:|||||  |  |::|| ||||| ||||:|| || |||||  | ||
Db         61 KCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVD 120

Qy        121 RDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQERQDTICHCHMGFFLKGAKCI 180
              |||||||||||| || |  |:| ||||| ||||:: |||:|:|:| || ||||:  :|:
Db        121 RDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECV 180

Qy        181 SCHDCKNK-ECEKLCPTRPSTGKDSQDPGTTVLLPLVIVFGLCLASFASVVLACRYQRWK 239
              || :||   || |||  :   | ::| |||||||||| |||||  :  |  ||||||
Db        181 SCSNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPLVIFFGLCLLSLLFIGLMYRYQRWK 240

Qy        240 PKLYSIICGQSTLVKEGEPE-----LLVPAPGFNP----TTTICFSSTPSSSPVSIPPYI 290
              |||||:||:||  |||| |      | | | |:|    | |: ||  |||:  |   |

Db        241 SKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPTPGFTPTLGFSPVPSSTFTSSSTYT 300

Qy        291 SCDRSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLC 350
              |  ||   |:|  | |||:  | |||                :| |      ||  :
Db        301 PGDCPNF---AAPRREVAPPYQGADPIL---------------ATAL------ASDPIP 335

Qy        351 TPVQKWEASAPSAPDQLADADPATLYAVVDGVPPSRWKELVRRLGLSEHEIERLELENGR 410
              |:|||| ||   | |   |||||||||: ||| |||| |||||||:|||:||||:|||
Db        336 NPLQKWEDSA-HKPQSLDTDDPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLELQNGR 394

Qy        411 HLREAQYSMLAAWRRRTPRREATLELLGRVLRDMDLLGCLENIEEALGGAARLASEPRLL 470
              |||||||||| |||||||||||||||||||||||||||:|||| | | |   | ||
Db        395 CLREAQYSMLATWRRRTPRREATLELLGRVLRDMDLLGCLEDIEEALCGPAALPPAPSLL 454


RESULT 7
US-09-840-707A-16
; Sequence 16, Application US/09840707A
; Patent No. US20020077276A1
; GENERAL INFORMATION:
;  APPLICANT: Fredeking, Terry M.
;  APPLICANT:  Ignatyev, George M.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING HEMORRHAGIC VIRUS
;  TITLE OF INVENTION:  INFECTIONS AND OTHER DISORDERS
;  FILE REFERENCE: 24881-301C
;  CURRENT APPLICATION NUMBER: US/09/840,707A
;  CURRENT FILING DATE:  2001-04-23
;  PRIOR APPLICATION NUMBER: 09/562,979
;  PRIOR FILING DATE: 2000-04-27
;  PRIOR APPLICATION NUMBER: 60/198,210
;  PRIOR FILING DATE: 1999-04-27
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
;   LENGTH: 455
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Tumor Necrosis Factor p55 Receptor
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: AAA36753/GenBank
;   DATABASE ENTRY DATE: 1995-08-03
US-09-840-707A-16

  Query Match           58.3%;  Score 1517;  DB 9;  Length 455;
  Best Local Similarity  62.9%;  Pred. No. 7.1e-101;
  Matches  302;  Conservative   38;  Mismatches  104;  Indels   36;  Gaps    7;

Qy          1 MGLPTVPGLLLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCT 60
              ||| ||| |||||||  ||  :||:|| ||||| || |||:| |||||| ||||::||||
Db          1 MGLSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCT 60

Qy         61 KCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCLSCSRCRDEMFQVEISPCVVD 120
              ||||||||||||||||:|||||  |  |::|| ||||| ||||:|| || |||||  | ||
Db         61 KCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVD 120

Qy        121 RDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQERQDTICHCHMGFFLKGAKCI 180
              |||||||||||| || |  |:| ||||| ||||:: |||:|:|:| || ||||:  :|:
Db        121 RDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECV 180

Qy        181 SCHDCKNK-ECEKLCPTRPSTGKDSQDPGTTVLLPLVIVFGLCLASFASVVLACRYQRWK 239
              || :||   || |||  :   | ::| |||||||||| |||||  :  |  ||||||
Db        181 SCSNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPLVIFFGLCLLSLLFIGLMYRYQRWK 240

Qy        240 PKLYSIICGQSTLVKEGEPE-----LLVPAPGFNP----TTTICFSSTPSSSPVSIPPYI 290
              |||||:||:||  |||| |      | | | |:|    | |: ||  |||:  |   |
Db        241 SKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPTPGFTPTLGFSPVPSSTFTSSSTYT 300

Qy        291 SCDRSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLC 350
              |  ||   |:|  | |||:  | |||                :| |      ||  :
Db        301 PGDCPNF---AAPRREVAPPYQGADPIL---------------ATAL------ASDPIP 335

Qy        351 TPVQKWEASAPSAPDQLADADPATLYAVVDGVPPSRWKELVRRLGLSEHEIERLELENGR 410
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Db        336 NPLQKWEDSA-HKPQSLDTDDPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLELQNGR 394

Qy        411 HLREAQYSMLAAWRRRTPRREATLELLGRVLRDMDLLGCLENIEEALGGAARLASEPRLL 470

Db        395 CLREAQYSMLATWRRRTPRREATLELLGRVLRDMDLLGCLEDIEEALCGPAALPPAPSLL 454


RESULT 8
US-09-252-656B-3
; Sequence 3, Application US/09252656B
; Patent No. US20020081647A1
; GENERAL INFORMATION:
;  APPLICANT: Ebner, Reinhard
;  APPLICANT:  Yu, Guo-Liang
;  APPLICANT:  Ruben, Steven M.
;  APPLICANT:  Zhang, Jun
;  APPLICANT:  Ullrich, Stephen
;  APPLICANT:  Zhai, Yifan
;  TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use
;  FILE REFERENCE: 1488.0650006
;  CURRENT APPLICATION NUMBER: US/09/252,656B
;  CURRENT FILING DATE:  1999-02-19
;  PRIOR APPLICATION NUMBER: US 60/075,409
;  PRIOR FILING DATE: 1998-02-20
;  PRIOR APPLICATION NUMBER: US 09/027,287
;  PRIOR PILING DATE: 1998-02-20
;  PRIOR APPLICATION NUMBER: US 09/003,886
;  PRIOR FILING DATE: 1998-01-07
;  PRIOR APPLICATION NUMBER: US 08/822,953
;  PRIOR FILING DATE: 1997-03-21
;  PRIOR APPLICATION NUMBER: US 60/013,923
;  PRIOR FILING DATE: 1996-03-22
;  PRIOR APPLICATION NUMBER: US 60/030,157
;  PRIOR FILING DATE: 1996-10-31
;  NUMBER OF SEQ ID NOS: 61
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 455
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-252-656B-3

  Query Match            58.3%;  Score 1517;  DB 9;  Length 455;
  Best Local Similarity  62.9%;  Pred. No. 7.1e-101;
  Matches  302;  Conservative   38;  Mismatches  104;  Indels   36;  Gaps    7;

Qy          1 MGLPTVPGLLLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCT 60

Db          1 MGLSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCT 60

Qy         61 KCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCLSCSRCRDEMFQVEISPCVVD 120

Db         61 KCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVD 120

Qy        121 RDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQERQDTICHCHMGFFLKGAKCI 180

Db        121 RDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECV 180

Qy        181 SCHDCKNK-ECEKLCPTRPSTGKDSQDPGTTVLLPLVIVFGLCLASFASVVLACRYQRWK 239

Db        181 SCSNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPLVIFFGLCLLSLLFIGLMYRYQRWK 240

Qy        240 PKLYSIICGQSTLVKEGEPE-----LLVPAPGFNP----TTTICFSSTPSSSPVSIPPYI 290

Db        241 SKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPTPGFTPTLGFSPVPSSTFTSSSTYT 300

Qy        291 SCDRSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLC 350

Db        301 PGDCPNF---AAPRREVAPPYQGADPIL---------------ATAL------ASDPIP 335

Qy        351 TPVQKWEASAPSAPDQLADADPATLYAVVDGVPPSRWKELVRRLGLSEHEIERLELENGR 410

Db        336 NPLQKWEDSA-HKPQSLDTDDPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLELQNGR 394

Qy        411 HLREAQYSMLAAWRRRTPRREATLELLGRVLRDMDLLGCLENIEEALGGAARLASEPRLL 470

Db        395 CLREAQYSMLATWRRRTPRREATLELLGRVLRDMDLLGCLEDIEEALCGPAALPPAPSLL 454


RESULT 9
US-09-899-422-2
; Sequence 2, Application US/09899422
; Patent No. US20020090676A1
; GENERAL INFORMATION:
;  APPLICANT: Hauptmann, Rudolph
;  APPLICANT:  Himmler, Adolph
;  APPLICANT:  Maurer-Fogy, Ingrid
;  APPLICANT:  Stratowa, Christian
;  TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
;  TITLE OF INVENTION:  Them
;  FILE REFERENCE: 98,385-H
;  CURRENT APPLICATION NUMBER: US/09/899,422
;  CURRENT FILING DATE:  2001-08-21
;  PRIOR APPLICATION NUMBER: 09/525,998
;  PRIOR FILING DATE: 2000-03-15
;  PRIOR APPLICATION NUMBER: 08/383,676
;  PRIOR FILING DATE: 1995-02-01
;  PRIOR APPLICATION NUMBER: 08/153,287
;  PRIOR FILING DATE: 1993-11-17
;  PRIOR APPLICATION NUMBER: 07/821,750
;  PRIOR FILING DATE: 1992-01-02
;  PRIOR APPLICATION NUMBER: 07/511,430
;  PRIOR FILING DATE: 1990-04-20
;  NUMBER OF SEQ ID NOS: 87
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 455
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-899-422-2

  Query Match            58.3%;  Score 1517;  DB 9;  Length 455;
  Best Local Similarity  62.9%;  Pred. No. 7.1e-101;
  Matches  302;  Conservative   38;  Mismatches  104;  Indels   36;  Gaps    7;

Qy          1 MGLPTVPGLLLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCT 60

Db          1 MGLSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCT 60

Qy         61 KCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCLSCSRCRDEMFQVEISPCVVD 120

Db         61 KCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVD 120

Qy        121 RDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQERQDTICHCHMGFFLKGAKCI 180

Db        121 RDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECV 180

Qy        181 SCHDCKNK-ECEKLCPTRPSTGKDSQDPGTTVLLPLVIVFGLCLASFASVVLACRYQRWK 239

Db        181 SCSNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPLVIFFGLCLLSLLFIGLMYRYQRWK 240

Qy        240 PKLYSIICGQSTLVKEGEPE-----LLVPAPGFNP----TTTICFSSTPSSSPVSIPPYI 290

Db        241 SKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPTPGFTPTLGFSPVPSSTFTSSSTYT 300

Qy        291 SCDRSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLC 350

Db        301 PGDCPNF---AAPRREVAPPYQGADPIL---------------ATAL------ASDPIP 335

Qy        351 TPVQKWEASAPSAPDQLADADPATLYAVVDGVPPSRWKELVRRLGLSEHEIERLELENGR 410

Db        336 NPLQKWEDSA-HKPQSLDTDDPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLELQNGR 394

Qy        411 HLREAQYSMLAAWRRRTPRREATLELLGRVLRDMDLLGCLENIEEALGGAARLASEPRLL 470
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Db        395 CLREAQYSMLATWRRRTPRREATLELLGRVLRDMDLLGCLEDIEEALCGPAALPPAPSLL 454


RESULT 10
US-09-899-422-17
; Sequence 17, Application US/09899422
; Patent No. US20020090676A1
; GENERAL INFORMATION:
;  APPLICANT: Hauptmann, Rudolph
;  APPLICANT:  Himmler, Adolph
;  APPLICANT:  Maurer-Fogy, Ingrid
;  APPLICANT:  Stratowa, Christian
;  TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
;  TITLE OF INVENTION:  Them
;  FILE REFERENCE: 98,385-H
;  CURRENT APPLICATION NUMBER: US/09/899,422
;  CURRENT FILING DATE:  2001-08-21
;  PRIOR APPLICATION NUMBER: 09/525,998
;  PRIOR FILING DATE: 2000-03-15
;  PRIOR APPLICATION NUMBER: 08/383,676
;  PRIOR FILING DATE: 1995-02-01
;  PRIOR APPLICATION NUMBER: 08/153,287
;  PRIOR FILING DATE: 1993-11-17
;  PRIOR APPLICATION NUMBER: 07/821,750
;  PRIOR FILING DATE: 1992-01-02
;  PRIOR APPLICATION NUMBER: 07/511,430
;  PRIOR FILING DATE: 1990-04-20
;  NUMBER OF SEQ ID NOS: 87
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
;   LENGTH: 455
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: human TNF-R in
;   OTHER INFORMATION: lTNF-R2
US-09-899-422-17

  Query Match           58.3%;  Score 1517;  DB 9;  Length 455;
  Best Local Similarity  62.9%;  Pred. No. 7.1e-101;
  Matches  302;  Conservative   38;  Mismatches  104;  Indels   36;  Gaps    7;

Qy          1 MGLPTVPGLLLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCT 60
              ||| ||| ||||||| || :||:|| ||||| || |||:| |||||| ||||::||||
Db          1 MGLSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCT 60

Qy         61 KCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCLSCSRCRDEMFQVEISPCVVD 120
              ||||||||||||||||:||||| |  |::|| ||||| |||||:|| || ||||| | ||
Db         61 KCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVD 120

Qy        121 RDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQERQDTICHCHMGFFLKGAKCI 180
              |||||||||||||| || |  |:| ||||| |||:: |||:|:|:| || ||||:  :|:
Db        121 RDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECV 180

Qy        181 SCHDCKNK-ECEKLCPTRPSTGKDSQDPGTTVLLPLVIVFGLCLASFASVVLACRYQRWK 239
              || :||  || |||  :    | ::| |||||||||| ||||| |  : |  ||||||
Db        181 SCSNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPLVIFFGLCLLSLLFIGLMYRYQRWK 240

Qy        240 PKLYSIICGQSTLVKEGEPE-----LLVPAPGFNP----TTTICFSSTPSSSPVSIPPYI 290
              |||||:||:||  |||| |      | | | |:|    | |: ||  |||:  |   |
Db        241 SKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPTPGFTPTLGFSPVPSSTFTSSSTYT 300

Qy        291 SCDRSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLC 350
              |  ||   |:|  | |||:  | |||                :| |      || :
Db        301 PGDCPNF---AAPRREVAPPYQGADPIL---------------ATAL------ASDPIP 335

Qy        351 TPVQKWEASAPSAPDQLADADPATLYAVVDGVPPSRWKELVRRLGLSEHEIERLELENGR 410
              |:|||| ||   |  |||||||||: ||| |||| ||||||:|||:||||:|||
Db        336 NPLQKWEDSA-HKPQSLDTDDPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLELQNGR 394

Qy        411 HLREAQYSMLAAWRRRTPRREATLELLGRVLRDMDLLGCLENIEEALGGAARLASEPRLL 470
              |||||||||| ||||||||||||||||||||||||||||:|||| | | |   | ||
Db        395 CLREAQYSMLATWRRRTPRREATLELLGRVLRDMDLLGCLEDIEEALCGPAALPPAPSLL 454


RESULT 11
US-09-935-727-5
; Sequence 5, Application US/09935727
; Patent No. US20020150583A1
; GENERAL INFORMATION:
;  APPLICANT: Human Genome Sciences, Inc.
;  TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
;  FILE REFERENCE: PF454P2
;  CURRENT APPLICATION NUMBER: US/09/935,727
;  CURRENT FILING DATE:  2001-08-24
;  PRIOR APPLICATION NUMBER: 60/303,224
;  PRIOR FILING DATE: 2001-07-06
;  PRIOR APPLICATION NUMBER: 60/252,131
;  PRIOR FILING DATE: 2000-11-21
;  PRIOR APPLICATION NUMBER: 60/227,598
;  PRIOR FILING DATE: 2000-08-25
;  PRIOR APPLICATION NUMBER: 09/518,931
;  PRIOR FILING DATE: 2000-03-03
;  PRIOR APPLICATION NUMBER: 60/168,235
;  PRIOR FILING DATE: 1999-12-01
;  PRIOR APPLICATION NUMBER: 60/146,371
;  PRIOR FILING DATE: 1999-08-02
;  PRIOR APPLICATION NUMBER: 60/131,964
;  PRIOR FILING DATE: 1999-04-30
;  PRIOR APPLICATION NUMBER: 60/131,270
;  PRIOR FILING DATE: 1999-04-27
;  PRIOR APPLICATION NUMBER: 60/124,092
;  PRIOR FILING DATE: 1999-03-12
;  PRIOR APPLICATION NUMBER: 60/121,774
;  PRIOR FILING DATE: 1999-03-04
;  PRIOR APPLICATION NUMBER: 09/006,352
;  PRIOR FILING DATE: 1998-01-13
;  PRIOR APPLICATION NUMBER: 60/035,496
;  PRIOR FILING DATE: 1997-01-14
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 455
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-935-727-5

  Query Match           58.3%;  Score 1517;  DB 10;  Length 455;
  Best Local Similarity  62.9%;  Pred. No. 7.1e-101;
  Matches  302;  Conservative   38;  Mismatches  104;  Indels   36;  Gaps    7;

Qy          1 MGLPTVPGLLLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCT 60
              ||| ||| ||||||| || :||:|| ||||| || |||:| |||||| ||||::||||
Db          1 MGLSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCT 60

Qy         61 KCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCLSCSRCRDEMFQVEISPCVVD 120
              ||||||||||||||||:||||| |  |::|| ||||| |||||:|| || ||||| | ||
Db         61 KCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVD 120

Qy        121 RDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQERQDTICHCHMGFFLKGAKCI 180
              |||||||||||||| || |  |:| ||||| |||:: |||:|:|:| || ||||:  :|:
Db        121 RDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECV 180

Qy        181 SCHDCKNK-ECEKLCPTRPSTGKDSQDPGTTVLLPLVIVFGLCLASFASVVLACRYQRWK 239
              || :||  || |||  :    | ::| |||||||||| ||||| |  : |  ||||||
Db        181 SCSNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPLVIFFGLCLLSLLFIGLMYRYQRWK 240

Qy        240 PKLYSIICGQSTLVKEGEPE-----LLVPAPGFNP----TTTICFSSTPSSSPVSIPPYI 290
              |||||:||:||  |||| |      | | | |:|    | |: ||  |||:  |   |
Db        241 SKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPTPGFTPTLGFSPVPSSTFTSSSTYT 300

Qy        291 SCDRSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLC 350
              |  ||   |:|  | |||:  | |||                :| |      || :
Db        301 PGDCPNF---AAPRREVAPPYQGADPIL---------------ATAL------ASDPIP 335

Qy        351 TPVQKWEASAPSAPDQLADADPATLYAVVDGVPPSRWKELVRRLGLSEHEIERLELENGR 410
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Db 336 NPLQKWEDSA-HKPQSLDTDDPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLELQNGR 394

Qy 411 HLREAQYSMLAAWRRRTPRREATLELLGRVLRDMDLLGCLENIEEALGGAARLASEPRLL 470

Db 395 CLREAQYSMLATWRRRTPRREATLELLGRVLRDMDLLGCLEDIEEALCGPAALPPAPSLL 454

RESULT 12
US-09-898-234-2
; Sequence 2, Application US/09898234
; Patent No. US20020155112A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stratowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; TITLE OF INVENTION: Them
; FILE REFERENCE: 98,385-I
; CURRENT APPLICATION NUMBER: US/09/898,234
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/525,998
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-898-234-2

Query Match 58.3%; Score 1517; DB 10; Length 455;
Best Local Similarity 62.9%; Pred. No. 7.1e-101;
Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

Qy 1 MGLPTVPGLLLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCT 60

Db 1 MGLSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCT 60

Qy 61 KCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCLSCSRCRDEMFQVEISPCVVD 120

Db 61 KCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVD 120

Qy 121 RDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQERQDTICHCHMGFFLKGAKCI 180

Db 121 RDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECV 180

Qy 181 SCHDCKNK-ECEKLCPTRPSTGKDSQDPGTTVLLPLVIVFGLCLASFASVVLACRYQRWK 239

Db 181 SCSNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPLVIFFGLCLLSLLFIGLMYRYQRWK 240

Qy 240 PKLYSIICGQSTLVKEGEPE-----LLVPAPGFNP----TTTICFSSTPSSSPVSIPPYI 290

Db 241 SKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPTPGFTPTLGFSPVPSSTFTSSSTYT 300

Qy 291 SCDRSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLC 350

Db 301 PGDCPNF---AAPRREVAPPYQGADPIL----------ATAL------ASDPIP 335

Qy 351 TPVQKWEASAPSAPDQLADADPATLYAVVDGVPPSRWKELVRRLGLSEHEIERLELENGR 410

Db 336 NPLQKWEDSA-HKPQSLDTDDPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLELQNGR 394

Qy 411 HLREAQYSMLAAWRRRTPRREATLELLGRVLRDMDLLGCLENIEEALGGAARLASEPRLL 470

Db 395 CLREAQYSMLATWRRRTPRREATLELLGRVLRDMDLLGCLEDIEEALCGPAALPPAPSLL 454

RESULT 13
US-09-898-234-17
; Sequence 17, Application US/09898234
; Patent No. US20020155112A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stratowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; TITLE OF INVENTION: Them
; FILE REFERENCE: 98,385-I
; CURRENT APPLICATION NUMBER: US/09/898,234
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/525,998
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: human TNF-R in
; OTHER INFORMATION: 1TNF-R2
US-09-898-234-17

Query Match 58.3%; Score 1517; DB 10; Length 455;
Best Local Similarity 62.9%; Pred. No. 7.1e-101;
Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

Qy 1 MGLPTVPGLLLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCT 60

Db 1 MGLSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCT 60

Qy 61 KCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCLSCSRCRDEMFQVEISPCVVD 120

Db 61 KCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVD 120

Qy 121 RDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQERQDTICHCHMGFFLKGAKCI 180

Db 121 RDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECV 180

Qy 181 SCHDCKNK-ECEKLCPTRPSTGKDSQDPGTTVLLPLVIVFGLCLASFASVVLACRYQRWK 239

Db 181 SCSNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPLVIFFGLCLLSLLFIGLMYRYQRWK 240

Qy 240 PKLYSIICGQSTLVKEGEPE-----LLVPAPGFNP----TTTICFSSTPSSSPVSIPPYI 290

Db 241 SKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPTPGFTPTLGFSPVPSSTFTSSSTYT 300

Qy 291 SCDRSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLC 350

Db 301 PGDCPNF---AAPRREVAPPYQGADPIL----------ATAL------ASDPIP 335

Qy 351 TPVQKWEASAPSAPDQLADADPATLYAVVDGVPPSRWKELVRRLGLSEHEIERLELENGR 410

Db 336 NPLQKWEDSA-HKPQSLDTDDPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLELQNGR 394

Qy 411 HLREAQYSMLAAWRRRTPRREATLELLGRVLRDMDLLGCLENIEEALGGAARLASEPRLL 470

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Db        395 CLREAQYSMLATWRRRTPRREATLELLGRVLRDMDLLGCLEDIEEALCGPAALPPAPSLL 454


RESULT 14
US-09-756-854-5
; Sequence 5, Application US/09756854
; Patent No. US20020164684A1
;   GENERAL INFORMATION:
;        APPLICANT: Ni, Jian
;                   Yu, Guo-Liang
;                   Fan, Ping
;                   Gentz, Reiner
;        TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Human Genome Sciences, Inc.
;             STREET: 9410 Key West Avenue
;             CITY: Rockville
;             STATE: MD
;             COUNTRY: US
;             ZIP: 20850
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/756,854
;             FILING DATE: 10-Jan-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/095,094
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Hoover, Kenley K.
;             REGISTRATION NUMBER: 40,302
;             REFERENCE/DOCKET NUMBER: PF375
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 301-309-8504
;             TELEFAX: 301-309-8439
;   INFORMATION FOR SEQ ID NO: 5:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 455 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-756-854-5

  Query Match           58.3%;  Score 1517;  DB 10;  Length 455;
  Best Local Similarity   62.9%;  Pred. No. 7.1e-101;
  Matches  302;  Conservative   38;  Mismatches  104;  Indels   36;  Gaps    7;

Qy          1 MGLPTVPGLLLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCT 60
              ||| ||| |||||||  ||  :||:|| ||||| || |||:| |||||| ||||::||||
Db          1 MGLSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCT 60

Qy         61 KCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCLSCSRCRDEMFQVEISPCVVD 120
              |||||||||||||||:|||||  |  |::|| ||||| |||||:|| || |||||  | ||
Db         61 KCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVD 120

Qy        121 RDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQERQDTICHCHMGFFLKGAKCI 180
              |||||||||||||| || |  |:| ||||| ||||:: |||:|:|:| || ||||:  :|:
Db        121 RDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECV 180

Qy        181 SCHDCKNK-ECEKLCPTRPSTGKDSQDPGTTVLLPLVIVFGLCLASFASVVLACRYQRWK 239
              || :||   || |||  :    | ::| |||||||||| ||||| |   :  |  ||||||
Db        181 SCSNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPLVIFFGLCLLSLLFIGLMYRYQRWK 240

Qy        240 PKLYSIICGQSTLVKEGEPE-----LLVPAPGFNP----TTTICFSSTPSSSPVSIPPYI 290
              |||||:||:||  |||| |      | | | |:|    | |: ||  |||:  |   |
Db        241 SKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPTPGFTPTLGFSPVPSSTFTSSSTYT 300

Qy        291 SCDRSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLC 350
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Db        301 PGDCPNF---AAPRREVAPPYQGADPIL----------------ATAL------ASDPIP 335

Qy        351 TPVQKWEASAPSAPDQLADADPATLYAVVDGVPPSRWKELVRRLGLSEHEIERLELENGR 410
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Db        336 NPLQKWEDSA-HKPQSLDTDDPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLELQNGR 394

Qy        411 HLREAQYSMLAAWRRRTPRREATLELLGRVLRDMDLLGCLENIEEALGGAARLASEPRLL 470
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Db        395 CLREAQYSMLATWRRRTPRREATLELLGRVLRDMDLLGCLEDIEEALCGPAALPPAPSLL 454


RESULT 15
US-09-899-429A-2
; Sequence 2, Application US/09899429A
; Patent No. US20020169118A1
; GENERAL INFORMATION:
;  APPLICANT: Hauptmann, Rudolph
;  APPLICANT:  Himmler, Adolph
;  APPLICANT:  Maurer-Fogy, Ingrid
;  APPLICANT:  Stratowa, Christian
;  TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
;  TITLE OF INVENTION:  Them
;  FILE REFERENCE: 98-385-J
;  CURRENT APPLICATION NUMBER: US/09/899,429A
;  CURRENT FILING DATE:  2001-07-03
;  PRIOR APPLICATION NUMBER: 09/792,356
;  PRIOR FILING DATE: 2000-02-23
;  PRIOR APPLICATION NUMBER: 08/477,639
;  PRIOR FILING DATE: 1955-06-07
;  PRIOR APPLICATION NUMBER: 08/383,676
;  PRIOR FILING DATE: 1995-02-01
;  PRIOR APPLICATION NUMBER: 08/153,287
;  PRIOR FILING DATE: 1993-11-17
;  PRIOR APPLICATION NUMBER: 07/821,750
;  PRIOR FILING DATE: 1992-01-02
;  PRIOR APPLICATION NUMBER: 07/511,430
;  PRIOR FILING DATE: 1990-04-20
;  NUMBER OF SEQ ID NOS: 97
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 455
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-899-429A-2

  Query Match           58.3%;  Score 1517;  DB 10;  Length 455;
  Best Local Similarity   62.9%;  Pred. No. 7.1e-101;
  Matches  302;  Conservative   38;  Mismatches  104;  Indels   36;  Gaps    7;

Qy          1 MGLPTVPGLLLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCT 60
              ||| ||| |||||||  ||  :||:|| ||||| || |||:| |||||| ||||::||||
Db          1 MGLSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCT 60

Qy         61 KCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCLSCSRCRDEMFQVEISPCVVD 120
              |||||||||||||||:|||||  |  |::|| ||||| |||||:|| || |||||  | ||
Db         61 KCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVD 120

Qy        121 RDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQERQDTICHCHMGFFLKGAKCI 180
              |||||||||||||| || |  |:| ||||| ||||:: |||:|:|:| || ||||:  :|:
Db        121 RDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECV 180

Qy        181 SCHDCKNK-ECEKLCPTRPSTGKDSQDPGTTVLLPLVIVFGLCLASFASVVLACRYQRWK 239
              || :||   || |||  :    | ::| |||||||||| ||||| |   :  |  ||||||
Db        181 SCSNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPLVIFFGLCLLSLLFIGLMYRYQRWK 240

Qy        240 PKLYSIICGQSTLVKEGEPE-----LLVPAPGFNP----TTTICFSSTPSSSPVSIPPYI 290
              |||||:||:||  |||| |      | | | |:|    | |: ||  |||:  |   |
Db        241 SKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPTPGFTPTLGFSPVPSSTFTSSSTYT 300

Qy        291 SCDRSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLC 350
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                 |  ||   |:|  | |||:  | |||               :| |      ||  :
Db        301 PGDCPNF---AAPRREVAPPYQGADPIL---------------ATAL------ASDPIP 335

Qy        351 TPVQKWEASAPSAPDQLADADPATLYAVVDGVPPSRWKELVRRLGLSEHEIERLELENGR 410
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Db        336 NPLQKWEDSA-HKPQSLDTDDPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLELQNGR 394

Qy        411 HLREAQYSMLAAWRRRTPRREATLELLGRVLRDMDLLGCLENIEEALGGAARLASEPRLL 470
               |||||||||| |||||||||||||||||||||||||||:||||| | | |   | ||
Db        395 CLREAQYSMLATWRRRTPRREATLELLGRVLRDMDLLGCLEDIEEALCGPAALPPAPSLL 454

Search completed: September 13, 2003, 07:10:54
Job time : 28 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 13, 2003, 07:02:24 ; Search time 20 Seconds
(without alignments)
2264.772 Million cell updates/sec

Title: US-09-970-532-2
Perfect score: 2603
Sequence: 1 MGLPTVPGLLLPLVLPALLA.....NIEEALGGAARLASEPRLLW 471

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1750	67.2	461	2	JC4302	tumor necrosis fac
2	1517	58.3	455	1	GQHUT1	tumor necrosis fac
3	1338.5	51.4	461	1	GQRTT1	tumor necrosis fac
4	1319	50.7	454	1	GQMST1	tumor necrosis fac
5	257	9.9	435	2	I54182	tumor necrosis fac
6	236	9.1	427	1	GQHUN	nerve growth facto
7	227.5	8.7	425	1	A26431	nerve growth facto
8	220	8.5	416	1	JN0006	nerve growth facto
9	199.5	7.7	651	2	JC7705	death receptor-6 -
10	199	7.6	461	1	A35356	tumor necrosis fac
11	193	7.4	595	2	A42086	CD30 antigen precu
12	181.5	7.0	324	2	JC2395	Fas antigen precur
13	181.5	7.0	325	2	B43692	T2 protein - rabbi
14	180	6.9	326	1	GQVZML	T2 protein - myxom
15	178.5	6.9	474	2	B38634	tumor necrosis fac
16	173	6.6	459	2	I48854	gene murine tumour
17	169	6.5	3635	2	T10053	laminin alpha 5 ch
18	168.5	6.5	305	2	A46476	B cell-associated
19	163.5	6.3	348	2	T28623	hypothetical prote
20	163.5	6.3	349	2	D72175	G2R protein - vari
21	163.5	6.3	349	2	D36858	gene G4R protein -
22	161	6.2	327	2	A46484	apoptosis-mediatin
23	155	6.0	1548	2	S34583	serine proteinase
24	150	5.8	1613	2	JE0272	low density lipopr
25	149	5.7	1613	2	JE0273	low density lipopr
26	147.5	5.7	1801	1	MMRTS	laminin beta-2 cha
27	147	5.6	335	2	A40036	apoptosis-mediatin
28	147	5.6	2321	2	S78549	notch3 protein - h
29	145.5	5.6	1299	2	T43251	furin (EC 3.4.21.7
30	145	5.6	260	1	A46517	CD27 antigen precu
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33	140.5	5.4	1111	2	T26972	hypothetical prote
34	140.5	5.4	1513	2	A54895	mucin 2, intestina
35	140.5	5.4	3020	2	A43932	mucin 2 precursor,
36	140	5.4	277	2	I37552	OX40 homolog - hum
37	140	5.4	1797	2	A55677	laminin beta-2 cha
38	139.5	5.4	3672	2	T23433	hypothetical prote
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44	136	5.2	826	2	A60385	monocyte surface a
45	135.5	5.2	937	2	I53282	gene PACE4 protein

ALIGNMENTS

RESULT 1
JC4302
tumor necrosis factor receptor p55 precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 29-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 23-Jul-1999
C;Accession: JC4302; PC4093
R;Suter, B.; Pauli, U.
Gene 163, 263-266, 1995
A;Title: Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor.
A;Reference number: JC4302; MUID:96011645; PMID:7590278
A;Accession: JC4302
A;Molecule type: mRNA
A;Residues: 1-461 <SUT>
A;Cross-references: GB:U19994; NID:g1141752; PIDN:AAC48499.1; PID:g1141753
A;Accession: PC4093
A;Molecule type: protein
A;Residues: 1-7 <SU2>
A;Experimental source: kidney cell line 15
C;Genetics:
A;Gene: tnfr
C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
C;Keywords: glycoprotein; kidney; receptor; transmembrane protein; tumor
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-461/Product: tumor necrosis factor receptor p55 #status predicted <MAT>
F;44-194/Domain: extracellular cysteine rich #status predicted <EXT>
F;44-82/Domain: NGF receptor repeat homology <NG1>
F;84-126/Domain: NGF receptor repeat homology <NGF>
F;211-231/Domain: transmembrane #status predicted <TMM>
F;361-447/Domain: signal transduction #status predicted <SIT>
F;54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 67.2%; Score 1750; DB 2; Length 461;
Best Local Similarity 70.2%; Pred. No. 6.5e-100;
Matches 339; Conservative 24; Mismatches 84; Indels 36; Gaps 5;

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Qy          1 MGLPTVPGLLLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCT 60
              ||| |||||||||||| ||| ||||||| ||| |||| ||||| ||||||:|||| :||||
Db          1 MGLSTVPGLLLPLVLRALLVDVYPAGVHGLVLHPGDREKRESLCPQGKYSHPQNRSICCT 60

Qy         61 KCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCLSCSRCRDEMFQVEISPCVVD 120
              ||||||||:||| ||| ||||| |  ||:|| |||| :|||||:|| || ||||||| ||
Db         61 KCHKGTYLHNDCLGPGLDTDCRECDNGTFTASENHLTQCLSCSKCRSEMSQVEISPCTVD 120

Qy        121 RDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQERQDTICHCHMGPFLKGAKCI 180
              ||||||||||||||:|| || |:|||||||||||| :|| |:|||||:|| |||||  :|:
Db        121 RDTVCGCRKNQYRKYWSETLFQCLNCSLCPNGTVQLPCLEKQDTICNCHSGFFLRDKECV 180

Qy        181 SCHDCKNKECEKLCPTRPSTGKDSQDPGTTVLLPLVIVFGLCLASFASVVLACRYQRWKP 240
              || :||| :|: |||    |  | || |||||||||| ||||||  |  | ||||||||||
Db        181 SCVNCKNADCKNLCPATSETRNDFQDTGTTVLLPLVIFFGLCLAFFLFVGLACRYQRWKP 240

Qy        241 KLYSIICGQSTLVKEGEPELLVPAPGFNPTTTI----------CFSSTPSSSPVSIPPYI 290
```

```
            ||||||||:|| ||||||| |  || | | ||           ||  || ||:| | :
Db        241 KLYSIICGKSTPVKEGEPEPLATAPSFGPITTFSPIPSFSPTTTFSPVPSFSPISSPTFT 300

Qy        291 SCDRSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLC 350
              || ||   | ||  | |||   |||||| ||||           || |
Db        301 PCDWSNI-KVTSPPKEIAPPPQGAGPILPMPPAS--------------TPVP------- 337

Qy        351 TPVQKWEA---SAPSAPDQLADADPATLYAVVDGVPPSRWKELVRRLGLSEHEIERLELE 407
              ||: ||     || ||| |||||||||||||||||:|||| ||||||||||||||:
Db        338 TPLPKWGGSAHSAHSAPAQLADADPATLYAVVDGVPPTRWKEFVRRLGLSEHEIERLELQ 397

Qy        408 NGRHLREAQYSMLAAWRRRTPRREATLELLGRVLRDMDLLGCLENIEEALGGAARLASEP 467
              ||| |||||||||| ||||| |||||||||| ||||||||||||:||||| | ||||  |
Db        398 NGRCLREAQYSMLAEWRRRTSRREATLELLGSVLRDMDLLGCLEDIEEALRGPARLAPAP 457

Qy        468 RLL 470
              ||
Db        458 HLL 460
```

RESULT 2
GQHUT1
tumor necrosis factor receptor 1 precursor [validated] - human
N;Alternate names: P55 tumor necrosis factor receptor; TNF receptor type 1
N;Contains: tumor necrosis factor alpha inhibitor; tumor necrosis factor binding protein
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 08-Dec-2000
C;Accession: A38208; A34899; A34900; A36555; C36555; A38281; S12057; JT0758; A60231; A38
R;Fuchs, P.; Strehl, S.; Dworzak, M.; Himmler, A.; Ambros, P.F.
Genomics 13, 219-224, 1992
A;Title: Structure of the human TNF receptor 1 (p60) gene (TNRF1) and localization to ch
A;Reference number: A38208; MUID:92250049; PMID:1315717
A;Accession: A38208
A;Molecule type: DNA
A;Residues: 1-455 <FUC>
A;Cross-references: GB:M75864; GB:M75865; GB:M75866; NID:g339748; PIDN:AAA61201.1; PID:g
R;Loetscher, H.; Pan, Y.C.E.; Lahm, H.W.; Gentz, R.; Brockhaus, M.; Tabuchi, H.; Lesslau
Cell 61, 351-359, 1990
A;Title: Molecular cloning and expression of the human 55 kd tumor necrosis factor recep
A;Reference number: A34899; MUID:90235284; PMID:2158862
A;Accession: A34899
A;Molecule type: mRNA
A;Residues: 1-455 <LOE>
A;Cross-references: GB:M58286; GB:M33480; NID:g339753; PIDN:AAA36753.1; PID:g339754
A;Experimental source: placenta
A;Note: part of this sequence, including the amino end of the mature protein, confirmed
R;Schall, T.J.; Lewis, M.; Koller, K.J.; Lee, A.; Rice, G.C.; Wong, G.H.W.; Gatanaga, T.
Cell 61, 361-370, 1990
A;Title: Molecular cloning and expression of a receptor for human tumor necrosis factor.
A;Reference number: A34900; MUID:90235285; PMID:2158863
A;Accession: A34900
A;Molecule type: mRNA
A;Residues: 1-455 <SCH>
A;Cross-references: GB:M33294; NID:g339744; PIDN:AAA03210.1; PID:g339745
R;Himmler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lantz, M.;
DNA Cell Biol. 9, 705-715, 1990
A;Title: Molecular cloning and expression of human and rat tumor necrosis factor recepto
A;Reference number: A36555; MUID:91090841; PMID:1702293
A;Accession: A36555
A;Molecule type: mRNA
A;Residues: 1-455 <HIM>
A;Cross-references: GB:M63121; NID:g339755; PIDN:AAA36754.1; PID:g339756
A;Accession: C36555
A;Molecule type: protein
A;Residues: 30-38;41-53,'X',55-79,'XX',82-94,'NK';'XX',100-104;107-128;162-167,'X',169-2
A;Note: the purified protein, called tumor necrosis factor binding protein, is a soluble
R;Gray, P.W.; Barrett, K.; Chantry, D.; Turner, M.; Feldmann, M.
Proc. Natl. Acad. Sci. U.S.A. 87, 7380-7384, 1990
A;Title: Cloning of human tumor necrosis factor (TNF) receptor cDNA and expression of re
A;Reference number: A38281; MUID:91017509; PMID:2170974
A;Accession: A38281
A;Molecule type: mRNA
A;Residues: 1-455 <GRA>
A;Cross-references: GB:M37764
A;Note: the authors translated the codon TGG for residue 371 as Thr, AAG for residue 372
R;Nophar, Y.; Kemper, O.; Brakebusch, C.; Engelmann, H.; Zwang, R.; Aderka, D.; Holtmann,
EMBO J. 9, 3269-3278, 1990
A;Title: Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA for the type
le form of the receptor.
A;Reference number: S12057; MUID:91006021; PMID:1698610
A;Accession: S12057
A;Molecule type: mRNA
A;Residues: 1-455 <NOP>
A;Cross-references: EMBL:X55313; NID:g37223; PIDN:CAA39021.1; PID:g37224
A;Note: parts of soluble TNF binding protein 1, including its amino and carboxyl ends, we
R;Kemper, O.; Wallach, D.
Gene 134, 209-216, 1993
A;Title: Cloning and partial characterization of the promoter for the human p55 tumor nec
A;Reference number: JT0758; MUID:94085779; PMID:8262379
A;Accession: JT0758
A;Molecule type: DNA
A;Residues: 1-13 <KEM>
R;Seckinger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayer, J.M.
Eur. J. Immunol. 20, 1167-1174, 1990
A;Title: Tumor necrosis factor inhibitor: purification, NH-2-terminal amino acid sequence
A;Reference number: A60231; MUID:90292116; PMID:2113477
A;Accession: A60231
A;Molecule type: protein
A;Residues: 41-43,'X',45-53,'X',55-57 <SEC>
R;Gatanaga, T.; Hwang, C.; Kohr, W.; Cappuccini, F.; Lucci III, J.A.; Jeffes, E.W.B.; Ler
Proc. Natl. Acad. Sci. U.S.A. 87, 8781-8784, 1990
A;Title: Purification and characterization of an inhibitor (soluble tumor necrosis factor
tients.
A;Reference number: A38258; MUID:91062364; PMID:2174164
A;Accession: A38258
A;Molecule type: protein
A;Residues: 41-60 <GAT>
A;Experimental source: cancer patient serum
R;Olsson, I.; Lantz, M.; Nilsson, E.; Peetre, C.; Thysell, H.; Grubb, A.; Adolf, G.
Eur. J. Haematol. 42, 270-275, 1989
A;Title: Isolation and characterization of a tumor necrosis factor binding protein from u
A;Reference number: A60594; MUID:89171156; PMID:2924890
A;Accession: A60594
A;Molecule type: protein
A;Residues: 41-43,'X',45-53,'V',55-57,'XK',60 <OLS>
A;Experimental source: renal failure patient urine
R;Engelmann, H.; Novick, D.; Wallach, D.
J. Biol. Chem. 265, 1531-1536, 1990
A;Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence f
A;Reference number: A35010; MUID:90110215; PMID:2153136
A;Accession: A35010
A;Molecule type: protein
A;Residues: 41-45 <ENG>
A;Experimental source: normal urine
R;Kajihara, J.; Asada, A.; Kirihara, S.; Kato, K.
Biosci. Biotechnol. Biochem. 58, 2266-2268, 1994
A;Title: Amino acid sequence of natural tumor necrosis factor alpha inhibitor purified fr
A;Reference number: JC2404; MUID:95128033; PMID:7765720
A;Accession: JC2404
A;Molecule type: protein
A;Residues: 41-53,'X',55-144,'X',146-150,'X',152-186,'X',188-201 <KAJ>
A;Experimental source: urine
C;Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and
C;Genetics:
A;Gene: GDB:TNFR1
A;Cross-references: GDB:125913; OMIM:191190
A;Map position: 12p13.2-12p13.2
A;Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1
C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
C;Keywords: duplication; glycoprotein; receptor; transmembrane protein
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-455/Product: tumor necrosis factor receptor 1 #status predicted <MAT>
F;30-211/Domain: extracellular #status predicted <EXT>
F;41-201/Product: TNF binding protein 1 (tumor necrosis factor alpha inhibitor) #status e
F;44-82/Domain: NGF receptor repeat homology <NG1>
F;84-126/Domain: NGF receptor repeat homology <NG2>
```
```

F;127-167/Domain: NGF receptor repeat homology <NG3>
F;168-196/Domain: NGF receptor repeat homology <NG4>
F;212-234/Domain: transmembrane #status predicted <MEM>
F;235-455/Domain: intracellular #status predicted <INT>
F;54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 58.3%; Score 1517; DB 1; Length 455;
Best Local Similarity 62.9%; Pred. No. 1.1e-85;
Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

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Qy          1 MGLPTVPGLLLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCT 60
              ||| ||| ||||||| ||  :||:|| ||||| || |||:| |||||| ||||::||||
Db          1 MGLSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCT 60

Qy         61 KCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCLSCSRCRDEMFQVEISPCVVD 120
              ||||||||||||||||:|||||  |  |::|| ||||| |||||:|| || |||||  | ||
Db         61 KCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVD 120

Qy        121 RDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQERQDTICHCHMGFFLKGAKCI 180
              |||||||||||| || |  |:| ||||| ||||:: |||:|:|:| || ||||:  :|:
Db        121 RDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECV 180

Qy        181 SCHDCKNK-ECEKLCPTRPSTGKDSQDPGTTVLLPLVIVFGLCLASFASVVLACRYQRWK 239
              || :||   || |||  :    | ::| |||||||||| ||||| |   : |  ||||||
Db        181 SCSNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPLVIFFGLCLLSLLFIGLMYRYQRWK 240

Qy        240 PKLYSIICGQSTLVKEGEPE-----LLVPAPGFNP----TTTICFSSTPSSSPVSIPPYI 290
              |||||:||:||  |||| |      | | | |:|    | |: ||  |||:  |   |
Db        241 SKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPTPGFTPTLGFSPVPSSTFTSSSTYT 300

Qy        291 SCDRSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLC 350
              |  ||   |:|  | |||:  | |||                :| |       ||  :
Db        301 PGDCPNF---AAPRREVAPPYQGADPIL---------------ATAL------ASDPIP 335

Qy        351 TPVQKWEASAPSAPDQLADADPATLYAVVDGVPPSRWKELVRRLGLSEHEIERLELENGR 410
              |:|||| ||   |  |  |||||||||: ||| |||| |||||||:|||:||||:|||
Db        336 NPLQKWEDSA-HKPQSLDTDDPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLELQNGR 394

Qy        411 HLREAQYSMLAAWRRRTPRREATLELLGRVLRDMDLLGCLENIEEALGGAARLASEPRLL 470
              |||||||||| ||||||||||L||||||||||||||||||:|||| | | |   | ||
Db        395 CLREAQYSMLATWRRRTPRREATLELLGRVLRDMDLLGCLEDIEEALCGPAALPPAPSLL 454
```

RESULT 3
GQRTT1
tumor necrosis factor receptor 1 precursor - rat
N;Contains: tumor necrosis factor binding protein 1 (TNF blocking factor)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1992 #sequence_revision 07-Oct-1994 #text_change 22-Jun-1999
C;Accession: B36555
R;Himmler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lantz, M.;
DNA Cell Biol. 9, 705-715, 1990
A;Title: Molecular cloning and expression of human and rat tumor necrosis factor recepto
A;Reference number: A36555; MUID:91090841; PMID:1702293
A;Accession: B36555
A;Molecule type: mRNA
A;Residues: 1-461 <HIM>
A;Cross-references: GB:M63122; NID:g207361; PIDN:AAA42256.1; PID:g207362
C;Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and
C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
C;Keywords: duplication; glycoprotein; receptor; transmembrane protein
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-461/Product: tumor necrosis factor receptor type 1 #status predicted <MAT>
F;30-211/Domain: extracellular #status predicted <EXT>
F;30-201/Product: tumor necrosis factor binding protein #status predicted <TBP>
F;44-82/Domain: NGF receptor repeat homology <NG1>
F;84-126/Domain: NGF receptor repeat homology <NG2>
F;127-167/Domain: NGF receptor repeat homology <NG3>
F;168-204/Domain: NGF receptor repeat homology <NG4>
F;212-234/Domain: transmembrane #status predicted <MEM>
F;235-461/Domain: intracellular #status predicted <INT>
F;54,151,201/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 51.4%; Score 1338.5; DB 1; Length 461;
Best Local Similarity 55.8%; Pred. No. 9.2e-75;
Matches 268; Conservative 51; Mismatches 114; Indels 47; Gaps 9;

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Qy          1 MGLPTVPGLLLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCT 60
              |||| |||||| ||| |||  ::|:|| ||||  || |||:: |||||| ||:|::||||
Db          1 MGLPIVPGLLLSLVLLALLMGIHPSGVTGLVPSLGDREKRDNLCPQGKYAHPKNNSICCT 60

Qy         61 KCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCLSCSRCRDEMFQVEISPCVVD 120
              |||||||| :||| ||::|  | ||  ||:|| :|||:|:|||  || ||||||||||  |
Db         61 KCHKGTYLVSDCPSPGQETVCEVCDKGTFTASQNHVRQCLSCKTCRKEMFQVEISPCKAD 120

Qy        121 RDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQERQDTICHCHMGFFLKGAKCI 180
              ||||||:|||:: |  || |:|::|| | |||| |||:|:|:|:|:|| |||| | :|
Db        121 MDTVCGCKKNQFQRYLSETHFQCVDCSPCFNGTVTIPCKEKQNTVCNCHAGFFLSGNECT 180

Qy        181 SCHDC-KNKECEKLCPTRPSTGKDSQDPGTTVLLPLVIVFGLCLASFASVVLACRYQRWK 239
              |  | ||:|| |||    :   : || || |||||||  |||| |  : | ||| :|:
Db        181 PCSHCKKNQECMKLCLPPVANVTNPQDSGTAVLLPLVIFLGLCLLFFICISLLCRYPQWR 240

Qy        240 PKLYSIICGQSTLVKEGEPELLV-------------PAPGFNPT----TTICFSSTPSSS 282
              |::|||||  |  ||| | | :|              | ||||||    ||  ||   ||:
Db        241 PRVYSIICRDSAPVKEVEGEGIVTKPLTPASIPAFSPNPGFNPTLGFSTTPRFSHPVSST 300

Qy        283 PVSIPPYISCDRSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPG 342
              |:| | :     ||:    | | |    | |:| |                      |
Db        301 PIS-PVF---GPSNWHNFVPPVREVVPTQ-GADPLLYGS----------------LNPV 338

Qy        343 P-PASTHLCTPVQKWEASAPSAPDQLADADPATLYAVVDGVPPSRWKELVRRLGLSEHEI 401
              | ||      ||:|||    : | :|  |||| ||||||||||:|||| :| ||||||||
Db        339 PIPA------PVRKWEDVVAAQPQRLDTADPAMLYAVVDGVPPTRWKEFMRLLGLSEHEI 392

Qy        402 ERLELENGRHLREAQYSMLAAWRRRTPRREATLELLGRVLRDMDLLGCLENIEEALGGAA 461
              |||||:||| |||| |||||||||| ||||:::|||| ||:| |||||| | |   |
Db        393 ERLELQNGRCLREAHYSMLEAWRRRTPRHEATLDVVGRVLCDMNLRGCLENIRETLESPA 452
```

RESULT 4
GQMST1
tumor necrosis factor receptor 1 precursor - mouse
N;Alternate names: tumor necrosis factor receptor, 55K
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 01-Dec-2000
C;Accession: A38634; B40254; S16677; S19021; I54532; I57826
R;Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E.
Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991
A;Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor re
A;Reference number: A38634; MUID:91187885; PMID:1849278
A;Accession: A38634
A;Molecule type: mRNA
A;Residues: 1-454 <LEW>
A;Cross-references: GB:M60468; NID:g199825; PIDN:AAA39751.1; PID:g199826
R;Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jenki
Mol. Cell. Biol. 11, 3020-3026, 1991
A;Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for t
A;Reference number: A40254; MUID:91246168; PMID:1645445
A;Accession: B40254
A;Molecule type: mRNA
A;Residues: 1-454 <GO2>
A;Cross-references: GB:M60468; NID:g199825; PIDN:AAA39751.1; PID:g199826
R;Barrett, K.; Taylor-Fishwick, D.A.; Cope, A.P.; Kissonerghis, A.M.; Gray, P.W.; Feldmar
Eur. J. Immunol. 21, 1649-1656, 1991
A;Title: Cloning, expression and cross-linking analysis of the murine p55 tumor necrosis
A;Reference number: S16677; MUID:91285014; PMID:1647956
A;Accession: S16677
A;Molecule type: mRNA
A;Residues: 1-454 <BAR>
A;Cross-references: EMBL:X59238; NID:g53578; PIDN:CAA41922.1; PID:g53579
R;Rothe, J.G.; Brockhaus, M.; Gentz, R.; Lesslauer, W.
Immunogenetics 34, 338-340, 1991
A;Title: Molecular cloning and expression of the mouse Tnf receptor type b.
A;Reference number: S19021; MUID:92039815; PMID:1657766
A;Accession: S19021

A;Molecule type: mRNA
A;Residues: 1-454 <ROT>
A;Cross-references: EMBL:X57796; NID:g54848; PIDN:CAA40936.1; PID:g54849
R;Bebo, B.F.
Immunogenetics 39, 450-451, 1994
A;Title: Nucleotide sequence of the TNF type I receptor from a mouse endothelioma cell l
A;Reference number: I54532; MUID:94245292; PMID:8188324
A;Accession: I54532
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-454 <RES>
A;Cross-references: GB:L26349; NID:g430732; PIDN:AAA59361.1; PID:g430733
R;Rothe, J.G.; Bluethmann, H.; Gentz, R.; Lesslauer, W.; Steinmetz, M.
Mol. Immunol. 30, 165-176, 1993
A;Title: Genomic organization and promoter function of the murine tumor necrosis factor
A;Reference number: I57826; MUID:93156721; PMID:8381516
A;Accession: I57826
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-393,'G',395-454 <RE2>
A;Cross-references: GB:M76656; NID:g202100; PIDN:AAA40465.1; PID:g202102
C;Comment: This protein is one of two distantly related receptors for both TNF-alpha (ca
C;Genetics:
A;Gene: TNFR-2
A;Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 210/1; 248/1; 257/3; 353/1
C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
C;Keywords: cytokine receptor; duplication; glycoprotein; receptor; transmembrane protei
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-454/Product: tumor necrosis factor receptor type 1 #status predicted <MAT>
F;30-212/Domain: extracellular #status predicted <EXT>
F;44-82/Domain: NGF receptor repeat homology <NG1>
F;84-126/Domain: NGF receptor repeat homology <NG2>
F;127-167/Domain: NGF receptor repeat homology <NG3>
F;168-204/Domain: NGF receptor repeat homology <NG4>
F;213-235/Domain: transmembrane #status predicted <MEM>
F;236-454/Domain: intracellular #status predicted <INT>
F;54,151,202/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 50.7%; Score 1319; DB 1; Length 454;
Best Local Similarity 56.5%; Pred. No. 1.4e-73;
Matches 268; Conservative 55; Mismatches 109; Indels 42; Gaps 12;

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Qy          1 MGLPTVPGLLLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCT 60
              |||||||||||  ||| |||  ::|:|| ||||  || |||:| |||||| | :|::||||
Db          1 MGLPTVPGLLLSLVLLALLMGIHPSGVTGLVPSLGDREKRDSLCPQGKYVHSKNNSICCT 60

Qy         61 KCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCLSCSRCRDEMFQVEISPCVVD 120
              |||||||| :||| ||||| || |  ||:|| :|:||:|||  || || |||||||  |
Db         61 KCHKGTYLVSDCPSPGRDTVCRECEKGTFTASQNYLRQCLSCKTCRKEMSQVEISPCQAD 120

Qy        121 RDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQERQDTICHCHMGFFLKGAKCI 180
              :||||||::||:: |  || |:|::|| | |||| |||:| |:|:|:|| ||||: ::|:
Db        121 KDTVCGCKENQFQRYLSETHPQCVDCSPCFNGTVTIPCKETQNTVCNCHAGFFLRESECV 180

Qy        181 SCHDC-KNKECEKLC-PTRPSTGKDSQDPGTTVLLPLVIVFGLCLASFASVVLACRYQRW 238
              |  | ||:|| ||| |   :   : || || |||||||: |||| ||  : | ||| ||
Db        181 PCSHCKKNEECMKLCLPPPLANVTNPQDSGTAVLLPLVILLGLCLLSFIFISLMCRYPRW 240

Qy        239 KPKLYSIICGQSTLVKE---GEPELLVPAPGFNPTT----TICFSSTPSSSPVSIPPYIS 291
              :|::|||||      |||   |:|    |:| |:||:    |: ||:   |||||  |
Db        241 RPEVYSIICRDPVPVKEEKAGKPLTPAPSPAFSPTSGFNPTLGFSTPGFSSPVSSTP--- 297

Qy        292 CDRSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTPG--PPASTHLCT-PGPPASTH 348
                    :  ||:     |          || |  : | |  |      ||: | |
Db        298 -----ISPIFGPSNW----HFM-------PPVSEVVPTQGADPLLYESLCSVPAP----- 336

Qy        349 LCTPVQKWEASA-PSAPDQLADADPATLYAVVDGVPPSRWKELVRRLGLSEHEIERLELE 407
              | ||||| || |  ||   :|| | ||||||||||:|||| :| :||||||||||::
Db        337 --TSVQKWEDSAHPQRPD---NADLAILYAVVDGVPPARWKEFMRFMGLSEHEIERLEMQ 391

Qy        408 NGRHLREAQYSMLAAWRRRTPRREATLELLGRVLRDMDLLGCLENIEEALGGAA 461
              ||| |||||||||  |||||||| | |||:| ||  |:| |||||| |||   |
Db        392 NGRCLREAQYSMLEAWRRRTPRHEDTLEVVGLVLSKMNLAGCLENILEALRNPA 445
```

RESULT 5
I54182
tumor necrosis factor receptor 2-related protein - human
C;Species: Homo sapiens (man)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 17-Mar-2000
C;Accession: I54182
R;Baens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.
Genomics 16, 214-218, 1993
A;Title: Construction and evaluation of a hncDNA library of human 12p transcribed sequenc
A;Reference number: I54182; MUID:93252381; PMID:8486360
A;Accession: I54182
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-435 <RES>
A;Cross-references: GB:L04270; NID:g339761; PIDN:AAA36757.1; PID:g339762
C;Genetics:
A;Gene: GDB:LTBR
A;Cross-references: GDB:1230195; OMIM:600979
A;Map position: 12p13.3-12p13.1
C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

Query Match 9.9%; Score 257; DB 2; Length 435;
Best Local Similarity 27.3%; Pred. No. 1.1e-08;
Matches 121; Conservative 37; Mismatches 158; Indels 128; Gaps 25;

```
Qy          1 MGLP---TVPGLLL-PLVLP--ALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQN 54
              | ||   : |||   ||||    |||   |  |       |   | :    : :|  ||:
Db          1 MLLPWATSAPGLAWGPLVLGLFGLLAASQPQAVP-----PYASENQTCRDQEKEYYEPQH 55

Qy         55 STICCTKCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCLSCSRCRDEMFQVEI 114
                |||::|  |||:   |    ||| |  ||  :|      :|  |  |  |   |  ||
Db         56 -RICCSRCPPGTYVSAKC-SRIRDTVCATCAENSYNEHWNYLTICQLCRPCDPVMGLEEI 113

Qy        115 SPCVVDRDTVCGCRKNQYREYWGETGFRCLNCSL---CPNGTVNIPCQERQDTI------ 165
              :||   | | | |:   :   |      | :| |   || ||      | :| :
Db        114 APCTSKRKTQCRCQPGMFCAAW---ALECTHCELLSDCPPGTE----AELKDEVGKGNNH 166

Qy        166 -CHCHMGFFLK----GAKCISCHDCKNKECEKLCP---TRPSTGKDSQDP------GT-- 209
               | | |        |:|     |:|:   :  |      :| |:  :|      ||
Db        167 CVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTCKNPLEPLPPEMSGTML 226

Qy        210 --TVLLPLVIVFGLCLASFASVVLACRYQRWKPKLYSIICGQSTLVKEGEPELLVPAPGF 267
                |||||   | | ||:  | :          ||   :  :| :   :  :  |:      |
Db        227 MLAVLLPL--AFFLLLATVFSCI-------WKS--HPSLCRKLGSLLKRRPQ----GEGP 271

Qy        268 NPTTTICFSSTPSSSPVSIPPY----------ISCDRS--NFGAVASPSSETAPP----- 310
              ||          |  |   ||          || | |  : |  |:|   |   |
Db        272 NPV-------AGSWEPPKAHPYFPDLVQPLLPISGDVSPVSTGLPAAPVLEAGVPQQQSP 324

Qy        311 ------------------------------------HLKAGPILPGPPASTHL-CTPGP 332
                                                 ::  ||:| |||    |  || |
Db        325 LDLTREPQLEPGEQSQVAHGTNGIHVTGGSMTITGNIYIYNGPVLGGPPGPGDLPATPEP 384

Qy        333 P-ASTHLCTPGPPASTHLCTPVQK 355
              |        ||||    | || |:
Db        385 PYPIPEEGDPGPPG---LSTPHQE 405
```

RESULT 6
GOHUN
nerve growth factor receptor precursor, low affinity (validated) - human
N;Alternate names: NGF receptor
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 08-Dec-2000
C;Accession: A25218; A60204; S21689; I57638
R;Johnson, D.; Lanahan, A.; Buck, C.R.; Sehgal, A.; Morgan, C.; Mercer, E.; Bothwell, M.;
Cell 47, 545-554, 1986
A;Title: Expression and structure of the human NGF receptor.
A;Reference number: A25218; MUID:87051725; PMID:3022937
A;Accession: A25218
A;Molecule type: mRNA

A;Residues: 1-427 <JOH>
A;Cross-references: GB:M14764; NID:g189204; PIDN:AAB59544.1; PID:g189205
R;Marano, N.; Dietzschold, B.; Earley Jr., J.J.; Schatteman, G.; Thompson, S.; Grob, P.;
J. Neurochem. 48, 225-232, 1987
A;Title: Purification and amino terminal sequencing of human melanoma nerve growth factc
A;Reference number: A60204; MUID:87085574; PMID:3025363
A;Accession: A60204
A;Molecule type: protein
A;Residues: 29-31,'T',33-42,'TT',45-46,'TX',50-51,'XX',54-56 <MAR>
A;Experimental source: melanoma cell line A875
A;Note: this sequence has been corrected by a note added in proof to follow the nucleoti
R;Vissavajjhala, P.; Leszyk, J.D.; Lin-Goerke, J.; Ross, A.H.
Arch. Biochem. Biophys. 294, 244-252, 1992
A;Title: Structural domains of the extracellular domain of human nerve growth factor rec
A;Reference number: S21689; MUID:92198017; PMID:1372492
A;Accession: S21689
A;Status: preliminary
A;Molecule type: protein
A;Residues: 183-208 <VIS>
R;Sehgal, A.; Patil, N.; Chao, M.
Mol. Cell. Biol. 8, 3160-3167, 1988
A;Title: A constitutive promoter directs expression of the nerve growth factor receptor
A;Reference number: I57638; MUID:89096903; PMID:2850481
A;Accession: I57638
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-22 <RES>
A;Cross-references: GB:M21621; NID:g189206; PIDN:AAA36363.1; PID:g189207
C;Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma c
C;Comment: The cysteine-rich region of the extracellular domain may form part or all of
C;Comment: This protein is thought to form a high-affinity receptor when it associates w
C;Comment: This receptor undergoes both N- and O-linked glycosylation.
C;Genetics:
A;Gene: GDB:NGFR
A;Cross-references: GDB:120234; OMIM:162010
A;Map position: 17q21-17q22
C;Superfamily: nerve growth factor receptor; NGF receptor repeat homology
C;Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; t
F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-427/Product: nerve growth factor receptor #status experimental <MAT>
F;29-250/Domain: extracellular #status predicted <EXT>
F;32-65/Domain: NGF receptor repeat homology <NG1>
F;67-108/Domain: NGF receptor repeat homology <NG2>
F;109-147/Domain: NGF receptor repeat homology <NG3>
F;149-189/Domain: NGF receptor repeat homology <NG4>
F;197-248/Region: serine/threonine-rich
F;251-272/Domain: transmembrane #status predicted <TRM>
F;273-427/Domain: intracellular #status predicted <INT>
F;60/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 9.1%; Score 236; DB 1; Length 427;
Best Local Similarity 22.9%; Pred. No. 2.1e-07;
Matches 111; Conservative 62; Mismatches 194; Indels 118; Gaps 22;

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Qy          7 PGLLLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCTKCHKGT 66
              | ||| |:|   |      |                  || | | |   |  ||  |: |
Db         13 PRLLLLLLLGVSLGGAKEA-----------------CPTGLYTH---SGECCKACNLGE 51

Qy         67 YLYNDCPGPGRDTDCRVCAPG-TYTALENHLRRCLSCSRCRDEMFQVEISPCVVDRDTVC 125
                :   |      | |  |    |:: : :    |  |: |      |   :|||   | ||
Db         52 GVAQPC--GANQTVCEPCLDSVTFSDVVSATEPCKPCTECVG--LQSMSAPCVEADDAVC 107

Qy        126 GCRKNQYREYWGETGFRCLNCSLCPNGT-VNIPCQERQDTIC-HCHMGFFLKGAK----C 179
                |    |  |  ||  ||  | :|  |: :   ||::|:|:|  |  | :  |      |
Db        108 RC---AYGYYQDETTGRCEACRVCEAGSGLVFSCQDKQNTVCEECPDGTYSDEANHVDPC 164

Qy        180 ISCHDCK------------NKECEKLCPTR------PSTGKDSQDPGTTVLLPLVIVFG 220
              : |  |:            : |||:: | |      |  | ||  | |    |
Db        165 LPCTVCEDTERQLRECTRWADAECEEI-PGRWITRSTPPEGSDSTAPSTQE--PEAPPEQ 221

Qy        221 LCLASFASVVLACRYQRWKPKLYSIICGQSTLVKEGEPELLVPAPGFNPTTTICFSSTPS 280
                :||  : |:            :::     :|  |  : |:|           : |  :
Db        222 DLIASTVAGVVT----------TVMGSSQPVVTRGTTDNLIPV----------YCSILA 260

Qy        281 SSPVSIPPYI------SCDRSNFGAVASPSSETAPP-----HLKAGPILPGPPASTHLCT 329
              :  | :  ||      || ::  || : | ::| ||     |  :|  :     | |
Db        261 AVVVGLVAYIAFKRWNSCKQNKQGANSRPVNQTPPPEGEKLHSDSG--ISVDSQSLHDQQ 318

Qy        330 PGPPASTHLCTPGPPASTHLCTPVQKWEASAPSAPDQLADADPATLYAVVDGVPPSRWKE 389
              |    ::    |      | :: |                        :::|     |:
Db        319 PHTQTASGQALKGDGGLYSSLPPAKREEVE----------------KLLNGSAGDTWRH 361

Qy        390 LVRRLGLS-EHEIERLELENGRHLREAQYSMLAAWRRRTPRREATLELLGRVLRDMDLLG 448
              |  ||  ||     :::  |     ::||:|     :  |||: |   || :
Db        362 LAGELGYQPEH------IDSFTHEACPVRALLASW---ATQDSATLDALLAALRRIQRAD 412

Qy        449 CLENI 453
                :|::
Db        413 LVESL 417
```

RESULT 7
A26431
nerve growth factor receptor precursor, low affinity - rat
N;Alternate names: NGF receptor
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A26431; PH1229
R;Radeke, M.J.; Misko, T.P.; Hsu, C.; Herzenberg, L.A.; Shooter, E.M.
Nature 325, 593-597, 1987
A;Title: Gene transfer and molecular cloning of the rat nerve growth factor receptor.
A;Reference number: A26431; MUID:87115859; PMID:3027580
A;Accession: A26431
A;Molecule type: mRNA
A;Residues: 1-425 <RAD>
A;Cross-references: GB:X05137; NID:g56755; PIDN:CAA28783.1; PID:g56756
R;Metsis, M.; Timmusk, T.; Allikmets, R.; Saarma, M.; Persson, H.
Gene 121, 247-254, 1992
A;Title: Regulatory elements and transcriptional regulation by testosterone and retinoic
A;Reference number: PH1229; MUID:93077038; PMID:1446821
A;Accession: PH1229
A;Molecule type: DNA
A;Residues: 1-20 <MET>
A;Cross-references: GB:X61269
C;Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma ce
C;Comment: The cysteine-rich region of the extracellular domain may form part or all of t
C;Comment: This protein is thought to form a high-affinity receptor when it associates wi
C;Genetics:
A;Introns: 20/3
C;Superfamily: nerve growth factor receptor; NGF receptor repeat homology
C;Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; t
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-425/Product: nerve growth factor receptor #status predicted <MAT>
F;30-251/Domain: extracellular #status predicted <EXT>
F;33-66/Domain: NGF receptor repeat homology <NG1>
F;68-109/Domain: NGF receptor repeat homology <NG2>
F;110-148/Domain: NGF receptor repeat homology <NG3>
F;150-190/Domain: NGF receptor repeat homology <NG4>
F;198-249/Region: serine/threonine-rich
F;252-273/Domain: transmembrane #status predicted <MEM>
F;274-425/Domain: intracellular #status predicted <INT>
F;61/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 8.7%; Score 227.5; DB 1; Length 425;
Best Local Similarity 23.4%; Pred. No. 6.8e-07;
Matches 107; Conservative 59; Mismatches 169; Indels 123; Gaps 24;

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Qy         44 CPQGKYNHPQNSTICCTKCHKGTYLYNDCPGPGRDTDCRVCAPG-TYTALENHLRRCLSC 102
              | | | |   | ||  |: |  :   |      | | |    |:: : :    | |
Db         33 CSTGLYTH---SGECCKACNLGEGVAQPC--GANQTVCEPCLDNVTFSDVVSATEPCKPC 87

Qy        103 SRCRDEMFQVEISPCVVDRDTVCGCRKNQYREYWGETGFRCLNCSLCPNGT-VNIPCQER 161
              : |    |  :|||   | || |    |::   |||  |  ||:|  |: :   ||::
Db         88 TECLG--LQSMSAPCVEADDAVCRCAYGYYQD--EETG-HCEACSVCEVGSGLVFSCQDK 142

Qy        162 QDTIC-HCHMGFFLKGAK----CISCHDCKNKECEKLCPTRPSTGKDSQD-PGTTVLLPL 215
```

```
Db        143 QNTVCEECPEGTYSDEANHVDPCLPCTVCEDTE-RQLRECTPWADAECEEIPG------- 194

Qy        216 VIVFGLCLASFASVVLACRYQRWKPKLYSIICGQSTLVKEGEPEL-----LVPAPGFNPT 270

Db        195 --------------------RWIPRSTPPEGSDSTAPSTQEPEVPPEQDLVPSTVADMV 233

Qy        271 TTICFSSTP-----------------SSSPVSIPPYI------SCDRSNFGAVASPSSE 306

Db        234 TTVMGSSQPVVTRGTTDNLIPVYCSILAAVVVGLVAYIAFKRWNSCKQNKQGANSRPVNQ 293

Qy        307 TAPP-----HLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPA-----STHLCTPVQKW 356

Db        294 TPPPEGEKLHSDSG--ISVDSQSLH------DQQTHTQTASGQALKGDGNLYSSLPLTKR 345

Qy        357 EASAPSAPDQLADADPATLYAVVDGVPPSRWKELVRRLGLS-EHEIERLELENGRHLREA 415

Db        346 E-----EVEKLLNGD-------------TWRHLAGELGYQPEH------IDSFTHEACP 380

Qy        416 QYSMLAAWRRRTPRREATLELLGRVLRDMDLLGCLENI 453

Db        381 VRALLASWGAQD---SATLDALLAALRRIQRADIVESL 415


RESULT 8
JN0006
nerve growth factor receptor, low affinity precursor - chicken
N;Alternate names: NGF receptor
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: JN0006; A60504
R;Large, T.H.; Weskamp, G.; Helder, J.C.; Radeke, M.J.; Misko, T.P.; Shooter, E.M.; Reic
Neuron 2, 1123-1134, 1989
A;Title: Structure and developmental expression of the nerve growth factor receptor in t
A;Reference number: JN0006; MUID:90166579; PMID:2560385
A;Accession: JN0006
A;Molecule type: mRNA
A;Residues: 1-416 <LAR>
A;Experimental source: embryonic chick brain
R;Heuer, J.G.; Fatemie-Nainie, S.; Wheeler, E.F.; Bothwell, M.
Dev. Biol. 137, 287-304, 1990
A;Title: Structure and developmental expression of the chicken NGF receptor.
A;Reference number: A60504; MUID:90152140; PMID:2154393
A;Accession: A60504
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 21-35,'Y',37-172,'K',174-275,'S',277-395,'R',397-416 <HEU>
C;Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma c
C;Comment: The cysteine-rich region of the extracellular domain may form part or all of
C;Comment: This protein is thought to form a high-affinity receptor when it associates w
C;Superfamily: nerve growth factor receptor; NGF receptor repeat homology
C;Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; t
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-416/Product: nerve growth factor receptor #status predicted <MAT>
F;21-239/Domain: extracellular #status predicted <EXT>
F;24-57/Domain: NGF receptor repeat homology <NG1>
F;59-100/Domain: NGF receptor repeat homology <NG2>
F;101-139/Domain: NGF receptor repeat homology <NG3>
F;141-181/Domain: NGF receptor repeat homology <NG4>
F;189-237/Region: serine/threonine-rich
F;240-261/Domain: transmembrane #status predicted <MEM>
F;262-416/Domain: intracellular #status predicted <INT>
F;52/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             8.5%;  Score 220;  DB 1;  Length 416;
  Best Local Similarity  23.3%;  Pred. No. 1.9e-06;
  Matches  116;  Conservative   46;  Mismatches  168;  Indels  168;  Gaps   25;

Qy          6 VPGLLLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCTKCHKG 65

Db          5 VPLLLLLL----------PAG-----PTWGSKEK----CLTKMYT---TSGECCKACNLG 42

Qy         66 TYLYNDCPGPGRDTDCRVCAPG-TYTALENHLRRCLSCSRCRDEMFQVEISPCVVDRDTV 124

Db         43 EGVVQPC--GVNQTVCEPCLDSVTYSDTVSATEPCKPCTQCVG--LHSMSAPCVESDDAV 98

Qy        125 CGCRKNQYREYWGETGFRCLNCSLCPNG-TVNIPCQERQDTIC-HCHMGFFLKGAK---- 178

Db         99 CRC---AYGYFQDELSGSCKECSICEVGFGLMFPCRDSQDTVCEECPEGTFSDEANFVDP 155

Qy        179 CISCHDCK------------NKECEKLCP-----TRPSTGKDSQDPGT----------T 210

Db        156 CLPCTICEENEVMVKECTATSDAECRDLHPRWTTHTPSLAGSDSPEPITRDPFNTEGMAT 215

Qy        211 VLLPLVIVFGLCLASFASVVLACRYQRWKPKLYSIICGQSTLVKEGEPELLVPAPGFNPT 270

Db        216 TLADIVT-------------------------TVMGSSQPVVSRGTADNLIPV------ 243

Qy        271 TTICFSSTPSSSPVSIPPYI------SCDRSNFGAVASPSSETAPP-----HLKAGPILP 319

Db        244 ----YCSILAAVVVGLVAYIAFKRWNSCKQNKQGANNRPVNQTPSPEGEKLHSDSGISVD 299

Qy        320 GPPASTHLCTPGPPASTHLCTPGPPASTHLCTPVQKWEASAPSAPDQLADADPATLYAVV 379

Db        300 ----SQSLHDQQPPNQS---TQGP----------------------APKGDGSLYA-- 326

Qy        380 DGVPPSR--------------WKELVRRLGLSEHEIERLELENGRHLREAQYSMLAAWR 424

Db        327 -SLPPSKQEEVEKLLSSSAEETWRQLAGELGYKEDLIDCFTRE-----ESPARALLADW- 379

Qy        425 RRTPRREATLELLGRVLR 442

Db        380 --SAKETATLDALLVALR 395


RESULT 9
JC7705
death receptor-6 - chicken
C;Species: Gallus gallus (chicken)
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C;Accession: JC7705
R;Bridgham, J.T.; Bobe, J.; Goetz, F.W.; Johnson, A.L.
Biochem. Biophys. Res. Commun. 284, 1109-1115, 2001
A;Title: Conservation of death receptor-6 in avian and piscine vertebrates.
A;Reference number: JC7705; MUID:21308433; PMID:11414698
A;Accession: JC7705
A;Molecule type: mRNA
A;Residues: 1-651 <BRI>
A;Cross-references: GB:AF349908
C;Comment: This receptor, a member of the tumor necrosis factor receptor family, belongs
tresia, activates a cell death and/or survival signaling cascade.
C;Genetics:
A;Gene: dr-6
C;Keywords: ovary
F;1-21/Domain: signal sequence #status predicted <SIG>
F;52-196/Domain: extracellular cysteine-rich, ligand-binding #status predicted <ECL>
F;332-350/Domain: transmembrane #status predicted <TMM>
F;410-475/Domain: death domain #status predicted <DED>
F;551-651/Region: conserved cytoplasmic #status predicted

  Query Match             7.7%;  Score 199.5;  DB 2;  Length 651;
  Best Local Similarity  22.9%;  Pred. No. 5.3e-05;
  Matches  125;  Conservative   57;  Mismatches  217;  Indels  147;  Gaps   30;

Qy         10 LLPLVLPALL----ADVYPAGVQGLVPHPGDLEKRESPCPQGKYNH---PQNSTICCTKC 62

Db          5 VLAAVLPLLVFLGTADAQPKLTS---------EQNAVSLPAGKYLHLDRATNQELICDKC 55

Qy         63 HKGTYLYNDCPGPGRDT--DCRVCAPGTYTALENHLRRCLSCSR-CRDEMFQVEISPCVV 119

Db         56 PAGTYVSKHCT---KSTLRECSPCPDGTFTKHENGIERCHPCRKPC--ELPMIEKTHCTA 110

Qy        120 DRDTVCGCRKNQYREYWGETGFRCLNCSLCPNG-TVNIPCQERQDTICH-CHMGFF---- 173

Db        111 LTDRECTCLSGTF-----QINDTCVPYTVCPVGWGVRKKGTETEDVRCKPCLRGTFSDVP 165
```

```
Qy        174 LKGAKCISCHDC--KN--------KECEKLC------PTRPSTGKDSQDPGTTVLLPLVI 217
              || :  ||  ||          || : :|      |   |  |:|  | |   |
Db        166 SSVMKCKTYTDCPGKNMVVVKPGTKESDNVCXSPASLPNTSLTSSDAQADGETYEAPPTA 225

Qy        218 VFGLCLASFASVVLACRYQRWKPKLYSIICGQSTLVKEGEPELLVPAPGFNPTTTICFSS 277
                | |                 :: :    :  |  |  |             |: ::
Db        226 YLPKGLNS--------------SVFDLSSSPAPRVSNGTAE-----------PTVDYND 259

Qy        278 TPSSSPVSIPPYISCDRSNFGAVAS-------------PSSETAPPHLKAGPILP---GP 321
              | ::  |  |  :|       |   |             |: | |      : |  |   ||
Db        260 TSANGTVGAPGSLS-SAGTAGQAQSYRHKHTSQAMGKQPAQEMAGGEKSSIPYRPPRRGP 318

Qy        322 P-ASTHLCTPGPPASTHL-----------------CTPGPPASTHLCTPVQKWEASAPSA 363
              |   |        : ||                 |:    : |     ::|     |||
Db        319 PNVHQHF-----DINEHLPWMIVLFLLLVLVVIVVCSVRKSSRT-----LKKGPRQDPSA 368

Qy        364 PDQLADADPAT---------LYAV----VDGVPP------SRWKELVRRL-GLSEHEIER 403
                : |    :|         :|      :| : |      |:||:: : |  .|| |:
Db        369 IVEKAIMKKSTTPTQNREKWIYYCNGHGIDILKPVAAQVGSQWKDIYQFLCNASEREV-- 426

Qy        404 LELENGRHL-REAQYSMLAAWRRRTPRREATLELLGRVLRDMDLLGCLENIEEALGGAAR 462
                ||      |  |: | |  | |  ||:|  |   ||       :| |   :
Db        427 AAFSNGYAADHERAYAALQHWTIRGP--EASLAQLISALRQHRRNDVVEKIRGLMEDTTP 484

Qy        463 LASEPR 468
              :  :|:
Db        485 VQMQPQ 490
```

```
RESULT 10
A35356
tumor necrosis factor receptor 2 precursor [validated] - human
N;Alternate names: 75K tumor necrosis factor receptor; TNF receptor type 2
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 08-Dec-2000
C;Accession: A35356; A36475; A48416; A36007; A23666; B35010; I38094
R;Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower, S.K
Science 248, 1019-1023, 1990
A;Title: A receptor for tumor necrosis factor defines an unusual family of cellular and
A;Reference number: A35356; MUID:90260639; PMID:2160731
A;Accession: A35356
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-461 <SMI>
A;Cross-references: GB:M32315; NID:g189185; PIDN:AAA59929.1; PID:g189186
R;Kohno, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squires,
Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990
A;Title: A second tumor necrosis factor receptor gene product can shed a naturally occur
A;Reference number: A36475; MUID:91045991; PMID:2172983
A;Accession: A36475
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-195,'R',197-461 <KOH>
A;Cross-references: GB:M55994; GB:M38549; NID:g339757; PIDN:AAA36755.1; PID:g339758
R;Dembic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus, M.
Cytokine 2, 231-237, 1990
A;Title: Two human TNF receptors have similar extracellular, but distinct intracellular,
A;Reference number: A48416; MUID:91370690; PMID:1966549
A;Accession: A48416
A;Status: preliminary
A;Molecule type: mRNA; protein
A;Residues: 23-461 <DEM>
A;Cross-references: GB:S63368; NID:g235648; PIDN:AAB19824.1; PID:g235649
A;Note: sequence extracted from NCBI backbone (NCBIN:63368, NCBIP:63371)
R;Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M.
Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990
A;Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demonstra
A;Reference number: A36007; MUID:90349572; PMID:2166946
A;Accession: A36007
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 116-140,'P',142-195,'R',197-362,'T',364-461 <HEL>
A;Cross-references: GB:M35857; NID:g339751; PIDN:AAA63262.1; PID:g339752
R;Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M.
J. Biol. Chem. 265, 20131-20138, 1990
A;Title: Purification and partial amino acid sequence analysis of two distinct tumor nec
A;Reference number: A23666; MUID:91056048; PMID:2173696
A;Accession: A23666
A;Status: preliminary
A;Molecule type: protein
A;Residues: 23-40;65-69;136-141;300-306 <LOE>
R;Engelmann, H.; Novick, D.; Wallach, D.
J. Biol. Chem. 265, 1531-1536, 1990
A;Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence
A;Reference number: A35010; MUID:90110215; PMID:2153136
A;Accession: B35010
A;Status: preliminary
A;Molecule type: protein
A;Residues: 27-31 <ENG>
R;Kuhnert, P.; Kemper, O.; Wallach, D.
Gene 150, 381-386, 1994
A;Title: Cloning, sequencing and partial functional characterization of the 5' region of
A;Reference number: I38094; MUID:95121934; PMID:7821811
A;Accession: I38094
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-37 <RES>
A;Cross-references: EMBL:X80021; NID:g666044; PIDN:CAA56324.1; PID:g825701
C;Genetics:
A;Gene: GDB:TNFR2
A;Cross-references: GDB:125914; OMIM:191191
A;Map position: 1p36.2-1p36.2
A;Introns: 26/3
A;Note: the list of introns is incomplete
C;Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
C;Keywords: duplication; glycoprotein; receptor; transmembrane protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-416/Product: tumor necrosis factor receptor 2 #status experimental <MAT>
F;40-76/Domain: NGF receptor repeat homology <NG1>
F;78-119/Domain: NGF receptor repeat homology <NG2>
F;120-162/Domain: NGF receptor repeat homology <NG3>
F;164-201/Domain: NGF receptor repeat homology <NG4>
F;262-279/Domain: transmembrane #status predicted <TMN>
F;280-461/Domain: intracellular #status predicted <INT>
F;171,193/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             7.6%;  Score 199;  DB 1;  Length 461;
  Best Local Similarity   25.3%;  Pred. No. 4.1e-05;
  Matches   77;  Conservative   26;  Mismatches  103;  Indels   98;  Gaps   14;
```

```
Qy         32 PHPGDLEKRESPCPQGKYNHPQNSTICCTKCHKGTYLYNDCPGPGRDTDCRVCAPGTYTA 91
              | ||       | |   :| : | : :||:||  | :     |      || |  |   ||
Db         34 PEPG------STCRLREY-YDQTAQMCCSKCSPGQHAKVFCTKTS-DTVCDSCEDSTYTQ 85

Qy         92 LENHLRRCLSC-SRCRDEMFQVEISPCVVDRDTVCGCRKNQYREYWGETGFRCLNCSLC- 149
              | | :  |||| |||  :  |||    |  ::: :| ||   |     :  |     | ||
Db         86 LWNWVPECLSCGSRCSSD--QVETQACTREQNRICTCRPGWYCALSKQEG-----CRLCA 138

Qy        150 ------PNGTVNIPCQERQDTICHCHMGFFLKGAKCISCHDCKNKECEKLCPTRPSTGKD 203
                   |   | |  | |  | :|                      | |
Db        139 PLRKCRPGFGVARPGTETSDVVC--------------------KPCA------------ 165

Qy        204 SQDPGTTVLLPLVIVFGLCLASFASVVLACRYQRWKPKLYSIICGQSTLVKEGEPELLVP 263
                 |||                ::  |    ||  :          ||           :|
Db        166 ---PGT-------------FSNTTSSTDICRPHQ--------ICN------------VVA 189

Qy        264 APGFNPTTTICFSSTPSSS----PVSIPPYISCDRSNFGAVASPSSETAPPHLKAGPILP 319
              ||      :| |::|: |     | :|  :|    :      ||  |||       |: |
Db        190 IPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPS--TAPSTSFLLPMGP 247

Qy        320 GPPA 323
              |||
Db        248 SPPA 251
```

RESULT 11

```
A42086
CD30 antigen precursor - human
N;Alternate names: Ki-1 antigen; nerve growth factor receptor family member CD30
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 21-Jul-2000
C;Accession: A42086
R;Durkop, H.; Latza, U.; Hummel, M.; Eitelbach, F.; Seed, B.; Stein, H.
Cell 68, 421-427, 1992
A;Title: Molecular cloning and expression of a new member of the nerve growth factor rec
A;Reference number: A42086; MUID:92154659; PMID:1310894
A;Accession: A42086
A;Molecule type: mRNA
A;Residues: 1-595 <DUR>
A;Cross-references: GB:M83554; NID:g180095; PIDN:AAA51947.1; PID:g180096
A;Experimental source: HUT-102 cell line
A;Note: sequence extracted from NCBI backbone (NCBIN:82088, NCBIP:82090)
C;Genetics:
A;Gene: GDB:CD30; D1S166E
A;Cross-references: GDB:131547; OMIM:153243
A;Map position: 1p36-1p36
C;Superfamily: NGF receptor repeat homology
C;Keywords: glycoprotein; growth factor receptor; transmembrane protein
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-383/Domain: extracellular #status predicted <EXT>
F;384-407/Domain: transmembrane #status predicted <TMM>
F;408-595/Domain: intracellular #status predicted <CYT>
F;101,276/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             7.4%;  Score 193;  DB 2;  Length 595;
  Best Local Similarity   24.6%;  Pred. No. 0.00012;
  Matches  101;  Conservative   42;  Mismatches  166;  Indels  102;  Gaps   24;

Qy         41 ESPCPQGKYNHPQNSTI--CCTKCHKGTYLYNDCPGPGRDTDCR-VCAPGTYTALENHLR 97
              |  |  | :|  :  :  || :|  | :    |  | | ||||  | |  |    :
Db         26 EDTC-HGNPSHYYDKAVRRCCYRCPMGLFPTQQC--PQRPTDCRKQCEPDYYL---DEAD 79

Qy         98 RCLSCSRC-RDEMFQVEISPCVVDRDTVCGCRKNQYREYWG-ETGFRCLNCSLCPNG-TV 154
              || :|  | ||::  || :||  :   || ||    :       :  ||   |:|| | |
Db         80 RCTACVTCSRDDL--VEKTPCAWNSSRVCECRPGMFCSTSAVNSCARCFFHSVCPAGMIV 137

Qy        155 NIPCQERQDTICH-CHMGFPLKGAKCISCHDCKNKEC-----EKLCPTRPST-------- 200
                |   :::|:|      |        | |  :||         |  |  |:|
Db        138 KFPGTAQKNTVCEPASPGV---SPACASPENCKEPSSGTIPQAKPTPVSPATSSASTMPV 194

Qy        201 ------------------------GKDSQDPGTTVLLPLVIVFGLCLASFASVVLACRYQ 236
                                      |: | ||| :   |     | |             :
Db        195 RGGTRLAQEAASKLTRAPDSPSSVGRPSSDPGLSPTQPCPEGSGDC------------RK 242

Qy        237 RWKPKLYSIICGQST-LVKEGEPELLVPAP-GFNPTTT-------ICFSSTPSSSPVSIP 287
              : :|  |    |: |  |     :|:   |  :| : |        || :|  :|    :
Db        243 QCEPDYYLDEAGRCTACVSCSRDDLVEKTPCAWNSSRTCECRPGMICATSATNSCARCV- 301

Qy        288 PYISCDRSNFGAVASPSSETAPPHL-KAGPILPGPPASTHL-CTPGP-----PASTHLCT 340
              ||  |          :  : | |  : :        ||  |   | | |     ||||
Db        302 PYPIC---------AAETVTKPQDMAEKDTTFEAPPLGTQPDCNPTPENGEAPAST---- 348

Qy        341 PGPPASTHLCTPVQKWEASAPSAPDQLADADPATLYAVVDGVPPSRWKELV 391
              |  |  : :    |      |||  |:    :|   |:|  |   |  ||
Db        349 -SPTQSLLVDSQASKTLPIPTSAPVALS----STGKPVLDAGPVLFWVILV 394


RESULT 12
JC2395
Fas antigen precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 05-Nov-1999
C;Accession: JC2395; PC2246
R;Kimura, K.; Wakatsuki, T.; Yamamoto, M.
Biochem. Biophys. Res. Commun. 198, 666-674, 1994
A;Title: A variant mRNA species encoding a truncated from of Fas antigen in the rat live
A;Reference number: JC2395; MUID:94128114; PMID:7507668
A;Accession: JC2395
A;Molecule type: mRNA
A;Residues: 1-324 <KIM>
A;Cross-references: DDBJ:D26112; NID:g468486; PIDN:BAA05108.1; PID:d1005650; PID:g468487
A;Experimental source: thymus
A;Accession: PC2246
A;Molecule type: mRNA
A;Residues: 1-62,'RFT' <KI2>
A;Cross-references: DDBJ:D26113; NID:g468488; PIDN:BAA05109.1; PID:d1005651; PID:g468489
A;Experimental source: liver
C;Genetics:
A;Introns: 62/1
C;Superfamily: NGF receptor repeat homology
C;Keywords: transmembrane protein
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-324/Product: Fas antigen #status predicted <MAT>
F;44-79/Domain:'NGF receptor repeat homology <NGF>
F;81-124/Domain: NGF receptor repeat homology <NG4>
F;171-188/Domain: transmembrane #status predicted <TMM>

  Query Match             7.0%;  Score 181.5;  DB 2;  Length 324;
  Best Local Similarity   23.5%;  Pred. No. 0.00034;
  Matches   71;  Conservative   39;  Mismatches  107;  Indels   85;  Gaps   13;

Qy         10 LLPLVLPALLADVYPAGVQGL---VPHPGDLEKRESPCPQGKYNHPQNSTICCTKCHKGT 66
              :|||||     :|    |   :   :      : : :: | :| |   |     ||  | |
Db          7 VLPLVLAGPELNVRMQGTDSIFEGLELKRSVRETDNNCSEGLY---QVGPFCCQPCQPGE 63

Qy         67 YLYNDCPGPGRDTDCRVCAPG-TYTALENHLRRCLSCSRCRDEMFQVEI-SPCVVDRDTV 124
                 ||   |    |  |  |  ||  :::  :|  |: | ||    :|: : |   ::|
Db         64 RKVKDCTTSGGAPTCHPCTEGEEYTDRKHYSDKCRRCAFC-DEGHGLEVETNCTRTQNTK 122

Qy        125 CGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQERQDTICHCHMGFFLKGAKCISCHD 184
              | |::| |              | ||| :                    |  |
Db        123 CRCKENFY-----------CNASLCDH-------------------------CYHCTS 144

Qy        185 CKNKECEKLCPTRPSTGKDSQDPGTTVLLPLVIVFGLCLASFASVVLACRYQRWKPKLYS 244
              |  ::  : | || |  |  :        || |:|: || :     | :  ||:: :|
Db        145 CGLEDILEPC-TRTSNTKCKKQSSNYKLLWLLILPGLAI---LFVFIYKRYRKRQP---- 196

Qy        245 IICGQSTLVKEGEPELLVPAPGFNPTTTICFSSTPSS-SPVSIPPYI--------SCDRS 295
                  |:||  :|:|           | | : | |::  ||          ||
Db        197 ----------GDPESGIPSP----------ESVPMNVSDVNLNKYIWRTAEKMKICDAK 235

Qy        296 NF 297
              |
Db        236 KF 237


RESULT 13
B43692
T2 protein - rabbit fibroma virus
C;Species: rabbit fibroma virus, Shope fibroma virus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: B43692
R;Upton, C.; DeLange, A.M.; McFadden, G.
Virology 160, 20-30, 1987
A;Title: Tumorigenic poxviruses: genomic organization and DNA sequence of the telomeric
A;Reference number: A43692; MUID:87321103; PMID:2820128
A;Accession: B43692
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-325 <UPT>
A;Cross-references: GB:M17433
C;Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
F;64-105/Domain: NGF receptor repeat homology <NG2>
F;106-147/Domain: NGF receptor repeat homology <NG3>

  Query Match             7.0%;  Score 181.5;  DB 2;  Length 325;
  Best Local Similarity   29.6%;  Pred. No. 0.00034;
  Matches   58;  Conservative   16;  Mismatches   81;  Indels   41;  Gaps   12;

Qy         14 VLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCTKCHKGTYLYNDCP 73
              ::  |:  ||  |   ||:     :  |   |   :  :|| || | |    |
Db          4 LIALLVCVVYVYGDD--VPY----SSNQGKCGGHDY---EKDGLCCASCHPGFYASRLC- 53
```

```
Qy          74 GPGRDTDCRVCAPGTYTALENHLRRCLSC-SRCRDEMFQVEISPCVVDRDTVCGCRKNQY 132
               ||| :| |  |  ||:||  ||   |:||   |   :   |  ||    | || |    |
Db          54 GPGSNTVCSPCEDGTFTASTNHAPACVSCRGPCTGHL--SESQPCDRTHDRVCNCSTGNY 111

Qy         133 REYWGETGFRCLNCSLCPNGTVNIPCQERQDTICHCHMGFFLKGAKCISCHD-CKNKECE 191
                 |: |     | :|   |               |  |: : |       |    :  ||
Db         112 CLLKGQNG-----CRICAPQT------------KCPAGYGVSG------HTRAGDTLCE 147

Qy         192 KLCPTRPSTGKDSQDP 207
               | ||  | |  ||  |
Db         148 K-CP--PHTYSDSLSP 160


RESULT 14
GQVZML
T2 protein - myxoma virus (strain Lausanne)
C;Species: myxoma virus
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 18-Jun-1999
C;Accession: A40566
R;Upton, C.; Macen, J.L.; Schreiber, M.; Mcfadden, G.
Virology 184, 370-382, 1991
A;Title: Myxoma virus expresses a secreted protein with homology to the tumor necrosis f
A;Reference number: A40566; MUID:91335768; PMID:1651597
A;Accession: A40566
A;Molecule type: DNA
A;Residues: 1-326 <UPT>
A;Cross-references: GB:M95181; GB:M37976; NID:g332309; PIDN:AAA46632.1; PID:g332310
C;Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
C;Keywords: glycoprotein
F;64-105/Domain: NGF receptor repeat homology <NG2>
F;106-147/Domain: NGF receptor repeat homology <NG3>
F;66,181,205,238/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             6.9%;  Score 180;  DB 1;  Length 326;
  Best Local Similarity   35.5%;  Pred. No. 0.00042;
  Matches   50;  Conservative   11;  Mismatches   64;  Indels   16;  Gaps    7;

Qy          14 VLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCTKCHKGTYLYNDCP 73
               :| | :| ||  |     |:  |  |    |    |   :   :||| |  |:|    |
Db           6 LLLAYVACVYGGG----APYGADRGK----CRGNDY---EKDGLCCTSCPPGSYASRLC- 53

Qy          74 GPGRDTDCRVCAPGTYTALENHLRRCLSC-SRCRDEMFQVEISPCVVDRDTVCGCRKNQY 132
               ||| || |  |   |:||  ||   |:|| ||   :   |  || || |    |
Db          54 GPGSDTVCSPCKNETFTASTNHAPACVSCRGRCTGHL--SESQSCDKTRDRVCDCSAGNY 111

Qy          133 REYWGETGFR-CLNCSLCPNG 152
                    |: | | |   : || |
Db          112 CLLKGQEGCRICAPKTKCPAG 132


RESULT 15
B38634
tumor necrosis factor receptor type 2 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
C;Accession: B38634; A40254; S54816
R;Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E.
Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991
A;Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor r
A;Reference number: A38634; MUID:91187885; PMID:1849278
A;Accession: B38634
A;Molecule type: mRNA
A;Residues: 1-474 <LEW>
A;Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828
R;Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jenk
Mol. Cell. Biol. 11, 3020-3026, 1991
A;Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for
A;Reference number: A40254; MUID:91246168; PMID:1645445
A;Accession: A40254
A;Molecule type: mRNA
A;Residues: 1-474 <GOO>
A;Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828
R;Kissonerghis, M.; Fellowes, R.; Feldmann, M.; Chernajovsky, Y.
submitted to the EMBL Data Library, May 1995
A;Description: Characterization of the promoter region of the murine p75-TNF receptor.
A;Reference number: S54816
A;Accession: S54816
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-22 <KIS>
A;Cross-references: EMBL:X87128; NID:g809043; PIDN:CAA60618.1; PID:g809044
C;Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
C;Keywords: cytokine receptor; transmembrane protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-474/Product: tumor necrosis factor receptor type 2 #status predicted <MAT>
F;40-77/Domain: NGF receptor repeat homology <NG1>
F;79-120/Domain: NGF receptor repeat homology <NG2>
F;166-203/Domain: NGF receptor repeat homology <NG4>

  Query Match             6.9%;  Score 178.5;  DB 2;  Length 474;
  Best Local Similarity   23.1%;  Pred. No. 0.00075;
  Matches   80;  Conservative   36;  Mismatches  138;  Indels   93;  Gaps   16;

Qy          32 PHPGDLEKRESPCPQGKYNHPQNSTICCTKCHKGTYLYNDCPGPGRDTDCRVCAPGTYTA 91
               | ||          |   :  : : : :|| ||  | |: : |     || |  |    ||
Db          34 PEPG------YECQISQEYYDRKAQMCCAKCPPGQYVKHFC-NKTSDTVCADCEASMYTQ 86

Qy          92 LENHLRRCLSC-SRCRDEMFQVEISPCVVDRDTVCGCRKNQYREYWGETGF--RCLNCSL 148
               : |  | |||| | |  :  ||||  |   :: || |   :|      :|   :|:  |
Db          87 VWNQFRTCLSCSSSCTTD--QVEIRACTKQQNRVCACEAGRYCALKTHSGSCRQCMRLSK 144

Qy         149 C-----------PNGTVNIPCQERQDTICHCHMGFFLKGAKCISCHDCKNKECEKLCPTR 197
               |           ||| |          :|                        | |
Db         145 CGPGFGVASSRAPNGNV----------LC------------------------KAC--A 167

Qy         198 PSTGKDSQDPGTTVLLPLVIVFGLCLASFASVVLACRYQRWKPKLYSIICGQSTLVKEGE 257
               | |  |:    | |  |  |   | :  ||    |  :   | | :|   ::  | : |
Db         168 PGTFSDTTS-STDVCRPHRICSILAIPGNASTDAVCAPE--SPTLSAI--PRTLYVSQPE 222

Qy         258 PEL-----LVPAPGFNPTTTICFSSTP-----SSSPVSIPPYISCDRSNFG--------A 299
               |         | |   |:       |||      :   :|:|  :    :: |
Db         223 PTRSQPLDQEPGPSQTPSILTSLGSTPIIEQSTKGGISLPIGLIVGVTSLGLLMLGLVNC 282

Qy         300 VASPSSETAPPHLKAGPILPGPP----------ASTHLCTPGPPAST 336
               :    :  |  |:     :| |           || |  | :|:
Db         283 IILVQRKKKPSCLQRDAKVPHVPDEKSQDAVGLEQQHLLTAPSSSS 329


Search completed: September 13, 2003, 07:06:06
Job time : 22 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 13, 2003, 06:56:04 ; Search time 17 Seconds
(without alignments)
1302.916 Million cell updates/sec

Title: US-09-970-532-2
Perfect score: 2603
Sequence: 1 MGLPTVPGLLLPLVLPALLA.....NIEEALGGAARLASEPRLLW 471

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2603	100.0	471	1	TR1A_BOVIN	O19131 bos taurus
2	1750	67.2	461	1	TR1A_PIG	P50555 sus scrofa
3	1517	58.3	455	1	TR1A_HUMAN	P19438 homo sapien
4	1338.5	51.4	461	1	TR1A_RAT	P22934 rattus norv
5	1319	50.7	454	1	TR1A_MOUSE	P25118 mus musculu
6	387.5	14.9	417	1	TR25_HUMAN	Q93038 h tumor nec
7	271.5	10.4	440	1	T10B_HUMAN	O14763 homo sapien
8	257	9.9	435	1	TNR3_HUMAN	P36941 homo sapien
9	247	9.5	415	1	TNR3_MOUSE	P50284 mus musculu
10	236	9.1	427	1	TR16_HUMAN	P08138 homo sapien
11	227.5	8.7	425	1	TR16_RAT	P07174 rattus norv
12	221.5	8.5	417	1	TR16_MOUSE	Q9z0w1 mus musculu
13	220	8.5	416	1	TR16_CHICK	P18519 gallus gall
14	199	7.6	461	1	TR1B_HUMAN	P20333 homo sapien
15	196	7.5	176	1	TR23_MOUSE	Q9er63 mus musculu
16	195	7.5	655	1	TR21_HUMAN	O75509 homo sapien
17	195	7.5	655	1	TR21_MOUSE	Q9epu5 mus musculu
18	194.5	7.5	180	1	TR22_MOUSE	Q9er62 mus musculu
19	193	7.4	595	1	TNR8_HUMAN	P28908 homo sapien
20	191.5	7.4	381	1	T10B_MOUSE	Q9qzm4 mus musculu
21	185	7.1	468	1	T10A_HUMAN	O00220 homo sapien
22	181.5	7.0	324	1	TNR6_RAT	Q63199 rattus norv
23	181.5	7.0	325	1	VT2_SFVKA	P25943 shope fibro
24	180	6.9	326	1	VT2_MYXVL	P29825 myxoma viru
25	178.5	6.9	474	1	TR1B_MOUSE	P25119 mus musculu
26	171.5	6.6	259	1	T10C_HUMAN	O14798 h tumor nec
27	171.5	6.6	283	1	TR14_HUMAN	Q92956 homo sapien
28	169	6.5	3718	1	LMA5_MOUSE	Q61001 mus musculu
29	168.5	6.5	289	1	TNR5_MOUSE	P27512 mus musculu
30	168.5	6.5	332	1	TNR6_PIG	O77736 sus scrofa
31	167	6.4	323	1	TNR6_BOVIN	P51867 bos taurus
32	167	6.4	351	1	CRMB_COWPX	O73559 cowpox viru
33	166	6.4	401	1	T11B_RAT	O08727 rattus norv
34	163.5	6.3	349	1	CRMB_CAMPS	Q8uya7 camelpox vi
35	163.5	6.3	349	1	CRMB_VARV	P34015 variola vir
36	162	6.2	386	1	T10D_HUMAN	Q9ubn6 homo sapien
37	161	6.2	327	1	TNR6_MOUSE	P25446 mus musculu
38	160.5	6.2	300	1	TR6B_HUMAN	O95407 homo sapien
39	160.5	6.2	1696	1	PCK5_BRACL	Q9nj15 branchiosto
40	160	6.1	401	1	T11B_MOUSE	O08712 mus musculu
41	158	6.1	824	1	AD08_HUMAN	P78325 homo sapien
42	155.5	6.0	269	1	TNR5_BOVIN	Q28203 bos taurus
43	155	6.0	1877	1	PCK5_MOUSE	Q04592 mus musculu
44	154	5.9	870	1	SRC2_HUMAN	Q96gp6 homo sapien
45	153.5	5.9	625	1	TR11_MOUSE	O35305 mus musculu

ALIGNMENTS

RESULT 1
TR1A_BOVIN
ID TR1A_BOVIN STANDARD; PRT; 471 AA.
AC O19131;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 1A precursor (p60)
DE (TNF-R1) (TNF-RI) (p55).
GN TNFRSF1A OR TNFR1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Aorta;
RX MEDLINE=98273505; PubMed=9613449;
RA Lee E.-K., Kehrli M.E. Jr., Taylor M.J.;
RT "Cloning and sequencing of cDNA encoding bovine tumor necrosis factor
RT (TNF)-receptor I.";
RL Vet. Immunol. Immunopathol. 61:379-385(1998).
CC -!- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric
CC TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits
CC caspase-8 to the activated receptor. The resulting death-inducing
CC signaling complex (DISC) performs caspase-8 proteolytic activation
CC which initiates the subsequent cascade of caspases (aspartate-
CC specific cysteine proteases) mediating apoptosis (By similarity).
CC -!- SUBUNIT: Binding of TNF to the extracellular domain leads to
CC homotrimerization. The aggregated death domains provide a novel
CC molecular interface that interacts specifically with the death
CC domain of TRADD. Various TRADD-interacting proteins such as TRAFS,
CC RIP and possibly FADD, are recruited to the complex by their
CC association with TRADD. This complex activates at least two
CC distinct signaling cascades, apoptosis and NF-kappa-B signaling.
CC Binds BAG4 (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC -!- SIMILARITY: Contains 1 death domain.
CC ---

CC ---
DR EMBL; U90937; AAB65143.1; -.
DR HSSP; P19438; 1TNR.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00005; DEATH; 1.

```
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT   SIGNAL        1    21       POTENTIAL.
FT   CHAIN        22   471       TUMOR NECROSIS FACTOR RECEPTOR
FT                               SUPERFAMILY MEMBER 1A.
FT   DOMAIN       22   210       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    211   233       POTENTIAL.
FT   DOMAIN      234   471       CYTOPLASMIC (POTENTIAL).
FT   REPEAT       43    82       TNFR-CYS 1.
FT   REPEAT       83   125       TNFR-CYS 2.
FT   REPEAT      126   166       TNFR-CYS 3.
FT   REPEAT      167   195       TNFR-CYS 4.
FT   DOMAIN      340   360       N-SMASE ACTIVATION DOMAIN (NSD).
FT   DOMAIN      372   457       DEATH.
FT   DISULFID     44    58       BY SIMILARITY.
FT   DISULFID     59    72       BY SIMILARITY.
FT   DISULFID     62    81       BY SIMILARITY.
FT   DISULFID     84    99       BY SIMILARITY.
FT   DISULFID    102   117       BY SIMILARITY.
FT   DISULFID    105   125       BY SIMILARITY.
FT   DISULFID    127   143       BY SIMILARITY.
FT   DISULFID    146   158       BY SIMILARITY.
FT   DISULFID    149   166       BY SIMILARITY.
FT   DISULFID    168   179       BY SIMILARITY.
FT   DISULFID    182   194       BY SIMILARITY.
FT   DISULFID    185   190       BY SIMILARITY.
FT   CARBOHYD     54    54       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    145   145       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    151   151       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   471 AA;  51367 MW;  5243EF514DFE81C4 CRC64;

  Query Match          100.0%;  Score 2603;  DB 1;  Length 471;
  Best Local Similarity  100.0%;  Pred. No. 4.3e-159;
  Matches  471;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGLPTVPGLLLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGLPTVPGLLLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCT 60

Qy         61 KCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCLSCSRCRDEMFQVEISPCVVD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCLSCSRCRDEMFQVEISPCVVD 120

Qy        121 RDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQERQDTICHCHMGFFLKGAKCI 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQERQDTICHCHMGFFLKGAKCI 180

Qy        181 SCHDCKNKECEKLCPTRPSTGKDSQDPGTTVLLPLVIVFGLCLASFASVVLACRYQRWKP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SCHDCKNKECEKLCPTRPSTGKDSQDPGTTVLLPLVIVFGLCLASFASVVLACRYQRWKP 240

Qy        241 KLYSIICGQSTLVKEGEPELLVPAPGFNPTTTICFSSTPSSSPVSIPPYISCDRSNFGAV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 KLYSIICGQSTLVKEGEPELLVPAPGFNPTTTICFSSTPSSSPVSIPPYISCDRSNFGAV 300

Qy        301 ASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLCTPVQKWEASA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLCTPVQKWEASA 360

Qy        361 PSAPDQLADADPATLYAVVDGVPPSRWKELVRRLGLSEHEIERLELENGRHLREAQYSML 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 PSAPDQLADADPATLYAVVDGVPPSRWKELVRRLGLSEHEIERLELENGRHLREAQYSML 420

Qy        421 AAWRRRTPRREATLELLGRVLRDMDLLGCLENIEEALGGAARLASEPRLLW 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AAWRRRTPRREATLELLGRVLRDMDLLGCLENIEEALGGAARLASEPRLLW 471


RESULT 2
TR1A_PIG
ID   TR1A_PIG     STANDARD;      PRT;   461 AA.
AC   P50555;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 1A precursor (p60)
DE   (TNF-R1) (TNF-RI) (p55).
GN   TNFRSF1A OR TNFR1.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RX   MEDLINE=96011645; PubMed=7590278;
RA   Suter B., Pauli U.H.;
RT   "Cloning of the cDNA encoding the porcine p55 tumor necrosis factor
RT   receptor.";
RL   Gene 163:263-266(1995).
CC   -!- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric
CC       TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits
CC       caspase-8 to the activated receptor. The resulting death-inducing
CC       signaling complex (DISC) performs caspase-8 proteolytic activation
CC       which initiates the subsequent cascade of caspases (aspartate-
CC       specific cysteine proteases) mediating apoptosis (By similarity).
CC   -!- SUBUNIT: Binding of TNF to the extracellular domain leads to
CC       homotrimerization. The aggregated death domains provide a novel
CC       molecular interface that interacts specifically with the death
CC       domain of TRADD. Various TRADD-interacting proteins such as TRAF5,
CC       RIP and possibly FADD, are recruited to the complex by their
CC       association with TRADD. This complex activates at least two
CC       distinct signaling cascades, apoptosis and NF-kappa-B signaling.
CC       Binds BAG4 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC   -!- SIMILARITY: Contains 1 death domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U19994; AAC48499.1; -.
DR   PIR; JC4302; JC4302.
DR   HSSP; P19438; 1TNR.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00531; death; 1.
DR   Pfam; PF00020; TNFR_c6; 3.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT   SIGNAL        1    21       POTENTIAL.
FT   CHAIN        22   461       TUMOR NECROSIS FACTOR RECEPTOR
FT                               SUPERFAMILY MEMBER 1A.
FT   DOMAIN       22   210       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    211   233       POTENTIAL.
FT   DOMAIN      234   461       CYTOPLASMIC (POTENTIAL).
FT   REPEAT       43    82       TNFR-CYS 1.
FT   REPEAT       83   125       TNFR-CYS 2.
FT   REPEAT      126   166       TNFR-CYS 3.
FT   REPEAT      167   195       TNFR-CYS 4.
FT   DOMAIN      340   350       N-SMASE ACTIVATION DOMAIN (NSD).
FT   DOMAIN      362   447       DEATH.
FT   DISULFID     44    58       BY SIMILARITY.
FT   DISULFID     59    72       BY SIMILARITY.
```

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FT   DISULFID     62     81       BY SIMILARITY.
FT   DISULFID     84     99       BY SIMILARITY.
FT   DISULFID    102    117       BY SIMILARITY.
FT   DISULFID    105    125       BY SIMILARITY.
FT   DISULFID    127    143       BY SIMILARITY.
FT   DISULFID    146    158       BY SIMILARITY.
FT   DISULFID    149    166       BY SIMILARITY.
FT   DISULFID    168    179       BY SIMILARITY.
FT   DISULFID    182    194       BY SIMILARITY.
FT   DISULFID    185    190       BY SIMILARITY.
FT   CARBOHYD     54     54       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     86     86       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    145    145       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    151    151       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   461 AA;  50696 MW;  CD72361EC60C9D43 CRC64;

  Query Match             67.2%;  Score 1750;  DB 1;  Length 461;
  Best Local Similarity   70.2%;  Pred. No. 9.7e-105;
  Matches  339;  Conservative   24;  Mismatches   84;  Indels   36;  Gaps    5;

Qy          1 MGLPTVPGLLLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCT 60
              ||| |||||||||| ||| ||||||| ||| |||| ||||| ||||||:|||| :||||
Db          1 MGLSTVPGLLLPLVLRALLVDVYPAGVHGLVLHPGDREKRESLCPQGKYSHPQNRSICCT 60

Qy         61 KCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCLSCSRCRDEMFQVEISPCVVD 120
              ||||||||:||| ||| ||||| |  ||:|| |||| :|||||:|| || |||||||||
Db         61 KCHKGTYLHNDCLGPGLDTDCRECDNGTFTASENHLTQCLSCSKCRSEMSQVEISPCTVD 120

Qy        121 RDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQERQDTICHCHMGFFLKGAKCI 180
              |||||||||||||:|| || |:|||||||||||| :|| |:|||||:|| ||||:  :|:
Db    .   121 RDTVCGCRKNQYRKYWSETLFQCLNCSLCPNGTVQLPCLEKQDTICNCHSGFFLRDKECV 180

Qy        181 SCHDCKNKECEKLCPTRPSTGKDSQDPGTTVLLPLVIVFGLCLASFASVVLACRYQRWKP 240
              || :||| :|: |||     |  | || ||||||||||| |||||| |  | ||||||||||
Db        181 SCVNCKNADCKNLCPATSETRNDFQDTGTTVLLPLVIFFGLCLAFFLFVGLACRYQRWKP 240

Qy        241 KLYSIICGQSTLVKEGEPELLVPAPGFNPTTTI----------CFSSTPSSSPVSIPPYI 290
              ||||||||:|| |||||||  |  || | | ||           ||  || ||:| | :
Db        241 KLYSIICGKSTPVKEGEPEPLATAPSFGPITTFSPIPSFSPTTTFSPVPSFSPISSPTFT 300

Qy        291 SCDRSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLC 350
               || ||   | ||  | |||   |||||| ||||               || |
Db        301 PCDWSNI-KVTSPPKEIAPPPQGAGPILPMPPAS---------------TPVP------- 337

Qy        351 TPVQKWEA---SAPSAPDQLADADPATLYAVVDGVPPSRWKELVRRLGLSEHEIERLELE 407
              ||: ||     || ||| ||||||||||||||||||:|||| ||||||||||||||||:
Db        338 TPLPKWGGSAHSAHSAPAQLADADPATLYAVVDGVPPTRWKEFVRRLGLSEHEIERLELQ 397

Qy        408 NGRHLREAQYSMLAAWRRRTPRREATLELLGRVLRDMDLLGCLENIEEALGGAARLASEP 467
              ||| |||||||||| ||||| |||||||||| ||||||||||:||||| | ||||  |
Db        398 NGRCLREAQYSMLAEWRRRTSRREATLELLGSVLRDMDLLGCLEDIEEALRGPARLAPAP 457

Qy        468 RLL 470
               ||
Db        458 HLL 460


RESULT 3
TR1A_HUMAN
ID   TR1A_HUMAN     STANDARD;      PRT;   455 AA.
AC   P19438;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 1A precursor (p60)
DE   (TNF-R1) (TNF-RI) (p55) (CD120a) [Contains: Tumor necrosis factor
DE   binding protein 1 (TBPI)].
GN   TNFRSF1A OR TNFR1 OR TNFAR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RX   MEDLINE=90235285; PubMed=2158863;
RA   Schall T.J., Lewis M., Koller K.J., Lee A., Rice G.C., Wong G.H.W.,
RA   Getanaga T., Granger G.A., Lentz R., Raab H., Kohr W.J., Goeddel D.V.;
RT   "Molecular cloning and expression of a receptor for human tumor
RT   necrosis factor.";
RL   Cell 61:361-370(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90235284; PubMed=2158862;
RA   Loetscher H., Pan Y.-C.E., Lahm H.-W., Gentz R., Brockhaus M.,
RA   Tabuchi H., Lesslauer W.;
RT   "Molecular cloning and expression of the human 55 kd tumor necrosis
RT   factor receptor.";
RL   Cell 61:351-359(1990).
RN   [3]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 41-53; 110-124 AND 199-201.
RX   MEDLINE=91006021; PubMed=1698610;
RA   Nophar Y., Kemper O., Brakebusch C., Engelmann H., Zwang R.,
RA   Aderka D., Holtmann H., Wallach D.;
RT   "Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA
RT   for the type I TNF-R, cloned using amino acid sequence data of its
RT   soluble form, encodes both the cell surface and a soluble form of the
RT   receptor.";
RL   EMBO J. 9:3269-3278(1990).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91090841; PubMed=1702293;
RA   Himmler A., Maurer-Fogy I., Kroenke M., Scheurich P., Pfizenmaier K.,
RA   Lantz M., Olsson I., Hauptmann R., Stratowa C., Adolf G.R.;
RT   "Molecular cloning and expression of human and rat tumor necrosis
RT   factor receptor chain (p60) and its soluble derivative, tumor
RT   necrosis factor-binding protein.";
RL   DNA Cell Biol. 9:705-715(1990).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RX   MEDLINE=91017509; PubMed=2170974;
RA   Gray P.W., Barrett K., Chantry D., Turner M., Feldman M.;
RT   "Cloning of human tumor necrosis factor (TNF) receptor cDNA and
RT   expression of recombinant soluble TNF-binding protein.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:7380-7384(1990).
RN   [6]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92250049; PubMed=1315717;
RA   Fuchs P., Strehl S., Dworzak M., Himmler A., Ambros P.F.;
RT   "Structure of the human TNF receptor 1 (p60) gene (TNFR1) and
RT   localization to chromosome 12p13.";
RL   Genomics 13:219-224(1992).
RN   [7]
RP   SEQUENCE FROM N.A.
RA   Rieder M.J., Armel T.Z., Carrington D.P., Ozuna M., Kuldanek S.A.,
RA   Rajkumar N.R., Toth E.J., Yi Q., Nickerson D.A.;
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
RN   [8]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Muscle;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
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RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [9]
RP   SEQUENCE OF 41-45.
RX   MEDLINE=90110215; PubMed=2153136;
RA   Engelmann H., Novick D., Wallach D.;
RT   "Two tumor necrosis factor-binding proteins purified from human
RT   urine. Evidence for immunological cross-reactivity with cell surface
RT   tumor necrosis factor receptors.";
RL   J. Biol. Chem. 265:1531-1536(1990).
RN   [10]
RP   INTERACTION WITH BAG4.
RX   MEDLINE=99115917; PubMed=9915703;
RA   Jiang Y., Woronicz J.D., Liu W., Goeddel D.V.;
RT   "Prevention of constitutive TNF receptor 1 signaling by silencer of
RT   death domains.";
RL   Science 283:543-546(1999).
RN   [11]
RP   X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS) OF 30-211 IN COMPLEX WITH TNFB.
RX   MEDLINE=93258809; PubMed=8387891;
RA   Banner D.W., D'Arcy A., Janes W., Gentz R., Schoenfeld H.-J.,
RA   Broger C., Loetscher H., Lesslauer W.;
RT   "Crystal structure of the soluble human 55 kd TNF receptor-human TNF
RT   beta complex: implications for TNF receptor activation.";
RL   Cell 73:431-445(1993).
RN   [12]
RP   X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 41-202.
RX   MEDLINE=97094982; PubMed=8939750;
RA   Naismith J.H., Devine T.Q., Khono H., Sprang S.R.;
RT   "Structures of the extracellular domain of the type I tumor necrosis
RT   factor receptor.";
RL   Structure 4:1251-1262(1996).
RN   [13]
RP   VARIANTS FHF ARG-59; TYR-62; MET-79; PHE-81; ARG-117 AND TYR-117.
RX   MEDLINE=99213501; PubMed=10199409;
RA   McDermott M.F., Aksentijevich I., Galon J., McDermott E.M.,
RA   Ogunkolade B.W., Centola M., Mansfield E., Gadina M., Karenko L.,
RA   Pettersson T., McCarthy J., Frucht D.M., Aringer M., Torosyan Y.,
RA   Teppo A.-M., Wilson M., Karaarslan H.M., Wan Y., Todd I., Wood G.,
RA   Schlimgen R., Kumarajeewa T.R., Cooper S.M., Vella J.P., Amos C.I.,
RA   Mulley J., Quane K.A., Molloy M.G., Rnaki A., Powell R.J.,
RA   Hitman G.A., O'Shea J., Kastner D.L.;
RT   "Germline mutations in the extracellular domains of the 55 kDa TNF
RT   receptor, TNFR1, define a family of dominantly inherited
RT   autoinflammatory syndromes.";
RL   Cell 97:133-144(1999).
CC   -!- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric
CC       TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits
CC       caspase-8 to the activated receptor. The resulting death-inducing
CC       signaling complex (DISC) performs caspase-8 proteolytic activation
CC       which initiates the subsequent cascade of caspases (aspartate-
CC       specific cysteine proteases) mediating apoptosis. Contributes to
CC       the induction of noncytocidal TNF effects including anti-viral
CC       state and activation of the acid sphingomyelinase.
CC   -!- SUBUNIT: Binding of TNF to the extracellular domain leads to
CC       homotrimerization. The aggregated death domains provide a novel
CC       molecular interface that interacts specifically with the death
CC       domain of TRADD. Various TRADD-interacting proteins such as TRAFS,
CC       RIP and possibly FADD, are recruited to the complex by their
CC       association with TRADD. This complex activates at least two
CC       distinct signaling cascades, apoptosis and NF-kappa-B signaling.
CC       Binds BAG4.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein and secreted.
CC   -!- DOMAIN: THE DOMAIN THAT INDUCES A-SMASE IS PROBABLY IDENTICAL TO
CC       THE DEATH DOMAIN. THE N-SMASE ACTIVATION DOMAIN (NSD) IS BOTH
CC       NECESSARY AND SUFFICIENT FOR ACTIVATION OF N-SMASE.
CC   -!- PTM: The soluble form is produced from the membrane form by
CC       proteolytic processing.
CC   -!- DISEASE: Defects in TNFRSF1A are a cause of autosomal dominant
CC       familial hibernian fever (FHF), a disease characterized by
CC       recurrent fever, abdominal pain, localized tender skin lesions and
CC       myalgia.
CC   -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC   -!- SIMILARITY: Contains 1 death domain.
CC   -!- DATABASE: NAME=PROW; NOTE=CD guide CD120a entry;
CC       WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd120a.htm".
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X55313; CAA39021.1; -.
DR   EMBL; M33294; AAA03210.1; -.
DR   EMBL; M58286; AAA36753.1; -.
DR   EMBL; M63121; AAA36754.1; -.
DR   EMBL; M75866; AAA61201.1; -.
DR   EMBL; M75864; AAA61201.1; JOINED.
DR   EMBL; M75865; AAA61201.1; JOINED.
DR   EMBL; M60275; AAA36756.1; -.
DR   EMBL; A21522; CAA01558.1; -.
DR   EMBL; AY131997; AAM77802.1; -.
DR   EMBL; BC010140; AAH10140.1; -.
DR   PIR; A38208; GQHUT1.
DR   PDB; 1TNR; 31-JUL-94.
DR   PDB; 1NCF; 07-DEC-95.
DR   PDB; 1EXT; 11-JAN-97.
DR   PDB; 1FT4; 12-OCT-01.
DR   PDB; 1ICH; 01-APR-02.
DR   Genew; HGNC:11916; TNFRSF1A.
DR   MIM; 191190; -.
DR   MIM; 142680; -.
DR   GO; GO:0005576; C:extracellular; TAS.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0005032; F:tumor necrosis factor receptor, type I acti. . .; TAS.
DR   GO; GO:0007165; P:signal transduction; TAS.

  Query Match             58.3%;  Score 1517;  DB 1;  Length 455;
  Best Local Similarity   62.9%;  Pred. No. 6.8e-90;
  Matches  302;  Conservative   38;  Mismatches  104;  Indels   36;  Gaps    7;

Qy          1 MGLPTVPGLLLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCT 60
              ||| ||| ||||||| || :||:|| ||||| || |||:| |||||| ||||::||||
Db          1 MGLSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCT 60

Qy         61 KCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCLSCSRCRDEMFQVEISPCVVD 120
              ||||||||||||||||:||||| |   |::|| ||||| |||||:|| || ||||| | ||
Db         61 KCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVD 120

Qy        121 RDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQERQDTICHCHMGFFLKGAKCI 180
              |||||||||||||| || |  |:| ||||| ||||:: |||:|:|:| || ||||:  :|:
Db        121 RDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECV 180

Qy        181 SCHDCKNK-ECEKLCPTRPSTGKDSQDPGTTVLLPLVIVFGLCLASFASVVLACRYQRWK 239
              || :||   || |||  :    | ::| |||||||||| ||||| |   : |  ||||||
Db        181 SCSNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPLVIFFGLCLLSLLFIGLMYRYQRWK 240

Qy        240 PKLYSIICGQSTLVKEGEPE-----LLVPAPGFNP----TTTICFSSTPSSSPVSIPPYI 290
              |||||:||:||  |||| |       | | | |:|    | |: ||  |||:  |   |
Db        241 SKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPTPGFTPTLGFSPVPSSTFTSSSTYT 300

Qy        291 SCDRSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLC 350
                |  ||   |:|  | |||:  | |||                 :| |      ||  :
Db        301 PGDCPNF---AAPRREVAPPYQGADPIL---------------ATAL------ASDPIP 335

Qy        351 TPVQKWEASAPSAPDQLADADPATLYAVVDGVPPSRWKELVRRLGLSEHEIERLELENGR 410
              |:|||| ||   |  |||||||||: ||| |||| |||||||:|||:||||:|||
Db        336 NPLQKWEDSA-HKPQSLDTDDPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLELQNGR 394
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Qy        411 HLREAQYSMLAAWRRRTPRREATLELLGRVLRDMDLLGCLENIEEALGGAARLASEPRLL 470
              |||||||||| |||||||||||||||||||||||||||||:|||| | | |   | ||
Db      .  395 CLREAQYSMLATWRRRTPRREATLELLGRVLRDMDLLGCLEDIEEALCGPAALPPAPSLL 454


RESULT 4
TR1A_RAT
ID   TR1A_RAT       STANDARD;      PRT;   461 AA.
AC   P22934; Q91V30; Q91Y93;
DT   01-AUG-1991 (Rel. 19, Created)
DT   01-MAR-1992 (Rel. 21, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 1A precursor (p60)
DE   (TNF-R1) (TNF-RI) (p55).
GN   TNFRSF1A OR TNFR1 OR TNFR-1.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91090841; PubMed=1702293;
RA   Himmler A., Maurer-Fogy I., Kroenke M., Scheurich P., Pfizenmaier K.,
RA   Lantz M., Olsson I., Hauptmann R., Stratowa C., Adolf G.R.;
RT   "Molecular cloning and expression of human and rat tumor necrosis
RT   factor receptor chain (p60) and its soluble derivative, tumor
RT   necrosis factor-binding protein.";
RL   DNA Cell Biol. 9:705-715(1990).
RN   [2]
RP   SEQUENCE FROM N.A., AND VARIANTS VAL-230 AND PRO-295.
RC   STRAIN=BB(DR)/Wor, LEW/NHsd, ACI/SegHsd, DA/Bkl, F344/NHsd, and
RC   BN/SsNHsd;
RA   Furuya T., Salstrom J.L., Bina J., Hashiramoto A., Dobbins D.E.,
RA   Wilder R.L., Remmers E.F.;
RT   "Polymorphisms of the tumor necrosis factor receptor type 1 locus
RT   among autoimmune susceptible and resistant inbred rat strains.";
RL   Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric
CC       TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits
CC       caspase-8 to the activated receptor. The resulting death-inducing
CC       signaling complex (DISC) performs caspase-8 proteolytic activation
CC       which initiates the subsequent cascade of caspases (aspartate-
CC       specific cysteine proteases) mediating apoptosis (By similarity).
CC   -!- SUBUNIT: Binding of TNF to the extracellular domain leads to
CC       homotrimerization. The aggregated death domains provide a novel
CC       molecular interface that interacts specifically with the death
CC       domain of TRADD. Various TRADD-interacting proteins such as TRAFS,
CC       RIP and possibly FADD, are recruited to the complex by their
CC       association with TRADD. This complex activates at least two
CC       distinct signaling cascades, apoptosis and NF-kappa-B signaling.
CC       Binds BAG4 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC   -!- SIMILARITY: Contains 1 death domain.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M63122; AAA42256.1; -.
DR   EMBL; AF329976; AAK53562.1; -.
DR   EMBL; AF329977; AAK53563.1; -.
DR   EMBL; AF329981; AAK53567.1; -.
DR   EMBL; AF329978; AAK53564.1; -.
DR   EMBL; AF329979; AAK53565.1; -.
DR   EMBL; AF329980; AAK53566.1; -.
DR   PIR; B36555; GQRTT1.
DR   HSSP; P19438; 1NCF.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00531; death; 1.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT   SIGNAL       1     21       POTENTIAL.
FT   CHAIN       22    461       TUMOR NECROSIS FACTOR RECEPTOR
FT                               SUPERFAMILY MEMBER 1A.
FT   DOMAIN      22    211       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   212    234       POTENTIAL.
FT   DOMAIN     235    461       CYTOPLASMIC (POTENTIAL).
FT   REPEAT      43     82       TNFR-CYS 1.
FT   REPEAT      83    125       TNFR-CYS 2.
FT   REPEAT     126    166       TNFR-CYS 3.
FT   REPEAT     167    196       TNFR-CYS 4.
FT   DOMAIN     344    354       N-SMASE ACTIVATION DOMAIN (NSD).
FT   DOMAIN     363    448       DEATH.
FT   DISULFID    44     58       BY SIMILARITY.
FT   DISULFID    59     72       BY SIMILARITY.
FT   DISULFID    62     81       BY SIMILARITY.
FT   DISULFID    84     99       BY SIMILARITY.
FT   DISULFID   102    117       BY SIMILARITY.
FT   DISULFID   105    125       BY SIMILARITY.
FT   DISULFID   127    143       BY SIMILARITY.
FT   DISULFID   146    158       BY SIMILARITY.
FT   DISULFID   149    166       BY SIMILARITY.
FT   DISULFID   168    179       BY SIMILARITY.
FT   DISULFID   182    195       BY SIMILARITY.
FT   DISULFID   185    191       BY SIMILARITY.
FT   CARBOHYD    54     54       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   151    151       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   201    201       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT    230    230       I -> V (IN STRAINS LEW/NHSD, ACI/SEGHSD,
FT                               DA/BKL AND F344/NHSD).
FT   VARIANT    295    295       H -> P (IN STRAINS LEW/NHSD, ACI/SEGHSD,
FT                               DA/BKL, F344/NHSD AND BN/SSNHSD).
SQ   SEQUENCE   461 AA;  50969 MW;  EB23C05450FBD202 CRC64;

  Query Match           51.4%;  Score 1338.5;  DB 1;  Length 461;
  Best Local Similarity 55.8%;  Pred. No. 1.6e-78;
  Matches  268;  Conservative   51;  Mismatches  114;  Indels   47;  Gaps    9;

Qy          1 MGLPTVPGLLLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCT 60
              |||| |||||| ||| |||  ::|:|| ||||  || |||:: |||||| ||:|:::|||
Db          1 MGLPIVPGLLLSLVLLALLMGIHPSGVTGLVPSLGDREKRDNLCPQGKYAHPKNNSICCT 60

Qy         61 KCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCLSCSRCRDEMFQVEISPCVVD 120
              |||||||| :||| ||::| | ||  ||:|| :||:|:|||| || ||||||||||  |
Db         61 KCHKGTYLVSDCPSPGQETVCEVCDKGTFTASQNHVRQCLSCKTCRKEMFQVEISPCKAD 120

Qy        121 RDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQERQDTICHCHMGFFLKGAKCI 180
              ||||||:|||:: |  || |:|::|| | |||| |||:|:|:|:|:|| |||| | :|
Db        121 MDTVCGCKKNQFQRYLSETHFQCVDCSPCFNGTVTIPCKEKQNTVCNCHAGFFLSGNECT 180

Qy        181 SCHDC-KNKECEKLCPTRPSTGKDSQDPGTTVLLPLVIVFGLCLASFASVVLACRYQRWK 239
              | | ||:|| |||    :   : || || ||||||  |||| |  : | ||| :|:
Db        181 PCSHCKKNQECMKLCLPPVANVTNPQDSGTAVLLPLVIFLGLCLLFFICISLLCRYPQWR 240

Qy        240 PKLYSIICGQSTLVKEGEPELLV----------PAPGFNPT----TTICFSSTPSSS 282
              |::|||||  | ||| | | :|           | ||||||    ||  ||   ||:
Db        241 PRVYSIICRDSAPVKEVEGEGIVTKPLTPASIPAFSPNPGFNPTLGFSTTPRFSHPVSST 300

Qy        283 PVSIPPYISCDRSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPG 342
              |:| | :    ||:     |  |  |    | |:| |                     |
Db        301 PIS-PVF---GPSNWHNFVPPVREVVPTQ-GADPLLYGS----------------LNPV 338

Qy        343 P-PASTHLCTPVQKWEASAPSAPDQLADADPATLYAVVDGVPPSRWKELVRRLGLSEHEI 401
              | ||      ||:|||    : | :|  |||| ||||||||||:|||| :| |||||||||
Db        339 PIPA------PVRKWEDVVAAQPQRLDTADPAMLYAVVDGVPPTRWKEFMRLLGLSEHEI 392
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Qy        402 ERLELENGRHLREAQYSMLAAWRRRTPRREATLELLGRVLRDMDLLGCLENIEEALGGAA 461
              |||||:||| |||| |||| |||||||| ||||:::|||| ||:| |||||| | |    |
Db        393 ERLELQNGRCLREAHYSMLEAWRRRTPRHEATLDVVGRVLCDMNLRGCLENIRETLESPA 452


RESULT 5
TR1A_MOUSE
ID   TR1A_MOUSE     STANDARD;      PRT;   454 AA.
AC   P25118;
DT   01-MAY-1992 (Rel. 22, Created)
DT   01-MAY-1992 (Rel. 22, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 1A precursor (p60)
DE   (TNF-R1) (TNF-RI) (p55).
GN   TNFRSF1A OR TNFR1 OR TNFR-1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91187885; PubMed=1849278;
RA   Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,
RA   Wong G.H., Chen E.Y., Goeddel D.V.;
RT   "Cloning and expression of cDNAs for two distinct murine tumor
RT   necrosis factor receptors demonstrate one receptor is species
RT   specific.";
RL   Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91246168; PubMed=1645445;
RA   Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,
RA   Copeland N.G., Jenkins N.A., Smith C.A.;
RT   "Molecular cloning and expression of the type 1 and type 2 murine
RT   receptors for tumor necrosis factor.";
RL   Mol. Cell. Biol. 11:3020-3026(1991).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91285014; PubMed=1647956;
RA   Barrett K., Taylor-Fishwick D.A., Cope A.P., Kissonerghis A.M.,
RA   Gray P.W., Feldmann M., Foxwell B.M.J.;
RT   "Cloning, expression and cross-linking analysis of the murine p55
RT   tumor necrosis factor receptor.";
RL   Eur. J. Immunol. 21:1649-1656(1991).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=92039815; PubMed=1657766;
RA   Rothe J.G., Brockhaus M., Gentz R., Lesslauer W.;
RT   "Molecular cloning and expression of the mouse Tnf receptor type b.";
RL   Immunogenetics 34:338-340(1991).
RN   [5]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94245292; PubMed=8188324;
RA   Bebo B.F., Linthicum D.S.;
RT   "Nucleotide sequence of the TNF type I receptor from a mouse
RT   endothelioma cell line.";
RL   Immunogenetics 39:450-451(1994).
RN   [6]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93156721; PubMed=8381516;
RA   Rothe J., Bluethmann H., Gentz R., Lesslauer W., Steinmetz M.;
RT   "Genomic organization and promoter function of the murine tumor
RT   necrosis factor receptor beta gene.";
RL   Mol. Immunol. 30:165-175(1993).
RN   [7]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko.L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric
CC       TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits
CC       caspase-8 to the activated receptor. The resulting death-inducing
CC       signaling complex (DISC) performs caspase-8 proteolytic activation
CC       which initiates the subsequent cascade of caspases (aspartate-
CC       specific cysteine proteases) mediating apoptosis (By similarity).
CC   -!- SUBUNIT: Binding of TNF to the extracellular domain leads to
CC       homotrimerization. The aggregated death domains provide a novel
CC       molecular interface that interacts specifically with the death
CC       domain of TRADD. Various TRADD-interacting proteins such as TRAFS,
CC       RIP and possibly FADD, are recruited to the complex by their
CC       association with TRADD. This complex activates at least two
CC       distinct signaling cascades, apoptosis and NF-kappa-B signaling.
CC       Binds BAG4 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC   -!- SIMILARITY: Contains 1 death domain.
CC   ---------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; M60468; AAA39751.1; -.
DR   EMBL; M59377; AAA40464.1; -.
DR   EMBL; X59238; CAA41922.1; -.
DR   EMBL; X57796; CAA40936.1; -.
DR   EMBL; L26349; AAA59361.1; -.
DR   EMBL; M76656; AAA40465.1; -.
DR   EMBL; M88067; AAA40465.1; JOINED.
DR   EMBL; M76655; AAA40465.1; JOINED.
DR   EMBL; BC004599; AAH04599.1; -.
DR   PIR; A38634; GQMST1.
DR   HSSP; P19438; 1EXT.
DR   MGD; MGI:1314884; Tnfrsf1a.
DR   GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; IMP.
DR   GO; GO:0006952; P:defense response; IMP.
DR   GO; GO:0006954; P:inflammatory response; IMP.
DR   GO; GO:0007515; P:lymph gland development; IMP.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00531; death; 1.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT   SIGNAL        1     21       POTENTIAL.
FT   CHAIN        22    454       TUMOR NECROSIS FACTOR RECEPTOR
FT                                 SUPERFAMILY MEMBER 1A.
FT   DOMAIN       22    212       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    213    235       POTENTIAL.
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FT   DOMAIN      236    454       CYTOPLASMIC (POTENTIAL).
FT   REPEAT       43     82       TNFR-CYS 1.
FT   REPEAT       83    125       TNFR-CYS 2.
FT   REPEAT      126    166       TNFR-CYS 3.
FT   REPEAT      167    196       TNFR-CYS 4.
FT   DOMAIN      339    349       N-SMASE ACTIVATION DOMAIN (NSD).
FT   DOMAIN      356    441       DEATH.
FT   DISULFID     44     58       BY SIMILARITY.
FT   DISULFID     59     72       BY SIMILARITY.
FT   DISULFID     62     81       BY SIMILARITY.
FT   DISULFID     84     99       BY SIMILARITY.
FT   DISULFID    102    117       BY SIMILARITY.
FT   DISULFID    105    125       BY SIMILARITY.
FT   DISULFID    127    143       BY SIMILARITY.
FT   DISULFID    146    158       BY SIMILARITY.
FT   DISULFID    149    166       BY SIMILARITY.
FT   DISULFID    168    179       BY SIMILARITY.
FT   DISULFID    182    195       BY SIMILARITY.
FT   DISULFID    185    191       BY SIMILARITY.
FT   CARBOHYD     54     54       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    151    151       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    202    202       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT    394    394       R -> G (IN REF. 6).
SQ   SEQUENCE   454 AA;  50129 MW;  0710C2E8C3C2B6D9 CRC64;

  Query Match           50.7%;  Score 1319;  DB 1;  Length 454;
  Best Local Similarity  56.5%;  Pred. No. 2.8e-77;
  Matches  268;  Conservative   55;  Mismatches  109;  Indels   42;  Gaps   12;

Qy          1 MGLPTVPGLLLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCT 60
              |||||||||| ||| |||  ::|:|| ||||  || |||:| |||||| | :|::||||
Db          1 MGLPTVPGLLLSLVLLALLMGIHPSGVTGLVPSLGDREKRDSLCPQGKYVHSKNNSICCT 60

Qy         61 KCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCLSCSRCRDEMPQVEISPCVVD 120
              |||||||| :||| ||||| || |  ||:|| :|:||:|||  || || |||||||  |
Db         61 KCHKGTYLVSDCPSPGRDTVCRECEKGTFTASQNYLRQCLSCKTCRKEMSQVEISPCQAD 120

Qy        121 RDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQERQDTICHCHMGFPLKGAKCI 180
              :||||||::||:: |  || |:|::|| | |||| |||:| |:|:|:|| ||||: ::|:
Db        121 KDTVCGCKENQFQRYLSETHFQCVDCSPCFNGTVTIPCKETQNTVCNCHAGFPLRESECV 180

Qy        181 SCHDC-KNKECEKLC-PTRPSTGKDSQDPGTTVLLPLVIVFGLCLASFASVVLACRYQRW 238
              |  | ||:|| ||| |   :   : || || ||||||: |||| ||  : | ||| ||
Db        181 PCSHCKKNEECMKLCLPPPLANVTNPQDSGTAVLLPLVILLGLCLLSFIFISLMCRYPRW 240

Qy        239 KPKLYSIICGQSTLVKE---GEPELLVPAPGFNPTT----TICFSSTPSSSPVSIPPYIS 291
              :|::|||||     |||   |:|   |:| |:||:    |: ||:   |||||  |
Db        241 RPEVYSIICRDPVPVKEEKAGKPLTPAPSPAFSPTSGFNPTLGFSTPGFSSPVSSTP--- 297

Qy        292 CDRSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTPG--PPASTHLCT-PGPPASTH 348
                  :  ||:     |          || |  : | |  |     ||: | |
Db        298 -----ISPIFGPSNW----HFM-------PPVSEVVPTQGADPLLYESLCSVPAP----- 336

Qy        349 LCTPVQKWEASA-PSAPDQLADADPATLYAVVDGVPPSRWKELVRRLGLSEHEIERLELE 407
              | ||||| || |  ||   :|| | |||||||||:|||| :| :|||||||||::
Db        337 --TSVQKWEDSAHPQRPD---NADLAILYAVVDGVPPARWKEFMRFMGLSEHEIERLEMQ 391

Qy        408 NGRHLRRAQYSMLAAWRRRTPRREATLELLGRVLRDMDLLGCLENIEEALGGAA 461
              ||| |||||||| |||||||| | |||:| ||  |:| |||||| |||   |
Db        392 NGRCLREAQYSMLEAWRRRTPRHEDTLEVVGLVLSKMNLAGCLENILEALRNPA 445


RESULT 6
TR25_HUMAN
ID   TR25_HUMAN     STANDARD;      PRT;   417 AA.
AC   Q93038; O00275; O00276; O00277; O00278; O00279; O00280; O14865;
AC   O14866; P78507; P78515; Q92983; Q93036; Q93037; Q99722; Q99830;
AC   Q99831; Q9BY86; Q9UME0; Q9UME1; Q9UME5;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 25 precursor
DE   (WSL-1 protein) (Apoptosis-mediating receptor DR3) (Apoptosis-
DE   mediating receptor TRAMP) (Death domain receptor 3) (WSL protein)
DE   (Apoptosis inducing receptor AIR) (Apo-3) (Lymphocyte associated
DE   receptor of death) (LARD).
GN   TNFRSF25 OR TNFRSF12 OR WSL1 OR WSL OR APO3 OR DR3 OR DDR3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS 1; 3 AND 4), AND MUTAGENESIS.
RC   TISSUE=Lymphoid;
RX   MEDLINE=97088617; PubMed=8934525;
RA   Kitson J., Raven T., Jiang Y.-P., Goeddel D.V., Giles K.M., Pun K.-T.,
RA   Grinham C.J., Brown R., Farrow S.N.;
RT   "A death-domain-containing receptor that mediates apoptosis.";
RL   Nature 384:372-375(1996).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   TISSUE=Umbilical vein endothelial cells;
RX   MEDLINE=97081063; PubMed=8875942;
RA   Chinnaiyan A.M., O'Rourke K., Yu G.-L., Lyons R.H., Garg M.,
RA   Duan D.R., Xing L., Gentz R., Ni J., Dixit V.M.;
RT   "Signal transduction by DR3, a death domain-containing receptor
RT   related to TNFR-1 and CD95.";
RL   Science 274:990-992(1996).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Degli-Esposti M.A., Din W.S., Cosman D., Smith C.A., Goodwin R.G.;
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   TISSUE=Heart;
RX   MEDLINE=97148200; PubMed=8994832;
RA   Marsters S.A., Sheridan J.P., Donahue C.J., Pitti R.M., Gray C.L.,
RA   Goddard A.D., Bauer K.D., Ashkenazi A.;
RT   "Apo-3, a new member of the tumor necrosis factor receptor family,
RT   contains a death domain and activates apoptosis and NF-kappa-B.";
RL   Curr. Biol. 6:1669-1676(1996).
RN   [5]
RP   SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4; 5; 6; 7; 8; 9 AND 10).
RX   MEDLINE=97272273; PubMed=9114039;
RA   Screaton G.R., Xu X.-N., Olsen A.L., Cowper A.E., Tan R.,
RA   McMichael A.J., Bell J.I.;
RT   "LARD: a new lymphoid-specific death domain containing receptor
RT   regulated by alternative pre-mRNA splicing.";
RL   Proc. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997).
RN   [6]
RP   SEQUENCE FROM N.A. (ISOFORMS 11 AND 12).
RX   MEDLINE=98113360; PubMed=9446802;
RA   Warzocha K., Ribeiro P., Charlot C., Renard N., Coiffier B.,
RA   Salles G.;
RT   "A new death receptor 3 isoform: expression in human lymphoid cell
RT   lines and non-Hodgkin's lymphomas.";
RL   Biochem. Biophys. Res. Commun. 242:376-379(1998).
RN   [7]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RA   Shiozawa S., Konishi Y., Murayama K., Mukae N., Yamamoto E.,
RA   Hayashi S., Sato M., Shiozawa K., Tsukamoto Y.;
RL   Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
RN   [8]
RP   SEQUENCE OF 4-417 FROM N.A.
RC   TISSUE=Brain, and Fetal lung;
RX   MEDLINE=97205335; PubMed=9052839;
RA   Bodmer J.-L., Burns K., Schneider P., Hofmann K., Steiner V.,
RA   Thome M., Bornand T., Hahne M., Schroeter M., Wilson A., French L.E.,
RA   Browning J.L., Macdonald H.R., Tschopp J.;
RT   "TRAMP, a novel apoptosis-mediating receptor with sequence homology
RT   to tumor necrosis factor receptor 1 and Fas(Apo-1/CD95).";
RL   Immunity 6:79-88(1997).
RN   [9]
RP   SEQUENCE OF 7-417 FROM N.A.
RC   TISSUE=Brain;
RA   Chaudhary P.M., Hood L.E.;
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RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
RN   [10]
RP   INTERACTION WITH BAG4.
RX   MEDLINE=99115917; PubMed=9915703;
RA   Jiang Y., Woronicz J.D., Liu W., Goeddel D.V.;
RT   "Prevention of constitutive TNF receptor 1 signaling by silencer of
RT   death domains.";
RL   Science 283:543-546(1999).
CC   -!- FUNCTION: Receptor for TNFSF12/APO3L/TWEAK. Interacts directly
CC       with the adaptor TRADD. Mediates activation of NF-kappaB and
CC       induces apoptosis. May play a role in regulating lymphocyte
CC       homeostasis.
CC   -!- SUBUNIT: Homodimer. Interacts strongly via the death domains with
CC       TNFRSF1 and TRADD to activate at least two distinct signaling
CC       cascades, apoptosis and NF-kappa-B signaling. Interacts with BAG4.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1, 2, 9
CC       and 11); Secreted (isoforms 3, 4, 5, 6, 7, 8, 10 and 12)
CC       (Potential).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=12;
CC       Name=1; Synonyms=WSL-1, LARD-1A;
CC         IsoId=Q93038-1; Sequence=Displayed;
CC       Name=2; Synonyms=LARD-1B;
CC         IsoId=Q93038-2; Sequence=VSP_006504;
CC       Name=3; Synonyms=WSL-S1, LARD-3;
CC         IsoId=Q93038-3; Sequence=VSP_006497, VSP_006498;
CC       Name=4; Synonyms=WSL-S2, LARD-2;
CC         IsoId=Q93038-4; Sequence=VSP_006501, VSP_006502;
CC       Name=5; Synonyms=LARD-4, LARD-11;
CC         IsoId=Q93038-5; Sequence=VSP_006495;
CC       Name=6; Synonyms=LARD-5;
CC         IsoId=Q93038-6; Sequence=VSP_006491, VSP_006495;
CC       Name=7; Synonyms=LARD-6;
CC         IsoId=Q93038-7; Sequence=VSP_006491, VSP_006493, VSP_006494;
CC       Name=8; Synonyms=LARD-7;
CC         IsoId=Q93038-8; Sequence=VSP_006492;
CC       Name=9; Synonyms=LARD-8;
CC         IsoId=Q93038-9; Sequence=VSP_006491;
CC       Name=10; Synonyms=LARD-9;
CC         IsoId=Q93038-10; Sequence=VSP_006503;
CC       Name=11; Synonyms=Beta;
CC         IsoId=Q93038-11; Sequence=VSP_006496;
CC       Name=12; Synonyms=Beta soluble;
CC         IsoId=Q93038-12; Sequence=VSP_006499, VSP_006500;
CC   -!- TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN THYMOCYTES AND
CC       LYMPHOCYTES. DETECTED IN LYMPHOCYTE-RICH TISSUES SUCH AS THYMUS,
CC       COLON, INTESTINE, AND SPLEEN. ALSO FOUND IN THE PROSTATE.
CC   -!- PTM: GLYCOSYLATED (PROBABLE).
CC   -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC   -!- SIMILARITY: Contains 1 death domain.
CC   -!- CAUTION: Ref.5 reports for isoform 4 at position 208 a serine
CC       residue instead of arginine.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Y09392; CAA70561.1; -.
DR   EMBL; Y09392; CAA70559.1; -.
DR   EMBL; Y09392; CAA70560.1; -.
DR   EMBL; U72763; AAC50819.1; -.
DR   EMBL; U83599; AAB41434.1; -.
DR   EMBL; U83600; AAB41435.1; -.
DR   EMBL; U78029; AAB40918.1; -.
DR   EMBL; U74611; AAB39714.1; -.
DR   EMBL; U94501; AAC51306.1; -.
DR   EMBL; U94504; AAC51309.1; -.
DR   EMBL; U94502; AAC51307.1; -.
DR   EMBL; U94503; AAC51308.1; -.
DR   EMBL; U94505; AAC51310.1; -.
DR   EMBL; U94506; AAC51311.1; -.
DR   EMBL; U94507; AAC51312.1; -.
DR   EMBL; U94508; AAC51313.1; -.
DR   EMBL; U94509; AAC51314.1; -.
DR   EMBL; U94510; AAC51315.1; -.
DR   EMBL; U94512; AAC51316.1; -.
DR   EMBL; U83598; AAB41433.1; -.
DR   EMBL; AF026070; AAC39556.1; -.
DR   EMBL; AF026071; AAB82288.1; -.
DR   EMBL; AB051850; BAB40662.1; -.
DR   EMBL; AB051851; BAB40663.1; -.
DR   EMBL; U75380; AAC51192.1; -.
DR   EMBL; U75381; AAC51193.1; -.
DR   EMBL; U83597; AAB41432.1; -.
DR   Genew; HGNC:11910; TNFRSF25.
DR   MIM; 603366; -.
DR   GO; GO:0005829; C:cytosol; NAS.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0016329; F:apoptosis regulator activity; NAS.
DR   GO; GO:0005027; F:NGF/TNF (6 C-domain) receptor activity; TAS.
DR   GO; GO:0004872; F:receptor activity; NAS.
DR   GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.
DR   GO; GO:0008624; P:induction of apoptosis by extracellular sig. . .; TAS.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00531; death; 1.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 1.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   Receptor; Apoptosis; Transmembrane; Alternative splicing; Signal;
KW   Repeat; Polymorphism.
FT   SIGNAL        1     24       POTENTIAL.
FT   CHAIN        25    417       TUMOR NECROSIS FACTOR RECEPTOR
FT                                 SUPERFAMILY MEMBER 25.
FT   DOMAIN       25    199       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    200    220       POTENTIAL.
FT   DOMAIN      221    417       CYTOPLASMIC (POTENTIAL).
FT   REPEAT       34     71       TNFR-CYS 1.
FT   REPEAT       72    115       TNFR-CYS 2.
FT   REPEAT      116    163       TNFR-CYS 3.
FT   REPEAT      164    192       TNFR-CYS 4.
FT   DOMAIN      332    413       DEATH.
FT   DISULFID     35     47       BY SIMILARITY.

  Query Match          14.9%;  Score 387.5;  DB 1;  Length 417;
  Best Local Similarity  26.9%;  Pred. No. 6.1e-18;
  Matches  130;  Conservative   47;  Mismatches  186;  Indels  121;  Gaps   18;

Qy         14 VLPALLADVYPAGVQGLVPHP-----GDLEKRESPCPQGKYNHPQNSTICCTKCHKGTYL 68
              |  |||  :  |  ||   '|      ||               | :    ||  |  | ||
Db         11 VAAALLLVLLGARAQGGTRSPRCDCAGDF------------HKKIGLFCCRGCPAGHYL 57

Qy         69 YNDCPGPGRDTDCRVCAPGTYTALENHLR-RCLSCSRCRDEMFQVEISPCVVDRDTVCGC 127
              |  |  :: | ||   |: | |||    |  |  | ::  || :  |    || |||
Db         58 KAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGC 117

Qy        128 RKN-----QYREYWGETGFRCLNCSLCPNGTVN----IPCQERQDTIC-HCHMGFFLKGA 177
              :  |     :  : | |  |  | ::    : |  |:|| |  |  ||: |
Db        118 KPGWFVECQVSQCVSSSPFYCQPCLDC--GALHRHTRLLC-SRRDTDCGTCLPGFYEHGD 174

Qy        178 KCISC-----HDCKNKECEKLCPTRPSTGKDSQDPGTTVLLPLVIVFGLCLASFASVVLA 232
              |:||       |  : |  :|  |              :    |:: || :       |
Db        175 GCVSCPTSTLGSCPER-CAAVCGWR-----------QMFWVQVLLAGLVVPLLLGATLT 221

Qy        233 CRYQR-WKPKLYSIICGQSTLVKEGEPELLVPAPGFNPTTTICFSSTPSSSPVSIPPYIS 291
              |:  |  |                                                | ::
Db        222 YTYRHCWPHK-------------------------------------------------PLVT 235

Qy        292 CDRSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLCT 351
              |  :  |:  |  :   |   |  :|  | :|  :||     ::   ||| | :
Db        236 ADEAGMEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNS--WTPGYPETQEALC 293
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Qy        352 PVQKW-------EASAPSAPDQLADADPA----------TLYAVVDGVPPSRWKELVRR 393
              |  |       |  |:|   |:   ||           || |:| ||  |||| ||
Db        294 PQVTWSWDQLPSRALGPAAAPTLSPESPAGSPAMMLQPGPQLYDVMDAVPARRWKEFVRT 353

Qy        394 LGLSEHEIERLELENGRHLREAQYSMLAAWRRRTPRREATLELLGRVLRDMDLLGCLENI 453
              ||| | ||| :|:| ||  |: || ||  ||:: |  | |  :  |  | | ||:|::
Db        354 LGLREAEIEAVEVEIGR-FRDQQYEMLKRWRQQQP---AGLGAVYAALERMGLDGCVEDL 409

Qy        454 EEAL 457
                |
Db        410 RSRL 413
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RESULT 7
T10B_HUMAN
ID   T10B_HUMAN     STANDARD;      PRT;   440 AA.
AC   O14763; O14720; O15508; O15517; O15531; Q9BVE0;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 10B precursor (Death
DE   receptor 5) (TNF-related apoptosis-inducing ligand receptor 2) (TRAIL
DE   receptor-2) (TRAIL-R2).
GN   TNFRSF10B OR DR5 OR TRAILR2 OR TRICK2 OR KILLER OR ZTNFR9.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM LONG), AND SEQUENCE OF N-TERMINUS.
RC   TISSUE=Foreskin fibroblast;
RX   MEDLINE=97459925; PubMed=9311998;
RA   Walczak H., Degli-Esposti M.A., Johnson R.S., Smolak P.J., Waugh J.Y.,
RA   Boiani N., Timour M.S., Gerhart M.J., Schooley K.A., Smith C.A.,
RA   Goodwin R.G., Rauch C.T.;
RT   "TRAIL-R2: a novel apoptosis-mediating receptor for TRAIL.";
RL   EMBO J. 16:5386-5397(1997).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT), AND ALTERNATIVE
RP   SPLICING.
RX   MEDLINE=97431692; PubMed=9285725;
RA   Screaton G.R., Mongkolsapaya J., Xu X.-N., Cowper A.E.,
RA   McMichael A.J., Bell J.I.;
RT   "TRICK2, a new alternatively spliced receptor that transduces the
RT   cytotoxic signal from TRAIL.";
RL   Curr. Biol. 7:693-696(1997).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM LONG), AND CHARACTERIZATION.
RC   TISSUE=Liver, and Spleen;
RX   MEDLINE=98039016; PubMed=9373179;
RA   Schneider P., Bodmer J.-L., Thome M., Hofmann K., Holler N.,
RA   Tschopp J.;
RT   "Characterization of two receptors for TRAIL.";
RL   FEBS Lett. 416:329-334(1997).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM SHORT).
RC   TISSUE=Ovary;
RX   MEDLINE=97467719; PubMed=9326928;
RA   Wu G.S., Burns T.F., McDonald E.R. III, Jiang W., Meng R.,
RA   Krantz I.D., Kao G., Gan D.D., Zhou J.Y., Muschel R., Hamilton S.R.,
RA   Spinner N.B., Markowitz S., Wu G., el-Deiry W.S.;
RT   "KILLER/DR5 is a DNA damage-inducible p53-regulated death receptor
RT   gene.";
RL   Nat. Genet. 17:141-143(1997).
RN   [5]
RP   SEQUENCE FROM N.A. (ISOFORM SHORT).
RX   MEDLINE=97390508; PubMed=9242610;
RA   Pan G., Ni J., Wei Y.-F., Yu G.-I., Gentz R., Dixit V.M.;
RT   "An antagonist decoy receptor and a death domain-containing receptor
RT   for TRAIL.";
RL   Science 277:815-818(1997).
RN   [6]
RP   SEQUENCE FROM N.A. (ISOFORM SHORT).
RX   MEDLINE=97467318; PubMed=9325248;
RA   MacFarlane M., Ahmad M., Srinivasula S.M., Fernandes-Alnemri T.,
RA   Cohen G.M., Alnemri E.S.;
RT   "Identification and molecular cloning of two novel receptors for the
RT   cytotoxic ligand TRAIL.";
RL   J. Biol. Chem. 272:25417-25420(1997).
RN   [7]
RP   SEQUENCE FROM N.A. (ISOFORM SHORT).
RX   MEDLINE=98090092; PubMed=9430227;
RA   Chaudhary P.M., Eby M., Jasmin A., Bookwalter A., Murray J., Hood L.;
RT   "Death receptor 5, a new member of the TNFR family, and DR4 induce
RT   FADD-dependent apoptosis and activate the NF-kappaB pathway.";
RL   Immunity 7:821-830(1997).
RN   [8]
RP   SEQUENCE FROM N.A. (ISOFORM SHORT).
RX   MEDLINE=97390509; PubMed=9242611;
RA   Sheridan J.P., Marsters S.A., Pitti R.M., Gurney A., Skubatch M.,
RA   Baldwin D., Ramakrishnan L., Gray C.L., Baker K., Wood W.I.,
RA   Goddard A.D., Godowski P., Ashkenazi A.;
RT   "Control of TRAIL-induced apoptosis by a family of signaling and decoy
RT   receptors.";
RL   Science 277:818-821(1997).
RN   [9]
RP   SEQUENCE FROM N.A. (ISOFORM LONG).
RA   Arai T., Akiyama Y., Okabe S., Saito K., Iwai T., Yuasa Y.;
RT   "Genomic structure and mutation analyses of the DR5/TRAIL receptor 2
RT   gene in colorectal carcinoma.";
RL   Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
RN   [10]
RP   SEQUENCE FROM N.A. (ISOFORM SHORT).
RA   Cao X., Zhang W., Wan T.;
RL   Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
RN   [11]
RP   SEQUENCE FROM N.A. (ISOFORM SHORT).
RA   Farrah T., Vu T., Gilbert T., Gross J., O'Hara P.;
RT   "Homo sapiens homolog of tumor necrosis factor receptor.";
RL   Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
RN   [12]
RP   SEQUENCE FROM N.A. (ISOFORM LONG).
RC   TISSUE=Cervix;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [13]
RP   X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 54-183.
RX   MEDLINE=20017054; PubMed=10549288;
RA   Hymowitz S.G., Christinger H.W., Fuh G., Ultsch M., O'Connell M.,
RA   Kelley R.F., Ashkenazi A., de Vos A.M.;
RT   "Triggering cell death: the crystal structure of Apo2L/TRAIL in a
RT   complex with death receptor 5.";
RL   Mol. Cell 4:563-571(1999).
RN   [14]
RP   X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 69-184.
RX   PubMed=10542098;
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RA   Mongkolsapaya J., Grimes J.M., Chen N., Xu X.-N., Stuart D.I.,
RA   Jones E.Y., Screaton G.R.;
RT   "Structure of the TRAIL-DR5 complex reveals mechanisms conferring
RT   specificity in apoptotic initiation.";
RL   Nat. Struct. Biol. 6:1048-1053(1999).
CC   -!- FUNCTION: Receptor for the cytotoxic ligand TNFSF10/TRAIL. The
CC       adaptor molecule FADD recruits caspase-8 to the activated
CC       receptor. The resulting death-inducing signaling complex (DISC)
CC       performs caspase-8 proteolytic activation which initiates the
CC       subsequent cascade of caspases (aspartate-specific cysteine
CC       proteases) mediating apoptosis. Promotes the activation of NF-
CC       kappaB.
CC   -!- SUBUNIT: Homotrimer. Can interact with TRADD and RIP.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=Long; Synonyms=TRICK2B;
CC         IsoId=O14763-1; Sequence=Displayed;
CC       Name=Short; Synonyms=TRICK2A;
CC         IsoId=O14763-2; Sequence=VSP_006490;
CC   -!- TISSUE SPECIFICITY: Widely expressed in adult and fetal tissues;
CC       very highly expressed in tumor cell lines such as HeLa S3, K562,
CC       HL-60, SW480, A549 and G361; highly expressed in heart, peripheral
CC       blood lymphocytes, liver, pancreas, spleen, thymus, prostate,
CC       ovary, uterus, placenta, testis, esophagus, stomach and throughout
CC       the intestinal tract; not detectable in brain.
CC   -!- INDUCTION: TNFRSF10B is regulated by the tumor suppressor p53.
CC   -!- DISEASE: Defects in TNFRSF10B may be a cause of squamous cell
CC       carcinoma of the head and neck.
CC   -!- SIMILARITY: Contains 3 TNFR-Cys repeats.
CC   -!- SIMILARITY: Contains 1 death domain.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF016849; AAC51778.1; -.
DR   EMBL; AF018657; AAB70577.1; -.
DR   EMBL; AF018658; AAB70578.1; -.
DR   EMBL; AF016266; AAB81180.1; -.
DR   EMBL; AF022386; AAB71949.1; -.
DR   EMBL; AF012628; AAB67109.1; -.
DR   EMBL; AF020501; AAB71412.1; -.
DR   EMBL; AF016268; AAC01565.1; -.
DR   EMBL; AF012535; AAB67103.1; -.
DR   EMBL; AB014718; BAA33723.1; -.
DR   EMBL; AB014710; BAA33723.1; JOINED.
DR   EMBL; AB014711; BAA33723.1; JOINED.
DR   EMBL; AB014712; BAA33723.1; JOINED.
DR   EMBL; AB014713; BAA33723.1; JOINED.
DR   EMBL; AB014714; BAA33723.1; JOINED.
DR   EMBL; AB014715; BAA33723.1; JOINED.
DR   EMBL; AB014716; BAA33723.1; JOINED.
DR   EMBL; AB014717; BAA33723.1; JOINED.
DR   EMBL; AF153687; AAF75587.1; -.
DR   EMBL; AF192548; AAF07175.1; -.
DR   EMBL; BC001281; AAH01281.1; -.
DR   PDB; 1D0G; 22-OCT-99.
DR   PDB; 1D4V; 01-NOV-99.
DR   Genew; HGNC:11905; TNFRSF10B.
DR   MIM; 603612; -.
DR   MIM; 601400; -.
DR   GO; GO:0016021; C:integral to membrane; IC.
DR   GO; GO:0016506; F:apoptosis activator activity; NAS.
DR   GO; GO:0008656; F:caspase activator activity; NAS.
DR   GO; GO:0004872; F:receptor activity; NAS.

  Query Match          10.4%;  Score 271.5;  DB 1;  Length 440;
  Best Local Similarity  25.5%;  Pred. No. 1.6e-10;
  Matches  123;  Conservative   57;  Mismatches  196;  Indels  107;  Gaps   25;

Qy          4 PTVPGLLLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCTKCH 63
              | ||  |: :|   ||        :  :    ||  ::   || | : |       |
Db         32 PRVPKTLVLVVAAVLLL----VSAESALITQQDLAPQQRAAPQQKRSSPSEGL-----CP 82

Qy         64 KGTYLYNDCPGPGRDTDCRVCAPG-TYTALENHLRRCLSCSRCRDEMFQVEISPCVVDRD 122
               | ::  |    ||  ||  |  |  |:   | |  || |:||  :  :||:|||   |:
Db         83 PGHHISED----GR--DCISCKYGQDYSTHWNDLLFCLRCTRC--DSGEVELSPCTTTRN 134

Qy        123 TVCGCRKNQYREYWGETGFRCLNCSL-CPNGTVNI-PCQERQDTIC-HCHMGFFLKGAKC 179
              ||| | :  :||   ::   |  |  || | | :  |    |  | |  |
Db        135 TVCQCEEGTFRE--EDSPEMCRKCRTGCPRGMVKVGDCTPWSDIECVHKESG-------- 184

Qy        180 ISCHDCKNKECEKLCPTRPSTGKDSQDPGTTVLLPLVIVFGLCLASFASV--VLACRYQR 237
               : |  :    |:  : | |      | :   |  :|: |: :|:  :  |  |:
Db        185 -TKHSGEAPAVEETVTSSPGT------PASPCSLSGIII-GVTVAAVVLIVAVFVCKSLL 236

Qy        238 WK---PKLYSIICGQSTLVKEGEPELLVPAPGFNPTTTICFSSTPSSSPVSIPPYISCDR 294
              ||   | | |  |       |:|| :                              ||
Db        237 WKKVLPYLKGICSGGG-----GDPERV------------------------------DR 260

Qy        295 SNFGAVASPSSETAPPHLKAGPILPG--PPASTHLCTPGPPASTHLCTPGPPASTHLCTP 352
              |:      | :|    :  :  : |   |      :  | |   :: :||   | ||  |
Db        261 SS----QRPGAEDNVLNEIVSILQPTQVPEQEMEVQEPAEPTGVNMLSPG--ESEHLLEP 314

Qy        353 VQKWEASAPSAPDQLADADPA-TLYAVVDG----VPPSRWKELVRRLGLSEHEIERLELE 407
               :   :          : ||  ||    |     ||   |: |:|:||| ::||:  : |
Db        315 AEAERSQRRRLLVPANEGDPTETLRQCFDDFADLVPFDSWEPLMRKLGLMDNEIKVAKAE 374

Qy        408 NGRHLREAQYSMLAAWRRRTPRREATLELLGRVLRDMDLLGCLENIEEALGGAARLASEP 467
              | |:  |:||  |  :|          ||      ||  || : | |   |:  |
Db        375 AAGH-RDTLYTMLIKWVNKT----------GRDASVHTLLDALETLGERL---AKQKIED 420

Qy        468 RLL 470
               ||
Db        421 HLL 423


RESULT 8
TNR3_HUMAN
ID   TNR3_HUMAN     STANDARD;      PRT;   435 AA.
AC   P36941;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 3 precursor
DE   (Lymphotoxin-beta receptor) (Tumor necrosis factor receptor 2 related
DE   protein) (Tumor necrosis factor C receptor).
GN   LTBR OR TNFRSF3 OR TNFCR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=93252381; PubMed=8486360;
RA   Baens M., Chaffanet M., Cassiman J.J., den Berghe H., Marynen P.;
RT   "Construction and evaluation of a hncDNA library of human 12p
RT   transcribed sequences derived from a somatic cell hybrid.";
RL   Genomics 16:214-218(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
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RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [3]
RP   FUNCTION.
RX   MEDLINE=94225209; PubMed=8171323;
RA   Crowe P.D., VanArsdale T.L., Walter B.N., Ware C.F., Hession C.,
RA   Ehrenfels B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.;
RT   "A lymphotoxin-beta-specific receptor.";
RL   Science 264:707-710(1994).
RN   [4]
RP   CHARACTERIZATION.
RX   MEDLINE=99223511; PubMed=10207006;
RA   Wu M.-Y., Wang P.-Y., Han S.-H., Hsieh S.-L.;
RT   "The cytoplasmic domain of the lymphotoxin-beta receptor mediates cell
RT   death in HeLa cells.";
RL   J. Biol. Chem. 274:11868-11873(1999).
RN   [5]
RP   FUNCTION.
RX   MEDLINE=20261554; PubMed=10799510;
RA   Rooney I.A., Butrovich K.D., Glass A.A., Borboroglu S., Benedict C.A.,
RA   Whitbeck J.C., Cohen G.H., Eisenberg R.J., Ware C.F.;
RT   "The lymphotoxin-beta receptor is necessary and sufficient for
RT   LIGHT-mediated apoptosis of tumor cells.";
RL   J. Biol. Chem. 275:14307-14315(2000).
RN   [6]
RP   INTERACTION WITH TRAF3.
RX   MEDLINE=96278943; PubMed=8663299;
RA   Nakano H., Oshima H., Chung W., Williams-Abbott L., Ware C.F.,
RA   Yagita H., Okumura K.;
RT   "TRAF5, an activator of NF-kappaB and putative signal transducer for
RT   the lymphotoxin-beta receptor.";
RL   J. Biol. Chem. 271:14661-14664(1996).
RN   [7]
RP   INTERACTION WITH TRAF4.
RX   PubMed=9626059;
RA   Krajewska M., Krajewski S., Zapata J.M., VanArsdale T.,
RA   Gascoyne R.D., Berern K., McFadden D., Shabaik A., Hugh J.,
RA   Reynolds A., Clevenger C.V., Reed J.C.;
RT   "TRAF-4 expression in epithelial progenitor cells. Analysis in normal
RT   adult, fetal, and tumor tissues.";
RL   Am. J. Pathol. 152:1549-1561(1998).
RN   [8]
RP   INTERACTION WITH TRAF5.
RX   MEDLINE=98172745; PubMed=9511754;
RA   Mizushima S.-I., Fujita M., Ishida T., Azuma S., Kato K., Hirai M.,
RA   Otsuka M., Yamamoto T., Inoue J.-I.;
RT   "Cloning and characterization of a cDNA encoding the human homolog of
RT   tumor necrosis factor receptor-associated factor 5 (TRAF5).";
RL   Gene 207:135-140(1998).
CC   -!- FUNCTION: Receptor for the heterotrimeric lymphotoxin containing
CC       LTA and LTB, and for TNFS14/LIGHT. Promotes apoptosis via TRAF3
CC       and TRAF5. May play a role in the development of lymphoid organs.
CC   -!- SUBUNIT: Self-associates. Associates with TRAF3, TRAF4 and TRAF5.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L04270; AAA36757.1; -.
DR   EMBL; BC026262; AAH26262.1; -.
DR   PIR; I54182; I54182.
DR   HSSP; P25942; 1CDF.
DR   Genew; HGNC:6718; LTBR.
DR   MIM; 600979; -.
DR   GO; GO:0007165; P:signal transduction; TAS.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
KW   Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT   SIGNAL       1     30       POTENTIAL.
FT   CHAIN       31    435       TUMOR NECROSIS FACTOR RECEPTOR
FT                               SUPERFAMILY MEMBER 3.
FT   DOMAIN      31    227       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   228    248       POTENTIAL.
FT   DOMAIN     249    435       CYTOPLASMIC (POTENTIAL).
FT   REPEAT      42     81       TNFR-CYS 1.
FT   REPEAT      82    124       TNFR-CYS 2.
FT   REPEAT     125    168       TNFR-CYS 3.
FT   REPEAT     169    211       TNFR-CYS 4.
FT   DISULFID    43     58       BY SIMILARITY.
FT   DISULFID    59     72       BY SIMILARITY.
FT   DISULFID    62     80       BY SIMILARITY.
FT   DISULFID    83     98       BY SIMILARITY.
FT   DISULFID   101    116       BY SIMILARITY.
FT   DISULFID   104    124       BY SIMILARITY.
FT   DISULFID   126    132       BY SIMILARITY.
FT   DISULFID   139    148       BY SIMILARITY.
FT   DISULFID   142    167       BY SIMILARITY.
FT   DISULFID   170    185       BY SIMILARITY.
FT   CARBOHYD    40     40       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   177    177       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   435 AA;  46709 MW;  624626E6022F656F CRC64;

  Query Match             9.9%;  Score 257;  DB 1;  Length 435;
  Best Local Similarity   27.3%;  Pred. No. 1.3e-09;
  Matches  121;  Conservative   37;  Mismatches  158;  Indels  128;  Gaps   25;

Qy          1 MGLP---TVPGLLL-PLVLP--ALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQN 54
              | ||    : |||   ||||    |||   |  |      |   | :     : :|  ||:
Db          1 MLLPWATSAPGLAWGPLVLGLFGLLAASQPQAVP-----PYASENQTCRDQEKEYYEPQH 55

Qy         55 STICCTKCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCLSCSRCRDEMPQVEI 114
                |||::|  |||:   |    ||| |  ||  :|    |:|  |  |  |   |   ||
Db         56 -RICCSRCPPGTYVSAKC-SRIRDTVCATCAENSYNEHWNYLTICQLCRPCDPVMGLEEI 113

Qy        115 SPCVVDRDTVCGCRKNQYREYWGETGFRCLNCSL---CPNGTVNIPCQERQDTI------ 165
              :||   | | |:   :   |       | :| |   || ||      | :| :
Db        114 APCTSKRKTQCRCQPGMFCAAW---ALECTHCELLSDCPPGTE----AELKDEVGKGNNH 166

Qy        166 -CHCHMGFFLK----GAKCISCHDCKNKECEKLCP---TRPSTGKDSQDP------GT-- 209
               | | |       |:|     |:|:   :  |      :| |:  :|       ||
Db        167 CVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTCKNPLEPLPPEMSGTML 226

Qy        210 --TVLLPLVIVFGLCLASFASVVLACRYQRWKPKLYSIICGQSTLVKEGEPELLVPAPGF 267
                |||||  | | ||:  | :       ||   :  :| :   :  :  |:      |
Db        227 MLAVLLPL--AFFLLLATVFSCI-------WKS--HPSLCRKLGSLLKRRPQ----GEGP 271

Qy        268 NPTTTICFSSTPSSSPVSIPPY----------ISCDRS--NFGAVASPSSETAPP----- 310
              ||          | |    ||          || | |  : |  |:|  |   |
Db        272 NPV-------AGSWEPPKAHPYFPDLVQPLLPISGDVSPVSTGLPAAPVLEAGVPQQQSP 324

Qy        311 ------------------------------------HLKAGPILPGPPASTHL-CTPGP 332
                                                 ::  ||:| |||    |  || |
Db        325 LDLTREPQLEPGEQSQVAHGTNGIHVTGGSMTITGNIYIYNGPVLGGPPGPGDLPATPEP 384

Qy        333 P-ASTHLCTPGPPASTHLCTPVQK 355
              |       ||||    | || |:
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Db        385 PYPIPEEGDPGPPG---LSTPHQE 405


RESULT 9
TNR3_MOUSE
ID   TNR3_MOUSE     STANDARD;      PRT;   415 AA.
AC   P50284;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 3 precursor
DE   (Lymphotoxin-beta receptor).
GN   LTBR OR TNFRSF3 OR TNFCR.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CVB; TISSUE=Lung;
RX   MEDLINE=96072804; PubMed=7594541;
RA   Force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,
RA   Browning J.L., Ware C.F.;
RT   "Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,
RT   and expression.";
RL   J. Immunol. 155:5280-5288(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96163885; PubMed=8586432;
RA   Nakamura T., Tashiro K., Nazarea M., Nakano T., Sasayama S.,
RA   Honjo T.;
RT   "The murine lymphotoxin-beta receptor cDNA: isolation by the signal
RT   sequence trap and chromosomal mapping.";
RL   Genomics 30:312-319(1995).
RN   [3]
RP   INTERACTION WITH TRAF5.
RC   STRAIN=BALB/c;
RX   MEDLINE=96278943; PubMed=8663299;
RA   Nakano H., Oshima H., Chung W., Williams-Abbott L., Ware C.F.,
RA   Yagita H., Okumura K.;
RT   "TRAF5, an activator of NF-kappaB and putative signal transducer for
RT   the lymphotoxin-beta receptor.";
RL   J. Biol. Chem. 271:14661-14664(1996).
CC   -!- FUNCTION: Receptor for the heterotrimeric lymphotoxin containing
CC       LTA and LTB, and for TNFS14/LIGHT. Promotes apoptosis via TRAF3
CC       and TRAF5. May play a role in the development of lymphoid organs
CC       (By similarity).
CC   -!- SUBUNIT: Self-associates (By similarity). Associates with TRAF5.
CC       Associates with TRAF3 and TRAF4 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U29173; AAA68964.1; -.
DR   EMBL; L38423; AAB00846.1; -.
DR   EMBL; U30798; AAA81334.1; -.
DR   HSSP; O14763; 1D0G.
DR   MGD; MGI:104875; Ltbr.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 3.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
KW   Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT   SIGNAL        1     30       POTENTIAL.
FT   CHAIN        31    415       TUMOR NECROSIS FACTOR RECEPTOR
FT                                SUPERFAMILY MEMBER 3.
FT   DOMAIN       31    223       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    224    244       POTENTIAL.
FT   DOMAIN      245    415       CYTOPLASMIC (POTENTIAL).
FT   REPEAT       42     81       TNFR-CYS 1.
FT   REPEAT       82    124       TNFR-CYS 2.
FT   REPEAT      125    170       TNFR-CYS 3.
FT   REPEAT      171    213       TNFR-CYS 4.
FT   DISULFID     43     58       BY SIMILARITY.
FT   DISULFID     59     72       BY SIMILARITY.
FT   DISULFID     62     80       BY SIMILARITY.
FT   DISULFID     83     98       BY SIMILARITY.
FT   DISULFID    101    116       BY SIMILARITY.
FT   DISULFID    104    124       BY SIMILARITY.
FT   DISULFID    126    132       BY SIMILARITY.
FT   DISULFID    139    150       BY SIMILARITY.
FT   DISULFID    142    169       BY SIMILARITY.
FT   DISULFID    172    187       BY SIMILARITY.
FT   CARBOHYD     40     40       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    179    179       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   415 AA;  44956 MW;  29B326A566AEF661 CRC64;

  Query Match             9.5%;  Score 247;  DB 1;  Length 415;
  Best Local Similarity   25.8%;  Pred. No. 5.5e-09;
  Matches  105;  Conservative   46;  Mismatches  168;  Indels   88;  Gaps   20;

Qy         12 PLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCTKCHKGTYLYND 71
              ||:|   |: :  |    ||| | :| :       :|  | :  :||::|  | :::
Db         16 PLLLG--LSGLLVASQPQLVP-PYRIENQTCWDQDKEYYEPMHD-VCCSRCPPGEFVFAV 71

Qy         72 CPGPGRDTDCRVCAPGTYTALENHLRRCLSCSRCRDEMFQVEISPCVVDRDTVCGCRKNQ 131
              |    :|| |: |   :|    |||  |  |  |   :   |::||  ||   | |:
Db         72 C-SRSQDTVCKTCPHNSYNEHWNHLSTCQLCRPCDIVLGFEEVAPCTSDRKAECRCQPGM 130

Qy        132 YREYWGETGFRCLNCS---LCPNGTVNIPCQERQDTICH---CHMGFFLK----GAKC 179
                |      |::|     || ||       | ||  :   | | |       |:|
Db        131 SCVYLDN---ECVHCEEERLVLCQPGTEAEVTDEIMDTDVNCVPCKPGHFQNTSSPRARC 187

Qy        180 ISCHDCKNKECEKLCPTRPSTG------KDSQDPGTTVLLPLVIVFGLCLASFASVVLAC 233
                |   | : |   | |       |:  :||  :|  | |:  | |    : ||||
Db        188 QPHTRC---EIQGLVEAAPGTSYSDTICKNPPEPGAMLL--LAILLSLVLFLLFTTVLAC 242

Qy        234 RYQRWKPKLYSIICGQ-STLVK---EGEPELLVPAPGFNP------TTTICFSSTPSSSP 283
              : |     :  :| :  ||:|   |||     |||  :|          :  |   | ||
Db        243 AWMR-----HPSLCRKLGTLLKRHPEGEESPPCPAPRADPHFPDLAEPLLPMSGDLSPSP 297

Qy        284 VSIPP-------------------YISCDRSNFGAVASPS----------SETAPPHLKA 314
                |                   :  :    | ||  :           : |   ::
Db        298 AGPPTAPSLEEVVLQQQSPLVQARELEAEPGEHGQVAHGANGIHVTGGSVTVTGNIYIYN 357

Qy        315 GPILPG------PPASTHLCTPGPPASTHLCTPGPPASTHLCTPVQK 355
              ||:| |      |||      | || |    | |  : | || |:
Db        358 GPVLGGTRGPGDPPA-----PPEPPYPTP--EEGAPGPSELSTPYQE 397


RESULT 10
TR16_HUMAN
ID   TR16_HUMAN     STANDARD;      PRT;   427 AA.
AC   P08138;
DT   01-AUG-1988 (Rel. 08, Created)
DT   01-AUG-1988 (Rel. 08, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 16 precursor (Low-
DE   affinity nerve growth factor receptor) (NGF receptor) (Gp80-LNGFR)
DE   (p75 ICD) (Low affinity neurotrophin receptor p75NTR).
GN   NGFR OR TNFRSF16.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87051725; PubMed=3022937;
```

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RA   Johnson D., Lanahan A., Buck C.R., Sehgal A., Morgan C., Mercer E.,
RA   Bothwell M., Chao M.;
RT   "Expression and structure of the human NGF receptor.";
RL   Cell 47:545-554(1986).
RN   [2]
RP   SEQUENCE OF 1-22 FROM N.A.
RX   MEDLINE=89096903; PubMed=2850481;
RA   Sehgal A., Patil N., Chao M.;
RT   "A constitutive promoter directs expression of the nerve growth factor
RT   receptor gene.";
RL   Mol. Cell. Biol. 8:3160-3167(1988).
RN   [3]
RP   INTERACTION WITH TRAF2; TRAF4 AND TRAF6.
RX   PubMed=10514511;
RA   Ye X., Mehlen P., Rabizadeh S., VanArsdale T., Zhang H., Shin H.,
RA   Wang J.J., Leo E., Zapata J.M., Hauser C.A., Reed J.C., Bredesen D.E.;
RT   "TRAF family proteins interact with the common neurotrophin receptor
RT   and modulate apoptosis induction.";
RL   J. Biol. Chem. 274:30202-30208(1999).
RN   [4]
RP   INTERACTION WITH TRAF6.
RX   PubMed=9915784;
RA   Khursigara G., Orlinick J.R., Chao M.V.;
RT   "Association of the p75 neurotrophin receptor with TRAF6.";
RL   J. Biol. Chem. 274:2597-2600(1999).
CC   -!- FUNCTION: Low affinity receptor which can bind to NGF, BDNF, NT-3,
CC       and NT-4. Can mediate cell survival as well as cell death of
CC       neural cells.
CC   -!- SUBUNIT: Homodimer; disulfide-linked. Interacts with p75NTR-
CC       associated cell death executor. Interacts with TRAF2, TRAF4 and
CC       TRAF6.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- PTM: N- AND O-glycosylated.
CC   -!- PTM: Phosphorylated on serine residues.
CC   -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC   -!- SIMILARITY: Contains 1 death domain.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M14764; AAB59544.1; -.
DR   EMBL; M21621; AAA36363.1; -.
DR   PIR; A25218; GQHUN.
DR   HSSP; P07174; 1NGR.
DR   Genew; HGNC:7809; NGFR.
DR   MIM; 162010; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0004888; F:transmembrane receptor activity; TAS.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00531; death; 1.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 4.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   Receptor; Apoptosis; Neurogenesis; Transmembrane; Glycoprotein;
KW   Repeat; Phosphorylation; Signal.
FT   SIGNAL       1    28
FT   CHAIN       29   427       TUMOR NECROSIS FACTOR RECEPTOR
FT                               SUPERFAMILY MEMBER 16.
FT   DOMAIN       29   250       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    251   272       POTENTIAL.
FT   DOMAIN      273   427       CYTOPLASMIC (POTENTIAL).
FT   REPEAT       31    64       TNFR-CYS 1.
FT   REPEAT       66   107       TNFR-CYS 2.
FT   REPEAT      108   146       TNFR-CYS 3.
FT   REPEAT      148   188       TNFR-CYS 4.
FT   DOMAIN      344   421       DEATH.
FT   DOMAIN      197   248       SER/THR-RICH.
FT   DISULFID     32    43       BY SIMILARITY.
FT   DISULFID     44    57       BY SIMILARITY.
FT   DISULFID     47    64       BY SIMILARITY.
FT   DISULFID     67    83       BY SIMILARITY.
FT   DISULFID     86    99       BY SIMILARITY.
FT   DISULFID     89   107       BY SIMILARITY.
FT   DISULFID    109   122       BY SIMILARITY.
FT   DISULFID    125   138       BY SIMILARITY.
FT   DISULFID    128   146       BY SIMILARITY.
FT   DISULFID    149   164       BY SIMILARITY.
FT   DISULFID    167   180       BY SIMILARITY.
FT   DISULFID    170   188       BY SIMILARITY.
FT   CARBOHYD     60    60       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   427 AA;  45183 MW;  B09FA143FB3D625B CRC64;

  Query Match           9.1%;  Score 236;  DB 1;  Length 427;
  Best Local Similarity  22.9%;  Pred. No. 2.8e-08;
  Matches  111;  Conservative   62;  Mismatches  194;  Indels  118;  Gaps   22;

Qy          7 PGLLLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCTKCHKGT 66
              | ||| |:|   |     |                  || | | |   | ||  |: |
Db         13 PRLLLLLLLGVSLGGAKEA-----------------CPTGLYTH---SGECCKACNLGE 51

Qy         67 YLYNDCPGPGRDTDCRVCAPG-TYTALENHLRRCLSCSRCRDEMFQVEISPCVVDRDTVC 125
               :  |     | |  |    |:: : :    |  |: |     |   :|||   | ||
Db.        52 GVAQPC--GANQTVCEPCLDSVTFSDVVSATEPCKPCTECVG--LQSMSAPCVEADDAVC 107

Qy        126 GCRKNQYREYWGETGFRCLNCSLCPNGT-VNIPCQERQDTIC-HCHMGFFLKGAK----C 179
              |    |  |  ||  ||  | :|  |: :   ||::|:|:|  |  | : |     |
Db        108 RC---AYGYYQDETTGRCEACRVCEAGSGLVFSCQDKQNTVCEECPDGTYSDEANHVDPC 164

Qy        180 ISCHDCK-------------NKECEKLCPTR------PSTGKDSQDPGTTVLLPLVIVFG 220
              : |  |:             : |||:: | |      |  | ||  | |    |
Db        165 LPCTVCEDTERQLRECTRWADAECEEI-PGRWITRSTPPEGSDSTAPSTQE--PEAPPEQ 221

Qy        221 LCLASFASVVLACRYQRWKPKLYSIICGQSTLVKEGEPELLVPAPGFNPTTTICFSSTPS 280
              :||  : |:           :::     :|  |  : |:|           : |  :
Db        222 DLIASTVAGVVT----------TVMGSSQPVVTRGTTDNLIPV----------YCSILA 260

Qy        281 SSPVSIPPYI------SCDRSNFGAVASPSSETAPP-----HLKAGPILPGPPASTHLCT 329
              :  | :  ||      || ::  || : | ::| ||      |  :|  :     | |
Db        261 AVVVGLVAYIAFKRWNSCKQNKQGANSRPVNQTPPPEGEKLHSDSG--ISVDSQSLHDQQ 318

Qy        330 PGPPASTHLCTPGPPASTHLCTPVQKWEASAPSAPDQLADADPATLYAVVDGVPPSRWKE 389
              |.   ::     |    .  | :: |                    :::|    |:
Db        319 PHTQTASGQALKGDGGLYSSLPPAKREEVE----------------KLLNGSAGDTWRH 361

Qy        390 LVRRLGLS-EHEIERLELENGRHLREAQYSMLAAWRRRTPRREATLELLGRVLRDMDLLG 448
              |  ||   ||      :::  |      ::||:|     :  |||: |   || :
Db        362 LAGELGYQPEH------IDSFTHEACPVRALLASW---ATQDSATLDALLAALRRIQRAD 412

Qy        449 CLENI 453
               :|::
Db        413 LVESL 417


RESULT 11
TR16_RAT
ID   TR16_RAT       STANDARD;      PRT;   425 AA.
AC   P07174;
DT   01-APR-1988 (Rel. 07, Created)
DT   01-APR-1988 (Rel. 07, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 16 precursor (Low-
DE   affinity nerve growth factor receptor) (NGF receptor) (Gp80-LNGFR)
DE   (p75 ICD) (Low affinity neurotrophin receptor p75NTR).
GN   NGFR OR TNFRSF16.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87115859; PubMed=3027580;
RA   Radeke M.J., Misko T.P., Hsu C., Herzenberg L.A., Shooter E.M.;
RT   "Gene transfer and molecular cloning of the rat nerve growth factor
RT   receptor.";
RL   Nature 325:593-597(1987).
RN   [2]
RP   SEQUENCE OF 1-22 FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=93077038; PubMed=1446821;
RA   Metsis M., Timmusk T., Allikmets R., Saarma M., Persson H.;
RT   "Regulatory elements and transcriptional regulation by testosterone
RT   and retinoic acid of the rat nerve growth factor receptor promoter.";
RL   Gene 121:247-254(1992).
RN   [3]
RP   STRUCTURE BY NMR OF 334-418.
RX   MEDLINE=97449145; PubMed=9305641;
RA   Liepinsh E., Ilag L.L., Otting G., Ibanez C.F.;
RT   "NMR structure of the death domain of the p75 neurotrophin receptor.";
RL   EMBO J. 16:4999-5005(1997).
CC   -!- FUNCTION: Low affinity receptor which can bind to NGF, BDNF, NT-3,
CC       and NT-4. Can mediate cell survival as well as cell death of
CC       neural cells.
CC   -!- SUBUNIT: Homodimer; disulfide-linked. Interacts with p75NTR-
CC       associated cell death executor. Interacts with TRAF2, TRAF4 and
CC       TRAF6 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- PTM: N- AND O-glycosylated.
CC   -!- PTM: Phosphorylated on serine residues.
CC   -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC   -!- SIMILARITY: Contains 1 death domain.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X05137; CAA28783.1; -.
DR   EMBL; X61269; -; NOT_ANNOTATED_CDS.
DR   PIR; A26431; A26431.
DR   PDB; 1NGR; 29-JUL-97.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00531; death; 1.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 4.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   Receptor; Apoptosis; Neurogenesis; Transmembrane; Glycoprotein;
KW   Repeat; Phosphorylation; Signal; 3D-structure.
FT   SIGNAL       1     29
FT   CHAIN       30    425       TUMOR NECROSIS FACTOR RECEPTOR
FT                               SUPERFAMILY MEMBER 16.
FT   DOMAIN      30    251       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   252    273       POTENTIAL.
FT   DOMAIN     274    425       CYTOPLASMIC (POTENTIAL).
FT   REPEAT      32     65       TNFR-CYS 1.
FT   REPEAT      67    108       TNFR-CYS 2.
FT   REPEAT     109    147       TNFR-CYS 3.
FT   REPEAT     149    189       TNFR-CYS 4.
FT   DOMAIN     354    419       DEATH.
FT   DOMAIN     198    249       SER/THR-RICH.
FT   DISULFID    33     44       BY SIMILARITY.
FT   DISULFID    45     58       BY SIMILARITY.
FT   DISULFID    48     65       BY SIMILARITY.
FT   DISULFID    68     84       BY SIMILARITY.
FT   DISULFID    87    100       BY SIMILARITY.
FT   DISULFID    90    108       BY SIMILARITY.
FT   DISULFID   110    123       BY SIMILARITY.
FT   DISULFID   126    139       BY SIMILARITY.
FT   DISULFID   129    147       BY SIMILARITY.
FT   DISULFID   150    165       BY SIMILARITY.
FT   DISULFID   168    181       BY SIMILARITY.
FT   DISULFID   171    189       BY SIMILARITY.
FT   CARBOHYD    61     61       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    71     71       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   425 AA;  45432 MW;  B2E152D94D3827F8 CRC64;

  Query Match             8.7%;  Score 227.5;  DB 1;  Length 425;
  Best Local Similarity   23.4%;  Pred. No. 9.8e-08;
  Matches  107;  Conservative   59;  Mismatches  169;  Indels  123;  Gaps   24;

Qy         44 CPQGKYNHPQNSTICCTKCHKGTYLYNDCPGPGRDTDCRVCAPG-TYTALENHLRRCLSC 102
              |  | | |   | ||  |: |  :   |      | | |    |:: : :   | |
Db         33 CSTGLYTH---SGECCKACNLGEGVAQPC--GANQTVCEPCLDNVTFSDVVSATEPCKPC 87

Qy        103 SRCRDEMFQVEISPCVVDRDTVCGCRKNQYREYWGETGFRCLNCSLCPNGT-VNIPCQER 161
              : |     |  :|||  | || |    |::  |||  |  ||:|  |: :  ||::
Db         88 TECLG--LQSMSAPCVEADDAVCRCAYGYYQD--EETG-HCEACSVCEVGSGLVFSCQDK 142

Qy        162 QDTIC-HCHMGFFLKGAK----CISCHDCKNKECEKLCPTRPSTGKDSQD-PGTTVLLPL 215
              |:|:|  |  | :   |      |: |  |:: |  :|    |    : :: ||
Db        143 QNTVCEECPEGTYSDEANHVDPCLPCTVCEDTE-RQLRECTPWADAECEEIPG------- 194

Qy        216 VIVFGLCLASFASVVLACRYQRWKPKLYSIICGQSTLVKEGEPEL-----LVPAPGFNPT 270
                                  || |:        ||     |||:     |||:  :
Db        195 --------------------RWIPRSTPPEGSDSTAPSTQEPEVPPEQDLVPSTVADMV 233

Qy        271 TTICFSSTP-----------------SSSPVSIPPYI------SCDRSNFGAVASPSSE 306
              ||:  || |                 ::  | :  ||      || ::  || : | ::
Db        234 TTVMGSSQPVVTRGTTDNLIPVYCSILAAVVVGLVAYIAFKRWNSCKQNKQGANSRPVNQ 293

Qy        307 TAPP-----HLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPA-----STHLCTPVQKW 356
              | ||     |  :|  :     | |        ||  |    |     : :   |: |
Db        294 TPPPEGEKLHSDSG--ISVDSQSLH------DQQTHTQTASGQALKGDGNLYSSLPLTKR 345

Qy        357 EASAPSAPDQLADADPATLYAVVDGVPPSRWKELVRRLGLS-EHEIERLELENGRHLREA 415
              |       ::| : |                |: |   ||   ||       :::  |
Db        346 E-----EVEKLLNGD-------------TWRHLAGELGYQPEH------IDSFTHEACP 380

Qy        416 QYSMLAAWRRRTPRREATLELLGRVLRDMDLLGCLENI 453
               ::||:|  :     |||: |   || :     :|::
Db        381 VRALLASWGAQD---SATLDALLAALRRIQRADIVESL 415


RESULT 12
TR16_MOUSE
ID   TR16_MOUSE     STANDARD;      PRT;   417 AA.
AC   Q9Z0W1;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 16 precursor (Low-
DE   affinity nerve growth factor receptor) (NGF receptor) (Low affinity
DE   neurotrophin receptor p75NTR).
GN   NGFR OR TNFRSF16.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A;
RX   MEDLINE=99077793; PubMed=9857182;
RA   Tuffereau C., Benejean J., Blondel D., Kieffer B., Flamand A.;
RT   "Low-affinity nerve-growth factor receptor (p75NTR) can serve as a
RT   receptor for rabies virus.";
RL   EMBO J. 17:7250-7259(1998).
CC   -!- FUNCTION: Low affinity receptor which can bind to NGF, BDNF, NT-3,
```

```
CC       AND NT-4. Can mediate cell survival as well as cell death of
CC       neural cells (By similarity). Binds to rabies virus glycoprotein
CC       Gs.
CC   -!- SUBUNIT: Homodimer; disulfide-linked. Interacts with p75NTR-
CC       associated cell death executor. Interacts with TRAF2, TRAF4 and
CC       TRAF6 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC   -!- PTM: N- AND O-glycosylated (By similarity).
CC   -!- PTM: Phosphorylated on serine residues (By similarity).
CC   -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC   -!- SIMILARITY: Contains 1 death domain.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF105292; AAD17943.1; -.
DR   HSSP; P07174; 1NGR.
DR   MGD; MGI:97323; Ngfr.
DR   GO; GO:0005035; F:death receptor activity; IDA.
DR   GO; GO:0005515; F:protein binding activity; IPI.
DR   GO; GO:0007411; P:axon guidance; IMP.
DR   GO; GO:0007417; P:central nervous system development; IMP.
DR   GO; GO:0006917; P:induction of apoptosis; IDA.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00531; death; 1.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 4.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   Receptor; Apoptosis; Neurogenesis; Transmembrane; Glycoprotein;
KW   Repeat; Signal.
FT   SIGNAL        1     21       BY SIMILARITY.
FT   CHAIN        22    417       TUMOR NECROSIS FACTOR RECEPTOR
FT                                SUPERFAMILY MEMBER 16.
FT   DOMAIN       22    246       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    247    265       POTENTIAL.
FT   DOMAIN      266    417       CYTOPLASMIC (POTENTIAL).
FT   REPEAT       24     57       TNFR-CYS 1.
FT   REPEAT       59    100       TNFR-CYS 2.
FT   REPEAT      101    139       TNFR-CYS 3.
FT   REPEAT      141    181       TNFR-CYS 4.
FT   DOMAIN      346    411       DEATH.
FT   DOMAIN      190    241       SER/THR-RICH.
FT   DISULFID     25     36       BY SIMILARITY.
FT   DISULFID     37     50       BY SIMILARITY.
FT   DISULFID     40     57       BY SIMILARITY.
FT   DISULFID     60     76       BY SIMILARITY.
FT   DISULFID     79     92       BY SIMILARITY.
FT   DISULFID     82    100       BY SIMILARITY.
FT   DISULFID    102    115       BY SIMILARITY.
FT   DISULFID    118    131       BY SIMILARITY.
FT   DISULFID    121    139       BY SIMILARITY.
FT   DISULFID    142    157       BY SIMILARITY.
FT   DISULFID    160    173       BY SIMILARITY.
FT   DISULFID    163    181       BY SIMILARITY.
FT   CARBOHYD     53     53       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   417 AA;  44686 MW;  5D7A4510DB8AF9B2 CRC64;

  Query Match             8.5%;  Score 221.5;  DB 1;  Length 417;
  Best Local Similarity   23.1%;  Pred. No. 2.3e-07;
  Matches  106;  Conservative   63;  Mismatches  166;  Indels  123;  Gaps   26;

Qy         44 CPQGKYNHPQNSTICCTKCHKGTYLYNDCPGPGRDTDCRVCAPG-TYTALENHLRRCLSC 102
              |  | | |   |  ||  |: |  :   |      | | |   |:: : :    | |
Db         25 CSTGMYTH---SGECCKACNLGEGVAQPC--GANQTVCEPCLDSVTFSDVVSATEPCKPC 79

Qy        103 SRCRDEMFQVEISPCVVDRDTVCGCRKNQYREYWGETGFRCLNCSLCPNGT-VNIPCQER 161
              : |     |   :|||   | || |    |::   ||| ||  ||:|  |: :   ||::
Db         80 TECLG--LQSMSAPCVEADDAVCRCSYGYYQD--EETG-RCEACSVCGVGSGLVFSCQDK 134

Qy        162 QDTIC-HCHMGPFLKGAK----CISCHDCK------------NKECEKLCPTR------ 197
              |:|:|  | | :   |      |: |  |:             : |||:: | |
Db        135 QNTVCEECPEGTYSDEANHVDPCLPCTVCEDTERQLRECTPWADAECEEI-PGRWITRST 193

Qy        198 PSTGKD-----SQDPGTTVLLPLVIVFGLCLASFASVVLACRYQRWKPKLYSIICGQSTL 252
              | | |     :|:|       |:          || |             : :::     :
Db        194 PPEGSDVTTPSTQEPEAPPERDLI----------ASTV--------ADTVTTVMGSSQPV 235

Qy        253 VKEGEPELLVPAPGFNPTTTICFSSTPSSSPVSIPPYI------SCDRSNFGAVASPSSE 306
              | | : |:|           : |  ::  | :  ||       || ::  || : | ::
Db        236 VTRGTADNLIPV----------YCSILAAVVVGLVAYIAFKRWNSCKQNKQGANSRPVNQ 285

Qy        307 TAPP-----HLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPA-----STHLCTPVQKW 356
              | ||     | :|  :     | |          ||  |     |     : :   |: |
Db        286 TPPPEGEKLHSDSG--ISVDSQSLH------DQQTHTQTASAQALKGDGNLYSSLPLTKR 337

Qy        357 EASAPSAPDQLADADPATLYAVVDGVPPSRWKELVRRLGLS-EHEIERLELENGRHLREA 415
              |       ::| : |             |: |   ||   ||        ::: |
Db        338 E-----EVEKLLNGD-------------TWRHLAGELGYQPEH------IDSFTHEACP 372

Qy        416 QYSMLAAWRRRTPRREATLELLGRVLRDMDLLGCLENI 453
                ::||:|  :    |||: |   || :    :|::
Db        373 VRALLASWGAQD---SATLDALLAALRRIQRADIVESL 407


RESULT 13
TR16_CHICK
ID   TR16_CHICK     STANDARD;      PRT;   416 AA.
AC   P18519;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 16 precursor (Low-
DE   affinity nerve growth factor receptor) (NGF receptor) (Gp80-LNGFR)
DE   (p75 ICD) (Low affinity neurotrophin receptor p75NTR).
GN   NGFR OR TNFRSP16.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=90166579; PubMed=2560385;
RA   Large T.H., Weskamp G., Helder J.C., Radeke M.J., Misko T.P.,
RA   Shooter E.M., Reichardt L.F.;
RT   "Structure and developmental expression of the nerve growth factor
RT   receptor in the chicken central nervous system.";
RL   Neuron 2:1123-1134(1989).
RN   [2]
RP   SEQUENCE OF 21-416 FROM N.A.
RX   MEDLINE=90152140; PubMed=2154393;
RA   Heuer J.G., Fatemie-Nainie S., Wheeler E.F., Bothwell M.;
RT   "Structure and developmental expression of the chicken NGF receptor.";
RL   Dev. Biol. 137:287-304(1990).
CC   -!- FUNCTION: Low affinity receptor which can bind to NGF, BDNF, NT-3,
CC       and NT-4. Can mediate cell survival as well as cell death of
CC       neural cells (By similarity).
CC   -!- SUBUNIT: Homodimer; disulfide-linked. Interacts with p75NTR-
CC       associated cell death executor. Interacts with TRAF2, TRAF4 and
CC       TRAF6 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- PTM: N- AND O-glycosylated.
CC   -!- PTM: Phosphorylated on serine residues.
CC   -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC   -!- SIMILARITY: Contains 1 death domain.
DR   PIR; JN0006; JN0006.
```

```
DR   HSSP; P07174; 1NGR.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00531; death; 1.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   Receptor; Apoptosis; Neurogenesis; Transmembrane; Glycoprotein;
KW   Repeat; Phosphorylation; Signal.
FT   SIGNAL        1     19       POTENTIAL.
FT   CHAIN        20    416       TUMOR NECROSIS FACTOR RECEPTOR
FT                                SUPERFAMILY MEMBER 16.
FT   DOMAIN       29    239       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    240    261       POTENTIAL.
FT   DOMAIN      262    416       CYTOPLASMIC (POTENTIAL).
FT   REPEAT       23     57       TNFR-CYS 1.
FT   REPEAT       58     99       TNFR-CYS 2.
FT   REPEAT      100    138       TNFR-CYS 3.
FT   REPEAT      140    180       TNFR-CYS 4.
FT   DOMAIN      333    410       DEATH.
FT   DOMAIN      188    236       SER/THR-RICH.
FT   DISULFID     24     35       BY SIMILARITY.
FT   DISULFID     36     49       BY SIMILARITY.
FT   DISULFID     39     56       BY SIMILARITY.
FT   DISULFID     59     75       BY SIMILARITY.
FT   DISULFID     78     91       BY SIMILARITY.
FT   DISULFID     81     99       BY SIMILARITY.
FT   DISULFID    101    114       BY SIMILARITY.
FT   DISULFID    117    130       BY SIMILARITY.
FT   DISULFID    120    138       BY SIMILARITY.
FT   DISULFID    141    156       BY SIMILARITY.
FT   DISULFID    159    172       BY SIMILARITY.
FT   DISULFID    162    180       BY SIMILARITY.
FT   CARBOHYD     52     52       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT     36     36       C -> Y (IN REF. 2).
FT   CONFLICT    173    173       T -> K (IN REF. 2).
FT   CONFLICT    276    276       N -> S (IN REF. 2).
FT   CONFLICT    396    396       K -> R (IN REF. 2).
SQ   SEQUENCE   416 AA;  44654 MW;  6BCEAAB54F4D2D56 CRC64;

  Query Match             8.5%;  Score 220;  DB 1;  Length 416;
  Best Local Similarity   23.3%;  Pred. No. 2.9e-07;
  Matches  116;  Conservative   46;  Mismatches  168;  Indels  168;  Gaps   25;

Qy          6 VPGLLLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCTKCHKG 65
              || ||| |           |||     |  |  ||    |    |     |  ||  |: |
Db          5 VPLLLLLL----------PAG-----PTWGSKEK----CLTKMYT---TSGECCKACNLG 42

Qy         66 TYLYNDCPGPGRDTDCRVCAPG-TYTALENHLRRCLSCSRCRDEMFQVEISPCVVDRDTV 124
               :  |       | | |    ||:   :     |  |::|          :|||   | |
Db         43 EGVVQPC--GVNQTVCEPCLDSVTYSDTVSATEPCKPCTQCVG--LHSMSAPCVESDDAV 98

Qy        125 CGCRKNQYREYWGETGFRCLNCSLCPNG-TVNIPCQERQDTIC-HCHMGFFLKGAK---- 178
              | |    |  :  |    |  ||:|  |  :  ||:: |||:|  |  | | |    |
Db         99 CRC---AYGYFQDELSGSCKECSICEVGPGLMFPCRDSQDTVCEECPEGTFSDEANFVDP 155

Qy        179 CISCHDCK------------NKECEKLCP-----TRPSTGKDSQDPGT----------T 210
              |: |  |:             : ||  | |     |   | || :| |          |
Db        156 CLPCTICEENEVMVKECTATSDAECRDLHPRWTTHTPSLAGSDSPEPITRDPFNTEGMAT 215

Qy        211 VLLPLVIVFGLCLASFASVVLACRYQRWKPKLYSIICGQSTLVKEGEPELLVPAPGFNPT 270
              |  :|                              :::     :|  |  : |:|
Db        216 TLADIVT-------------------------TVMGSSQPVVSRGTADNLIPV------ 243

Qy        271 TTICFSSTPSSSPVSIPPYI------SCDRSNFGAVASPSSETAPP-----HLKAGPILP 319
                :|  ::  | :  ||      || ::  ||   | ::|  |     |  :|  :
Db        244 ----YCSILAAVVVGLVAYIAFKRWNSCKQNKQGANNRPVNQTPSPEGEKLHSDSGISVD 299

Qy        320 GPPASTHLCTPGPPASTHLCTPGPPASTHLCTPVQKWEASAPSAPDQLADADPATLYAVV 379
                  |  |    ||  :   | ||                              |     :|||

Db        300 ----SQSLHDQQPPNQS---TQGP-----------------------APKGDGSLYA-- 326

Qy        380 DGVPPSR---------------WKELVRRLGLSEHEIERLELENGRHLREAQYSMLAAWR 424
                :|||:                |::|   ||  |  |:  |              ::|| |
Db        327 -SLPPSKQEEVEKLLSSSAEETWRQLAGELGYKEDLIDCFTRE-----ESPARALLADW- 379

Qy        425 RRTPRREATLELLGRVLR 442
                : :  |||: |   ||
Db        380 --SAKETATLDALLVALR 395


RESULT 14
TR1B_HUMAN
ID   TR1B_HUMAN     STANDARD;      PRT;   461 AA.
AC   P20333; Q16042; Q9UIH1;
DT   01-FEB-1991 (Rel. 17, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 1B precursor (Tumor
DE   necrosis factor receptor 2) (p80) (TNF-R2) (p75) (CD120b) (Etanercept)
DE   [Contains: Tumor necrosis factor binding protein 2 (TBPII)].
GN   TNFRSF1B OR TNFR2 OR TNFBR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90260639; PubMed=2160731;
RA   Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy R.,
RA   Dower S.K., Cosman D., Goodwin R.G.;
RT   "A receptor for tumor necrosis factor defines an unusual family of
RT   cellular and viral proteins.";
RL   Science 248:1019-1023(1990).
RN   [2]
RP   SEQUENCE FROM N.A., AND VARIANT ARG-196.
RX   MEDLINE=91045991; PubMed=2172983;
RA   Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W.,
RA   Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.;
RT   "A second tumor necrosis factor receptor gene product can shed a
RT   naturally occurring tumor necrosis factor inhibitor.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96299745; PubMed=8661109;
RA   Beltinger C.P., White P.S., Maris J.M., Sulman E.P., Jensen S.J.,
RA   Lepaslier D., Stallard B.J., Goeddel D.V., Desauvage F.J.,
RA   Brodeur G.M.;
RT   "Physical mapping and genomic structure of the human TNFR2 gene.";
RL   Genomics 35:94-100(1996).
RN   [4]
RP   SEQUENCE OF 37-461 FROM N.A.
RX   MEDLINE=91370690; PubMed=1966549;
RA   Dembic Z., Loetscher H., Gubler U., Pan Y.C., Lahm H.-W., Gentz R.,
RA   Brockhaus M., Lesslauer W.;
RT   "Two human TNF receptors have similar extracellular, but distinct
RT   intracellular, domain sequences.";
RL   Cytokine 2:231-237(1990).
RN   [5]
RP   SEQUENCE OF 116-461 FROM N.A., PARTIAL SEQUENCE, AND VARIANT ARG-196.
RX   MEDLINE=90349572; PubMed=2166946;
RA   Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang D.,
RA   Ringold G.M.;
RT   "Complementary DNA cloning of a receptor for tumor necrosis factor
RT   and demonstration of a shed form of the receptor.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990).
RN   [6]
RP   SEQUENCE OF 154-183 FROM N.A., AND VARIANTS ARG-196 AND LYS-232.
RX   MEDLINE=21069356; PubMed=11197692;
RA   Tsuchiya N., Komata T., Matsushita M., Ohashi J., Tokunaga K.;
RT   "New single nucleotide polymorphisms in the coding region of human
RT   TNFR2: association with systemic lupus erythematosus.";
RL   Genes Immun. 1:501-503(2000).
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RN   [7]
RP   SEQUENCE OF 27-31.
RX   MEDLINE=90110215; PubMed=2153136;
RA   Engelmann H., Novick D., Wallach D.;
RT   "Two tumor necrosis factor-binding proteins purified from human
RT   urine. Evidence for immunological cross-reactivity with cell surface
RT   tumor necrosis factor receptors.";
RL   J. Biol. Chem. 265:1531-1536(1990).
RN   [8]
RP   SEQUENCE OF 23-40; 65-69; 136-141; 300-306 AND 346-362.
RX   MEDLINE=91056048; PubMed=2173696;
RA   Loetscher H., Schlaeger E.J., Lahm H.-W., Pan Y.-C.E., Lesslauer W.,
RA   Brockhaus M.;
RT   "Purification and partial amino acid sequence analysis of two
RT   distinct tumor necrosis factor receptors from HL60 cells.";
RL   J. Biol. Chem. 265:20131-20138(1990).
RN   [9]
RP   CHARACTERIZATION.
RX   MEDLINE=93016040; PubMed=1328224;
RA   Pennica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M.,
RA   Lipari M.T., Goeddel D.V.;
RT   "Biochemical properties of the 75-kDa tumor necrosis factor receptor.
RT   Characterization of ligand binding, internalization, and receptor
RT   phosphorylation.";
RL   J. Biol. Chem. 267:21172-21178(1992).
RN   [10]
RP   INTERACTION WITH TRAF2.
RX   MEDLINE=94349371; PubMed=8069916;
RA   Rothe M., Wong S.C., Henzel W.J., Goeddel D.V.;
RT   "A novel family of putative signal transducers associated with the
RT   cytoplasmic domain of the 75 kDa tumor necrosis factor receptor.";
RL   Cell 78:681-692(1994).
RN   [11]
RP   X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 419-428 IN COMPLEX WITH
RP   TRAF2.
RX   MEDLINE=99221490; PubMed=10206649;
RA   Park Y.C., Burkitt V., Villa A.R., Tong L., Wu H.;
RT   "Structural basis for self-association and receptor recognition of
RT   human TRAF2.";
RL   Nature 398:533-538(1999).
CC   -!- FUNCTION: Receptor with high affinity for TNFSF2/TNF-alpha and
CC       approximately 5-fold lower affinity for homotrimeric
CC       TNFSF1/lymphotoxin-alpha. The TRAF1/TRAF2 complex recruits the
CC       apoptotic suppressors BIRC2 and BIRC3 to TNFRSF1B/TNFR2.
CC   -!- SUBUNIT: Binds to TRAF2.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein and secreted.
CC   -!- PTM: Phosphorylated; mainly on serine residues and with a very low
CC       level on threonine residues.
CC   -!- PTM: A soluble form (tumor necrosis factor binding protein 2) is
CC       produced from the membrane form by proteolytic processing.
CC   -!- PHARMACEUTICAL: Available under the name Enbrel (Immunex and
CC       Wyeth-Ayerst). Used to treat moderate to servere rheumatoid
CC       arthritis (RA). Enbrel consist of the extracellular ligand-binding
CC       portion of TNFR2 linked to an Immuglobulin Fc chain. It binds to
CC       TNF-alpha and blocks its interactions with receptors.
CC   -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC   -!- DATABASE: NAME=PROW; NOTE=CD guide CD120b entry;
CC       WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd120b.htm".
CC   -!- DATABASE: NAME=Enbrel; NOTE=Clinical information on Enbrel;
CC       WWW="http://www.enbrel.com/".
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit. institutions as long as its content is in no way
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M32315; AAA59929.1; -.
DR   EMBL; U52165; AAC50622.1; -.
DR   EMBL; U52156; AAC50622.1; JOINED.
DR   EMBL; U52157; AAC50622.1; JOINED.
DR   EMBL; U52158; AAC50622.1; JOINED.
DR   EMBL; U52159; AAC50622.1; JOINED.
DR   EMBL; U52160; AAC50622.1; JOINED.
DR   EMBL; U52161; AAC50622.1; JOINED.
DR   EMBL; U52162; AAC50622.1; JOINED.
DR   EMBL; U52163; AAC50622.1; JOINED.
DR   EMBL; U52164; AAC50622.1; JOINED.
DR   EMBL; M55994; AAA36755.1; -.
DR   EMBL; S63368; AAB19824.2; -.
DR   EMBL; M35857; AAA63262.1; -.
DR   EMBL; AB030950; BAA89053.1; -.
DR   PIR; A35356; A35356.
DR   PDB; 1CA9; 12-APR-99.
DR   Genew; HGNC:11917; TNFRSF1B.
DR   MIM; 191191; -.
DR   GO; GO:0005031; F:tumor necrosis factor receptor activity; TAS.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
KW   Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal;
KW   Phosphorylation; Pharmaceutical; Polymorphism; 3D-structure.
FT   SIGNAL       1    22
FT   CHAIN       23   461       TUMOR NECROSIS FACTOR RECEPTOR
FT                               SUPERFAMILY MEMBER 1B, MEMBRANE FORM.
FT   CHAIN       27     ?       TUMOR NECROSIS FACTOR BINDING PROTEIN 2.
FT   DOMAIN      23   257       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   258   287       POTENTIAL.
FT   DOMAIN     288   461       CYTOPLASMIC (POTENTIAL).
FT   REPEAT      39    76       TNFR-CYS 1.
FT   REPEAT      77   118       TNFR-CYS 2.
FT   REPEAT     119   162       TNFR-CYS 3.
FT   REPEAT     163   201       TNFR-CYS 4.
FT   DISULFID    40    53       BY SIMILARITY.
FT   DISULFID    54    67       BY SIMILARITY.
FT   DISULFID    57    75       BY SIMILARITY.
FT   DISULFID    78    93       BY SIMILARITY.
FT   DISULFID    96   110       BY SIMILARITY.
FT   DISULFID   100   118       BY SIMILARITY.
FT   DISULFID   120   126       BY SIMILARITY.
FT   DISULFID   134   143       BY SIMILARITY.
FT   DISULFID   137   161       BY SIMILARITY.
FT   DISULFID   164   179       BY SIMILARITY.
FT   CARBOHYD   171   171       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   193   193       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT    196   196       M -> R.
FT                               /FTId=VAR_015434.
FT   VARIANT    232   232       E -> K.
FT                               /FTId=VAR_015435.
FT   CONFLICT   141   141       R -> P (IN REF. 5).
FT   CONFLICT   363   363       A -> T (IN REF. 5).
SQ   SEQUENCE   461 AA;  48291 MW;  603D0AE1CD69ACBF CRC64;

  Query Match             7.6%;  Score 199;  DB 1;  Length 461;
  Best Local Similarity   25.3%;  Pred. No. 7e-06;
  Matches   77;  Conservative   26;  Mismatches  103;  Indels   98;  Gaps   14;

Qy         32 PHPGDLEKRESPCPQGKYNHPQNSTICCTKCHKGTYLYNDCPGPGRDTDCRVCAPGTYTA 91
              | ||      | |   :| : | : :||:||  | :    |     || |  |   |||
Db         34 PEPG------STCRLREY-YDQTAQMCCSKCSPGQHAKVFCTKTS-DTVCDSCEDSTYTQ 85

Qy         92 LENHLRRCLSC-SRCRDEMFQVEISPCVVDRDTVCGCRKNQYREYWGETGFRCLNCSLC- 149
              | | :  |||| |||  :  |||   |  ::: :| ||   |     : |    | ||
Db         86 LWNWVPECLSCGSRCSSD--QVETQACTREQNRICTCRPGWYCALSKQEG-----CRLCA 138

Qy        150 ------PNGTVNIPCQERQDTICHCHMGFFLKGAKCISCHDCKNKECEKLCPTRPSTGKD 203
                   |   | | |  | :|                      | |
Db        139 PLRKCRPGFGVARPGTETSDVVC--------------------KPCA------------ 165

Qy        204 SQDPGTTVLLPLVIVFGLCLASFASVVLACRYQRWKPKLYSIICGQSTLVKEGEPELLVP 263
                 |||                ::  |    ||  :       ||             :|
Db        166 ---PGT------------FSNTTSSTDICRPHQ--------ICN------------VVA 189
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Qy        264 APGFNPTTTICFSSTPSSS----PVSIPPYISCDRSNPGAVASPSSETAPPHLKAGPILP 319
              ||      :| |::|: |     | :|  :|    :     ||  |||      |: |
Db        190 IPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPS--TAPSTSFLLPMGP 247

Qy        320 GPPA 323
              |||
Db        248 SPPA 251


RESULT 15
TR23_MOUSE
ID   TR23_MOUSE     STANDARD;      PRT;   176 AA.
AC   Q9ER63; Q8VHC0;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 23 (Tumor necrosis
DE   factor receptor p60 homolog 1) (TNF receptor family member SOB).
GN   TNFRSF23 OR TNFRSF1AL1 OR TNFRH1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/Sv; TISSUE=Embryonic stem cells;
RX   MEDLINE=20519229; PubMed=11063728;
RA   Engemann S., Stroedicke M., Paulsen M., Franck O., Reinhardt R.,
RA   Lane N., Reik W., Walter J.;
RT   "Sequence and functional comparison in the Beckwith-Wiedemann region:
RT   implications for a novel imprinting centre and extended imprinting.";
RL   Hum. Mol. Genet. 9:2691-2706(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Pan G., Mao W., Risser P.;
RT   "Characterization of SOB, a member of the TNFR family.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC   -!- TISSUE SPECIFICITY: Ubiquitous.
CC   -!- SIMILARITY: Contains 3 TNFR-Cys repeats.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   ---------------------------------------------------------------------
DR   EMBL; AJ278264; CAC16405.1; -.
DR   EMBL; AJ276505; CAC27352.1; -.
DR   EMBL; AY046550; AAL05072.1; -.
DR   HSSP; P19438; 1EXT.
DR   MGD; MGI:1930269; Tnfrsf23.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 3.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
KW   Receptor; Signal-anchor; Transmembrane; Glycoprotein; Repeat.
FT   DOMAIN        1      9       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM      10     30      SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
FT                                 (POTENTIAL).
FT   DOMAIN        31     176     EXTRACELLULAR (POTENTIAL).
FT   REPEAT        37     72      TNFR-CYS 1.
FT   REPEAT        74     114     TNFR-CYS 2.
FT   REPEAT        115    155     TNFR-CYS 3.
FT   DISULFID      38     49      BY SIMILARITY.
FT   DISULFID      50     63      BY SIMILARITY.
FT   DISULFID      53     72      BY SIMILARITY.
FT   DISULFID      75     90      BY SIMILARITY.
FT   DISULFID      93     106     BY SIMILARITY.
FT   DISULFID      96     114     BY SIMILARITY.
FT   DISULFID      116    131     BY SIMILARITY.
FT   DISULFID      134    147     BY SIMILARITY.
FT   DISULFID      137    155     BY SIMILARITY.
FT   CARBOHYD      148    148     N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   176 AA;  19594 MW;  EE30D617F49DDB7D CRC64;

  Query Match             7.5%;  Score 196;  DB 1;  Length 176;
  Best Local Similarity   31.1%;  Pred. No. 4e-06;
  Matches   51;  Conservative   18;  Mismatches   63;  Indels   32;  Gaps    8;

Qy          9 LLLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCTKCHKGTYL 68
              ||| | || : |           :|      |      || |:|    |:: :||  |  ||::
Db         18 LLLNLFLPVIFA----------MP-----ESYSFNCPDGEY---QSNDVCCKTCPSGTFV 59

Qy         69 YNDCPGPGRDTDCRVCAPGTYTALENHLRRCLSCSRCRDEMFQVEISPCVVDRDTVCGCR 128
               |  |      |  | |||:|  :| |  |  || |  :  |  :: |    |  | | |
Db         60 KAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCSTCDKD--QNMVADCSATSDRKCEC- 116

Qy        129 KNQYREYWGETGF--RCLNCSLCPNGTVNIP----CQERQDTIC 166
              |   |: :  |   |  |: || |   ||     |    :|:|
Db        117 --QIGLYYYDPKFPESCRPCTKCPQG---IPVLQECNSTANTVC 155


Search completed: September 13, 2003, 07:04:40
Job time : 18 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 13, 2003, 07:01:54 ; Search time 39 Seconds
(without alignments)
3116.481 Million cell updates/sec

Title: US-09-970-532-2
Perfect score: 2603
Sequence: 1 MGLPTVPGLLLPLVLPALLA.....NIEEALGGAARLASEPRLLW 471

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1589.5	61.1	446	6	Q95ND3	Q95nd3 felis silve
2	790	30.3	189	6	Q95185	Q95185 felis silve
3	776	29.8	189	6	O97530	O97530 canis famil
4	400.5	15.4	413	11	Q99MM1	Q99mm1 mus musculu
5	360	13.8	387	11	Q8VD70	Q8vd70 mus musculu
6	220.5	8.5	417	11	Q8BYY1	Q8byy1 mus musculu
7	220.5	8.5	427	11	Q8CFT3	Q8cft3 mus musculu
8	211.5	8.1	368	13	O57408	O57408 meleagris g
9	210	8.1	368	13	Q9IAR7	Q9iar7 gallus gall
10	206.5	7.9	387	13	Q9PVD4	Q9pvd4 xenopus lae
11	201.5	7.7	433	11	Q91ZM6	Q91zm6 rattus norv
12	200	7.7	368	13	Q9PW79	Q9pw79 gallus gall
13	199.5	7.7	651	13	Q98SM6	Q98sm6 gallus gall
14	191	7.3	322	12	O72761	O72761 cowpox viru
15	187.5	7.2	302	13	Q9PUS0	Q9pus0 salvelinus
16	187.5	7.2	357	13	Q9DF34	Q9df34 brachydanio
17	185.5	7.1	283	6	Q9XSZ8	Q9xsz8 cercopithec
18	185	7.1	320	12	O57079	O57079 cowpox viru
19	180.5	6.9	401	13	Q9PRG7	Q9prg7 xenopus lae
20	178	6.8	350	12	O57123	O57123 cowpox viru
21	177.5	6.8	267	6	O02764	O02764 oryctolagus
22	176	6.8	347	12	O57119	O57119 cowpox viru
23	176	6.8	351	12	O57121	O57121 cowpox viru
24	175	6.7	360	12	O57118	O57118 cowpox viru
25	174	6.7	316	12	O57092	O57092 ectromelia
26	174	6.7	317	13	Q8JFV6	Q8jfv6 brachydanio
27	174	6.7	320	12	O57091	O57091 ectromelia
28	174	6.7	320	12	O57300	O57300 ectromelia
29	173.5	6.7	289	11	Q8K2X6	Q8k2x6 mus musculu
30	173.5	6.7	347	12	O57115	O57115 cowpox viru
31	173	6.6	459	11	Q62327	Q62327 mus musculu
32	172	6.6	351	12	O57117	O57117 cowpox viru
33	172	6.6	438	13	Q9DFV0	Q9dfv0 brachydanio
34	169.5	6.5	349	12	O57305	O57305 cowpox viru
35	169	6.5	326	12	O57122	O57122 cowpox viru
36	168.5	6.5	482	11	O88734	O88734 mus musculu
37	165	6.3	457	4	Q8IVS6	Q8ivs6 homo sapien
38	164.5	6.3	349	12	O57109	O57109 variola vir
39	164	6.3	547	5	Q8I8V2	Q8i8v2 giardia lam
40	164	6.3	547	5	Q8I8V1	Q8i8v1 giardia lam
41	163.5	6.3	320	6	Q9XS29	Q9xs29 oryctolagus
42	163.5	6.3	348	12	O57112	O57112 variola vir
43	163.5	6.3	349	12	O57111	O57111 variola vir
44	163.5	6.3	349	12	O57098	O57098 camelpox vi
45	163.5	6.3	349	12	O57284	O57284 camelpox vi

ALIGNMENTS

RESULT 1
Q95ND3
ID Q95ND3 PRELIMINARY; PRT; 446 AA.
AC Q95ND3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Tumor necrosis factor type I.
GN TNFR I.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA Mizuno T., Goto Y., Baba K., Masuda K., Ohno K., Tsujimoto H.;
RT "Molecular cloning of feline tumor necrosis factor receptor type I
RT (TNFR I) and expression of TNFR I and TNFR II in various disease in
RT cats.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AB051103; BAB55455.1; -.
DR InterPro; IPR000345; CytC_heme_bind.
DR InterPro; IPR000488; Death.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_c6; 4.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00190; CYTOCHROME_C; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
SQ SEQUENCE 446 AA; 49563 MW; 217BD331DD8A74AA CRC64;

Query Match 61.1%; Score 1589.5; DB 6; Length 446;
Best Local Similarity 66.0%; Pred. No. 1e-125;
Matches 311; Conservative 39; Mismatches 94; Indels 27; Gaps 6;

```
Qy          1 MGLPTVPGLLLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCT 60
              |||||||||| |||| ||| ::|| | ||||| | ||| |||||||| |||:::||||
Db          1 MGLPTVPGLLQPLVLLALLVEIYPLRVTGLVPHLRDREKRAIPCPQGKYIHPQDNSICCT 60

Qy         61 KCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCLSCSRCRDEMFQVEISPCVVD 120
              |||||||||||| ||| ||||| | ||:|| ||:||:|||||:|| ||:||||||| |
Db         61 KCHKGTYLYNDCAGPGLDTDCRECENGTFTASENYLRQCLSCSKCRKEMYQVEISPCTVY 120

Qy        121 RDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQERQDTICHCHMGFFLKGAKCI 180
              |||||||||||| || || |:|||||| |||| | |:| |:|:| || ||||:| :|:
Db        121 RDTVCGCRKNQYRYYWSETHFQCLNCSLCLNGTVQISCKETQNTVCTCHAGFFLRGNECV 180

Qy        181 SCHDC-KNKECEKLCPTRPSTGKDSQDPGTTVLLPLVIVFGLCLASFASVVLACRYQRWK 239
              || :| || || |||      | || |||||||||||| ||:|: || |: | ||||| |
Db        181 SCVNCKKNTECTKLCVPIVETVKDPQDPGTTVLLPLVIFFGICVLSF-SIGLMCRYQRRK 239

Qy        240 PKLYSIICGQSTLVKEGEPELLVPAPGFNPTTTICFSSTPSSSPVSIPPYISCDRSNFGA 299
              ||:||:||:||  |||||: |   |||:|  :  || :|: :|   | :   | :|  |
Db        240 SKLFSIVCGKSTPTKEGEPQPLATGPGFSPIPSPTFSPSPTFTP--SPTFTPSDWANLRA 297

Qy        300 VASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLCTPVQKWEAS 359
              || | | |||:  |||||   |||:                  | |    |||||||  |
Db        298 -ASVSREMAPPYQGAGPILSAAPASS----------------PIS----TPVQKWEDS 334

Qy        360 APSAPDQLADADPATLYAVVDGVPPSRWKELVRRLGLSEHEIERLELENGRHLREAQYSM 419
              :  :  ||||||||||||||||||| ||||||||||||||:||| |||| |||
Db        335 THTQRPEADPADPATLYAVVDGVPPSRWKEFVRRLGLSEHEIERLELQNGRCLREAHYSM 394

Qy        420 LAAWRRRTPRREATLELLGRVLRDMDLLGCLENIEEALGGAARLASEPRLL 470
              |||||||||||||||||||||||||||||:|||||   | |:  ||||
Db        395 LAAWRRRTPRREATLELLGRVLRDMDLLGCLEDIEEALCAPASLSPAPRLL 445


RESULT 2
Q95185
ID   Q95185      PRELIMINARY;      PRT;   189 AA.
AC   Q95185;
DT   01-FEB-1997 (TrEMBLrel. 02, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Tumour necrosis factor receptor p60 (Fragment).
GN   TNFR-1.
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Duthie S., Nasir L., Eckersall P.D.;
RT   "Felis catus tumour necrosis factor receptor p60 (TNFR-1) mRNA,
RT   partial cds.";
RL   Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U72344; AAB95089.1; -.
DR   HSSP; P19438; 1EXT.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 3.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS01186; EGF_2; 1.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
KW   Receptor.
FT   NON_TER     189    189
SQ   SEQUENCE   189 AA;  21420 MW;  F3FBE0CE809D7DBE CRC64;

  Query Match            30.3%;  Score 790;  DB 6;  Length 189;
  Best Local Similarity  73.1%;  Pred. No. 9.2e-59;
  Matches  136;  Conservative   18;  Mismatches   32;  Indels    0;  Gaps    0;

Qy          1 MGLPTVPGLLLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCT 60
              |||||||||| |||| ||| ::|| | ||||| | ||| |||||||| |||:::||||
Db          1 MGLPTVPGLLQPLVLLALLVEIYPLRVTGLVPHLRDREKRAIPCPQGKYIHPQDNSICCT 60

Qy         61 KCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCLSCSRCRDEMFQVEISPCVVD 120
              |||||||||||| ||| ||||| | ||:|| ||:||:|||||:|| ||:||||||| |
Db         61 KCHKGTYLYNDCAGPGLDTDCRECENGTFTASENYLRQCLSCSKCRKEMYQVEISPCTVY 120

Qy        121 RDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQERQDTICHCHMGFFLKGAKCI 180
              |||||||||||| || || |:|||||| |||| | |:| |:|:| || ||||:| :|:
Db        121 RDTVCGCRKNQYRYYWSETHFQCLNCSLCLNGTVQISCKETQNTVCTCHAGFFLRGNECV 180

Qy        181 SCHDC-KNKECEKLCPTRPSTGKDSQDPGTTVLLPLVIVFGLCLASFASVVLACRYQRWK 239
              || :| || || |||      | || |||||||||||| ||:|: || |: | ||||| |
Db        181 SCVNCKKNTECTKLCVPIVETVKDPQDPGTTVLLPLVIFFGICVLSF-SIGLMCRYQRRK 239

Qy        240 PKLYSIICGQSTLVKEGEPELLVPAPGFNPTTTICFSSTPSSSPVSIPPYISCDRSNFGA 299
              ||:||:||:||  |||||: |   |||:|  :  || :|: :|   | :   | :|  |
Db        240 SKLFSIVCGKSTPTKEGEPQPLATGPGFSPIPSPTFSPSPTFTP--SPTFTPSDWANLRA 297

Qy        300 VASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLCTPVQKWEAS 359
              || | | |||:  |||||   |||:                  | |    |||||||  |
Db        298 -ASVSREMAPPYQGAGPILSAAPASS----------------PIS----TPVQKWEDS 334

Qy        360 APSAPDQLADADPATLYAVVDGVPPSRWKELVRRLGLSEHEIERLELENGRHLREAQYSM 419
              :  :  ||||||||||||||||||| ||||||||||||||:||| |||| |||
Db        335 THTQRPEADPADPATLYAVVDGVPPSRWKEFVRRLGLSEHEIERLELQNGRCLREAHYSM 394

Qy        420 LAAWRRRTPRREATLELLGRVLRDMDLLGCLENIEEALGGAARLASEPRLL 470
              |||||||||||||||||||||||||||||:|||||   | |:  ||||
Db        395 LAAWRRRTPRREATLELLGRVLRDMDLLGCLEDIEEALCAPASLSPAPRLL 445


RESULT 3
O97530
ID   O97530      PRELIMINARY;      PRT;   189 AA.
AC   O97530;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Tumor necrosis factor receptor p60 (Fragment).
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=21109092; PubMed=11182158;
RA   Campbell S.E., Nasir L., Argyle D.J., Gault E.A., Duthie S.,
RA   Bennett D.;
RT   "Cloning of canine IL-1ra, TNFR and TIMP-2.";
RL   Vet. Immunol. Immunopathol. 78:207-214(2001).
DR   EMBL; AF013955; AAD01516.1; -.
DR   HSSP; P19438; 1TNR.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 3.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS01186; EGF_2; 1.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor.
FT   NON_TER     189    189
SQ   SEQUENCE   189 AA;  21324 MW;  5D3AD6A5676BFE99 CRC64;

  Query Match            29.8%;  Score 776;  DB 6;  Length 189;
  Best Local Similarity  73.1%;  Pred. No. 1.4e-57;
  Matches  136;  Conservative   15;  Mismatches   35;  Indels    0;  Gaps    0;

Qy          1 MGLPTVPGLLLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCT 60
              |||||||||||||||| ||| ::|| | ||||| : || |||||| |||: :||||
Db          1 MGLPTVPGLLLPLVLLALLLEIYPISVTALVPHPRNRVKRAILCPQGKYIHPQDDSICCT 60

Qy         61 KCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCLSCSRCRDEMFQVEISPCVVD 120
              |||||||||||||||| ||||| | ||:|| |||||:|||||:|| || ||||||| | .
Db         61 KCHKGTYLYNDCPGPGLDTDCRECENGTFTASENHLRQCLSCSKCRKEMNQVEISPCTVY 120

Qy        121 RDTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVNIPCQERQDTICHCHMGFFLKGAKCI 180
              |||||||||||| || || |:| ||||| |||| | |||:|:||| || ||||:  :|:
Db        121 RDTVCGCRKNQYRFYWSETLFQCNNCSLCLNGTVQISCQEKQNTICTCHAGFFLREHECV 180

Qy        181 SCHDCK 186
              || :||
Db        181 SCVNCK 186


RESULT 4
Q99MM1
ID   Q99MM1      PRELIMINARY;      PRT;   413 AA.
AC   Q99MM1;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
```

```
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   WSL-1-like protein.
GN   TNFRSF25 OR TNFRSF12.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/Sv;
RX   MEDLINE=21158384; PubMed=11261933;
RA   Wang E.C.Y., Kitson J., Thern A., Williamson J., Farrow S.N.,
RA   Owen M.J.;
RT   "Genomic structure, expression, and chromosome mapping of the mouse
RT   homologue for the WSL-1 (DR3, Apo3, TRAMP, LARD, TR3, TNFRSF12)
RT   gene.";
RL   Immunogenetics 53:59-63(2001).
DR   EMBL; AF329969; AAK11256.1; -.
DR   HSSP; Q92956; 1JMA.
DR   MGD; MGI:1934667; Tnfrsf25.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00531; death; 1.
DR   Pfam; PF00020; TNFR_c6; 3.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
DR   PROSITE; PS01186; EGF_2; 1.
DR   PROSITE; PS00652; TNFR_NGFR_1; 1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 1.
SQ   SEQUENCE   413 AA;  44453 MW;  69F21B85D0DABABF CRC64;

  Query Match             15.4%;  Score 400.5;  DB 11;  Length 413;
  Best Local Similarity   27.9%;  Pred. No. 1.5e-25;
  Matches  135;  Conservative   47;  Mismatches  175;  Indels  127;  Gaps   21;

Qy          9 LLLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCTKCHKGTYL 68
Db         18 LLLLLLLLLLLGGQGQGGMSGRCDCASESQKRYGP-------------FCCRGCPKGHYM 64

Qy         69 YNDCPGPGRDTDCRVCAPGTYTALENHLRR-CLSCSRCRDEMFQVEISPCVVDRDTVCGC 127
Db         65 KAPCAEPCGNSTCLPCPSDTFLTRDNHFKTDCTRCQVCDEEALQVTLENCSAKSDTHCGC 124

Qy        128 RKNQYREYWGETGFRCLNCSLCPNGTVN----IPC-----QERQDTICHCHMGFFLKGAK 178
Db        125 QSG-----W------CVDCSTVPCGKSSPFSCVPCGATTPVHEAPTPRPCLPGFYIRGND 173

Qy        179 CISCHDCKNKECEKLCPTRPSTGKDSQDPGTTVLLPLVIVFGLCLASFASVVLACRYQRW 238
Db        174 CTSCPTGFSSVCPKAC-TAVCGWK--QMFWVQVLLGVAFLFG--------AILICAYCRW 222

Qy        239 KPKLYSIICGQSTLVKEGEPELLVPAPGFNPTTTICFSSTPSSSPVSIPPYISCDRSNFG 298
Db        223 Q---------------------------PCKAVVTADTAGTEPLASP----------- 242

Qy        299 AVASPSSETAPPHLKAGP---ILPGPPAST-HLC----------TPGPPASTH-LC---- 339
Db        243 -------QTA--HLSASDSAHTLLAPPSSTGKICTTVQLVGNNWTPGLSQTQEVVCGQAS 293

Qy        340 -----TPGPPASTHLCTPVQKWEASAPSAPDQLADADPA-TLYAVVDGVPPSRWKELVRR 393
Db        294 QPWDQLPNRTLGTPLASPL----SPAPPAGSPAAVLQPGPQLYDVMDAVPARRWKEFVRT 349

Qy        394 LGLSEHEIERLELENGRHLREAQYSMLAAWRRRTPRREATLELLGRVLRDMDLLGCLENI 453
Db        350 LGLREAEIEAVEVEICR-FRDQQYEMLKRWRQQQP---AGLGAIYAALERKGLEGCAEDL 405

Qy        454 EEAL 457
Db        406 RSRL 409
```

```
RESULT 5
Q8VD70
ID   Q8VD70      PRELIMINARY;      PRT;   387 AA.
AC   Q8VD70;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Similar to tumor necrosis factor receptor superfamily, member 12.
GN   TNFRSF25 OR TNFRSF12.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Salivary gland;
RA   Strausberg R.;
RL   Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC017526; AAH17526.1; -.
DR   MGD; MGI:1934667; Tnfrsf25.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00531; death; 1.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
DR   PROSITE; PS01186; EGF_2; 1.
DR   PROSITE; PS00652; TNFR_NGFR_1; 1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 1.
KW   Receptor.
SQ   SEQUENCE   387 AA;  41640 MW;  F16644666BAD68D3 CRC64;

  Query Match             13.8%;  Score 360;  DB 11;  Length 387;
  Best Local Similarity   27.0%;  Pred. No. 3.7e-22;
  Matches  130;  Conservative   46;  Mismatches  161;  Indels  144;  Gaps   22;

Qy          7 PG----LLLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCTKC 62
Db         17 PGSTARVLQPLFLPLLLLLLLLGGQG----QGGMSGR---CDCASESQKRYGPFCCRGC 69

Qy         63 HKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRR-CLSCSRCRDEMFQVEISPCVVDR 121
Db         70 PKGHYMKAPCAEPCGNSTCLPCPSDTFLTRDNHFKTDCTRCQVCDEEALQVTLENCSAKS 129

Qy        122 DTVCGCRKNQYREYWGETGFRCLNCSLCPNGTVN----IPCQERQDTICHCHMGFFLKGA 177
Db        130 DTHCGCQSG-----W------CVDCSTEPCGKSSPFSCVPC-----------------GA 161

Qy        178 KCISCHDCKNKECEKLCPTRPSTGKDSQDPGTTVLLPLVIVFGLCLASFASVVLACRYQR 237
Db        162 -----------------TTPVHEAPTPLFWVQVLLGVAFLFG--------AILICAYCR 195

Qy        238 WKP---KLYSIICGQSTL---------VKEGEPELLVPAPGFNPTTT--ICFSS------ 277
Db        196 WQPCKAVVTADTAGTETLASPQTAHLSASDSAHTLLAP-----PSSTGKICTTVQLVGNN 250

Qy        278 -TPSSSPVSIPPYISCDRSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPAST 336
Db        251 WTPGLSQTQ---EVVCGQASQPWDQLPNRTLGTP--LASPLSPAPPA-------GSPAA- 297

Qy        337 HLCTPGPPASTHLCTPVQKWEASAPSAPDQLADADPATLYAVVDGVPPSRWKELVRRLGL 396
Db        298 -VLQPGP---------------------------QLYDVMDAVPARRWKEFVRTLGL 326

Qy        397 SEHEIERLELENGRHLREAQYSMLAAWRRRTPRREATLELLGRVLRDMDLLGCLENIEEA 456
Db        327 REAEIEAVEVEICR-FRDQQYEMLKRWRQQQP---AGLGAIYAALERMGLEGCAEDLRSR 382

Qy        457 L 457
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Db        383 L 383


RESULT 6
Q8BYY1
ID   Q8BYY1      PRELIMINARY;      PRT;   417 AA.
AC   Q8BYY1;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Tumor necrosis factor receptor 16.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Skin;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AK037248; BAC29775.1; -.
SQ   SEQUENCE   417 AA;  44672 MW;  CD0440EF7E70A617 CRC64;

  Query Match             8.5%;  Score 220.5;  DB 11;  Length 417;
  Best Local Similarity   23.1%;  Pred. No. 2.3e-10;
  Matches  106;  Conservative   63;  Mismatches  166;  Indels  123;  Gaps   26;

Qy         44 CPQGKYNHPQNSTICCTKCHKGTYLYNDCPGPGRDTDCRVCAPG-TYTALENHLRRCLSC 102
              |  |  |  |   |  ||  |: |  :   |       | |  |     |:: : :   | |
Db         25 CSTGMYTH---SGECCKACNLGEGVAQPC--GANQTVCEPCLDSVTFSDVVSATEPCKPC 79

Qy        103 SRCRDEMFQVEISPCVVDRDTVCGCRKNQYREYWGETGFRCLNCSLCPNGT-VNIPCQER 161
              : |    |   :|||   | || |    |::   ||| ||  ||:|  |: :   ||::
Db         80 TECLG--LQSMSAPCVEADDAVCRCSYGYYQD--EETG-RCEACSVCGVGSGLVFSCQDK 134

Qy        162 QDTIC-HCHMGFFLKGAK----CISCHDCK------------NKECEKLCPTR------ 197
              |:|:|  |  | :   |      |: |  |:             : |||:: | |
Db        135 QNTVCEECPEGTYSDEANHVDPCLPCTVCEDTERQLRECTPWADAECEEI-PGRWITRST 193

Qy        198 PSTGKD-----SQDPGTTVLLPLVIVFGLCLASFASVVLACRYQRWKPKLYSIICGQSTL 252
              |  | |      :|:|       |:           || |           : :::     :
Db        194 PPEGSDVTTPSTQEPEAPPERDLI----------ASTV--------ADTVTTVMGSSQPV 235

Qy        253 VKEGEPELLVPAPGFNPTTTICFSSTPSSSPVSIPPYI------SCDRSNFGAVASPSSE 306
              |  | : |:|           :|  ::  | :  ||      || ::  || : | ::
Db        236 VTRGTADNLIPV----------YCSILAAVVVGLVAYIAFKRWNSCKQNKQGANSRPVNQ 285

Qy        307 TAPP-----HLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPA-----STHLCTPVQKW 356
              | ||     |  :|  :      | |          ||  |     |     : :   |: |
Db        286 TPPPEGEKLHSDSG--ISVDSQSLH------DQQTHTQTASGQALKGDGNLYSSLPLTKR 337

Qy        357 EASAPSAPDQLADADPATLYAVVDGVPPSRWKELVRRLGLS-EHEIERLELENGRHLREA 415
              |       ::| : |                |: |   ||   ||       :::  |
Db        338 E-----EVEKLLNGD-------------TWRHLAGELGYQPEH------IDSFTHEACP 372

Qy        416 QYSMLAAWRRRTPRREATLELLGRVLRDMDLLGCLENI 453
                ::||:|  :     |||: |   || :     :|::
Db        373 VRALLASWGAQD---SATLDALLAALRRIQRADIVESL 407


RESULT 7
Q8CFT3
ID   Q8CFT3      PRELIMINARY;      PRT;   427 AA.
AC   Q8CFT3;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Similar to nerve growth factor receptor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Eye;
RA   Strausberg R.;
RL   Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC038365; AAH38365.1; -.
KW   Receptor.
SQ   SEQUENCE   427 AA;  45647 MW;  7AC73263F7B31436 CRC64;

  Query Match             8.5%;  Score 220.5;  DB 11;  Length 427;
  Best Local Similarity   23.1%;  Pred. No. 2.4e-10;
  Matches  106;  Conservative   63;  Mismatches  166;  Indels  123;  Gaps   26;

Qy         44 CPQGKYNHPQNSTICCTKCHKGTYLYNDCPGPGRDTDCRVCAPG-TYTALENHLRRCLSC 102
              |  |  |  |   |  ||  |: |  :   |       | |  |     |:: : :   | |
Db         35 CSTGMYTH---SGECCKACNLGEGVAQPC--GANQTVCEPCLDSVTFSDVVSATEPCKPC 89

Qy        103 SRCRDEMFQVEISPCVVDRDTVCGCRKNQYREYWGETGFRCLNCSLCPNGT-VNIPCQER 161
              : |    |   :|||   | || |    |::   ||| ||  ||:|  |: :   ||::
Db         90 TECLG--LQSMSAPCVEADDAVCRCSYGYYQD--EETG-RCEACSVCGVGSGLVFSCQDK 144

Qy        162 QDTIC-HCHMGFFLKGAK----CISCHDCK------------NKECEKLCPTR------ 197
              |:|:|  |  | :   |      |: |  |:             : |||:: | |
Db        145 QNTVCEECPEGTYSDEANHVDPCLPCTVCEDTERQLRECTPWADAECEEI-PGRWITRST 203

Qy        198 PSTGKD-----SQDPGTTVLLPLVIVFGLCLASFASVVLACRYQRWKPKLYSIICGQSTL 252
              |  | |      :|:|       |:           || |           : :::     :
Db        204 PPEGSDVTTPSTQEPEAPPERDLI----------ASTV--------ADTVTTVMGSSQPV 245

Qy        253 VKEGEPELLVPAPGFNPTTTICFSSTPSSSPVSIPPYI------SCDRSNFGAVASPSSE 306
              |  | : |:|           :|  ::  | :  ||      || ::  || : | ::
Db        246 VTRGTADNLIPV----------YCSILAAVVVGLVAYIAFKRWNSCKQNKQGANSRPVNQ 295

Qy        307 TAPP-----HLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPA-----STHLCTPVQKW 356
              | ||     |  :|  :      | |          ||  |     |     : :   |: |
Db        296 TPPPEGEKLHSDSG--ISVDSQSLH------DQQTHTQTASGQALKGDGNLYSSLPLTKR 347

Qy        357 EASAPSAPDQLADADPATLYAVVDGVPPSRWKELVRRLGLS-EHEIERLELENGRHLREA 415
              |       ::| : |                |: |   ||   ||       :::  |
Db        348 E-----EVEKLLNGD-------------TWRHLAGELGYQPEH------IDSFTHEACP 382

Qy        416 QYSMLAAWRRRTPRREATLELLGRVLRDMDLLGCLENI 453
                ::||:|  :     |||: |   || :     :|::
Db        383 VRALLASWGAQD---SATLDALLAALRRIQRADIVESL 417


RESULT 8
O57408
ID   O57408      PRELIMINARY;      PRT;   368 AA.
AC   O57408;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Subgroup E ALV receptor.
OS   Meleagris gallopavo (Common turkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
OX   NCBI_TaxID=9103;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97471016; PubMed=9326659;
RA   Adkins H.B., Brojatsch J., Naughton J., Rolls M.M., Pesola J.M.,
RA   Young J.A.;
RT   "Identification of a cellular receptor for subgroup E avian leukosis
RT   virus.";
RL   Proc. Natl. Acad. Sci. U.S.A. 94:11617-11622(1997).
DR   EMBL; AF006002; AAB93987.1; -.
DR   HSSP; O14763; 1D0G.
DR   InterPro; IPR001450; 4Fe4S_ferredoxin.
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DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001865; Ribosomal_S2.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00531; death; 1.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS00198; 4FE4S_FERREDOXIN; 1.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
DR   PROSITE; PS00962; RIBOSOMAL_S2_1; 1.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor.
SQ   SEQUENCE   368 AA;  41020 MW;  5701AC2A6D4F87E2 CRC64;

  Query Match             8.1%;  Score 211.5;  DB 13;  Length 368;
  Best Local Similarity   22.5%;  Pred. No. 1.1e-09;
  Matches  112;  Conservative   40;  Mismatches  141;  Indels  205;  Gaps   24;

Qy         14 VLPALLADVYPAGVQGLVPHPGD---LEKRE------SPCPQGKYNHPQNSTICCTKCHK 64
Db         11 VLLLLLAKV----------HLGSAAAVKKRAVKSDVLKPDPYSK-----------KCPM 48

Qy         65 GTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCLSCSRCRDEMFQVEISPCVVDRDTV 124
Db         49 GTYLAND------SSRCLPCKKDEYTEYPNDFPKCLGCRTCRED--QVEVSPCNSTRNTR 100

Qy        125 CGCRKNQYREYWGETGFRCL---NCSL-------CPNGTVNI-PCQERQDTICHCHMGFF 173
Db        101 CACKNGTF----------CLPDHPCEMCQKCQTRCPKGQVRIAACTQQSDLRC------- 143

Qy        174 LKGAKCISCHDCKNKECEKLCPTRPSTGKDSQDPGTTVL----LPLVIVFGLCLASFASV 229
Db        144 ----------------------GPPLDNSSSFTTTGIIISTVLPVVLVFLL-------V 173

Qy        230 VLAC----RYQRW-------KPKLYSIICGQSTLVKEG-----------EPELLVPAP 265
Db        174 LLCCCCCRRYSAGSGGVLSRKPRAMVKILLQRMGIQDNNCNEQIYQQQQQQQQLLTTEQ 233

Qy        266 GFNPTTTICFSSTPSSSPVSIPPYISCDRSNFGAVASPSSETAPPHLKAGPILPGPPAST 325
Db        234 G---------SEVPRGVEVEV----------------EEVAPR--------------- 251

Qy        326 HLCTPGPPASTHLC-TPGPPASTHLCTPVQKWEASAPSAPDQLADADPATLYA-----VV 379
Db        252 ---TPNVETQRNLVPVPG-------------------------KDPITVLSSSFNTPV 281

Qy        380 DGVPPSRWKELVRRLGLSEHEIERLELENGRHLREAQYSMLAAWRRRTPRREATLELLGR 439
Db        282 DLVPFPQWRRFGRALGLRENNLYQAE-QNDRESGEPLYQMLIMWLNKEGSK-ASVNTLLE 339

Qy        440 VLRDMDLLGCLENIEEAL 457
Db        340 TLSQISLSGVADIIASEL 357


RESULT 9
Q9IAR7
ID   Q9IAR7      PRELIMINARY;      PRT;   368 AA.
AC   Q9IAR7;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   TvbS1.
GN   TVB.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20193796; PubMed=10729132;
RA   Adkins H.B., Brojatsch J., Young J.A.T.;
RT   "Identification and Characterization of a TNFR-related Receptor for
RT   Subgroups B/D/E Avian Leukosis Viruses Reveals Cysteine Residues
RT   Required Specifically for Subgroup E Virus Entry.";
RL   J. Virol. 74:3572-3578(2000).
DR   EMBL; AF161713; AAF60221.1; -.
DR   HSSP; O14763; 1D0G.
DR   InterPro; IPR001450; 4Fe4S_ferredoxin.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00531; death; 1.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS00198; 4FE4S_FERREDOXIN; 1.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
SQ   SEQUENCE   368 AA;  41531 MW;  0553CE531DEB47C6 CRC64;

  Query Match             8.1%;  Score 210;  DB 13;  Length 368;
  Best Local Similarity   21.5%;  Pred. No. 1.5e-09;
  Matches   91;  Conservative   36;  Mismatches  129;  Indels  168;  Gaps   18;

Qy         61 KCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCLSCSRCRDEMFQVEISPCVVD 120
Db         45 KCPMGTYEAND------SIQCLPCKKDEYTEYPNDFPKCLGCRTCRED--QVEVSPCIPT 96

Qy        121 RDTVCGCRKNQYREYWGETGFRCL---NCSL-------CPNGTVNI-PCQERQDTICHCH 169
Db         97 RNTQCACKNGTF----------CLPDHPCEMCQKCQTECPKGQVRLAPCTQHSDLLC--- 143

Qy        170 MGFFLKGAKCISCHDCKNKECEKLCPTRPSTGKDSQDPGTTVLLPLVIVFGLCLASFASV 229
Db        144 ------------------------------GPPLEISSSSSTLWIIITFTVLLAVILGL 172

Qy        230 VLA----CRYQR----------WKPK----------LYSIICGQSTLVKEGEPELLVPA 264
Db        173 VLVFWKRCSSRHHGAGDDGELSWKPSAVVNRLLQRLGIQDNRCNEQIYQNQQQQELLFTA 232

Qy        265 PGFNPTTTICFSSTPSSSPVSIPPYISCDRSNFGAVASPSSETAPPHLKAGPILPGPPAS 324
Db        233 QG-----------------------------------SEV--PH---GVEMEG---- 245

Qy        325 THLCTPGPPASTH-----LCTPGPPASTHLCTPVQKWEASAPSAPDQLADADPATLYAVV 379
Db        246 TERRTPDPKVETQRKLVPVLGENPIALLH----------------------RSFNTFV 281

Qy        380 DGVPPSRWKELVRRLGLSEHEIERLELENGRHLREAQYSMLAAWRRRTPRREAT---LEL 436
Db        282 DYVPFPEWKRFGRALDLQENDLYLAE-QHDRVSCEPFYQMLNTWLNQQGSKASVNTLLET 340

Qy        437 LGRV 440
Db        341 LPRI 344


RESULT 10
Q9PVD4
ID   Q9PVD4      PRELIMINARY;      PRT;   387 AA.
AC   Q9PVD4;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   P75-like transmembrane protein fullback.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Hick E., Sun B.I., Collins-Racie L., LaVallie E., Sive H.L.;
RT   "Identification and Characterization of fullback, a Novel Posteriorly-
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RT   Expressed Xenopus Gene.";
RL   Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF131890; AAD54072.1; -.
DR   HSSP; P07174; 1NGR.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00531; death; 1.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 4.
KW   Transmembrane.
SQ   SEQUENCE   387 AA;  42066 MW;  1A386A239C7C8A82 CRC64;

  Query Match             7.9%;  Score 206.5;  DB 13;  Length 387;
  Best Local Similarity   22.8%;  Pred. No. 3.2e-09;
  Matches  101;  Conservative   52;  Mismatches  173;  Indels  117;  Gaps   23;

Qy         41 ESPCPQGKYNHPQNSTICCTKCHKGTYLYNDCPGPGRDTDCRVCAP-GTYTALENHLRRC 99
              |  |  | |    ||  ||: |  |  :   |     || |  |    |:: : :  :|
Db         22 EDVCESGLYT---NSGKCCSLCPAGFGVVVPC--GDSDTKCEPCIENSTFSDVRSAKAKC 76

Qy        100 LSCSRCRDEMFQVEISPCVVDRDTVCGCRKNQYREYWGETGFRCLNCSLCPNG-TVNIPC 158
                |  |:     :| | |  ::|||| | : || :  |      || | ||  | |  |
Db         77 QPCFTCQSPSLTLE-SNCTREQDTVCRCPERQYLDSNG----ICLPCQLCSKGHGVVSQC 131

Qy        159 QERQDTICH-CHMGFF--LKGAK--CISCH-DCKNKE-----C----EKLCP-------T 196
               ::|:|  |  ||:  :| ::  |: |  :|| |       |    : ||
Db        132 THNKNTVCQLCSSGFYSEVKSSESPCLPCRTECKETEVQIGDCVPQHDILCMDKDVPILK 191

Qy        197 RPSTGKDSQDPGTTVLLP------LVIVFGLCLASFASVVLACRYQRWKPKLYSIICGQS 250
              |   |::    |:   :|      :: |:  |    | ||    |  :  | |:   :
Db        192 RTEGGENGTSAGSPHFIPQDNSKNIIPVY--CSILAAVVVGLIAYVAF--KCYTTCKQKK 247

Qy        251 TLVKEGEPELLVPAPGFNPTTTICFSSTPSSSPVSIPPYISCDRSNFGAVASPSSETAPP 310
              | |    ||     |                                :: |    |  |
Db        248 QLAKARAGELATSTEGEKL----------------------HNDSGVFLDTHSLQEPN 283

Qy        311 HLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLCTPVQKWEASAPSAPDQLADA 370
              ||    | |                  |   ||   |  : |::  |        |
Db        284 HLSKAKIEP----------------KLYINLPP---HKQSEVERLLADTSLGKD----- 318

Qy        371 DPATLYAVVDGVPPSRWKELVRRLGLSEHEIERLELENGRHLREAQYSMLAAWRRRTPRR 430
                      |: |   || |  |:      ||   :  :::|  |   : :
Db        319 ---------------WQRLASLLGYEEETIDTF----GRG-EDPVHTLLTDW---SSKE 354

Qy        431 EATLELLGRVLRDMDLLGCLENI 453
              :|||:|   | :|:    :||:
Db        355 SSTLEVLCAALVNMERADVVENL 377


RESULT 11
Q91ZM6
ID   Q91ZM6      PRELIMINARY;      PRT;   433 AA.
AC   Q91ZM6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Tumor necrosis factor receptor type II (Fragment).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley;
RA   Osburg B., Peiser C., Doemling D., Schomburg L., Voigt K., Bickel U.;
RT   "TNF-receptors p60 and p80 are constitutively expressed by rat brain
RT   capillary endothelial cells and participate in TNF-alpha transport
RT   through the blood-brain barrier.";
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF420214; AAL16021.1; -.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
KW   Receptor.
FT   NON_TER       1      1
FT   NON_TER     433    433
SQ   SEQUENCE   433 AA;  45723 MW;  75736D835E72CA4A CRC64;

  Query Match             7.7%;  Score 201.5;  DB 11;  Length 433;
  Best Local Similarity   24.6%;  Pred. No. 9.6e-09;
  Matches   84;  Conservative   33;  Mismatches  143;  Indels   81;  Gaps   16;

Qy         32 PHPGDLEKRESPCPQGKYNHPQNSTICCTKCHKGTYLYNDCPGPGRDTDCRVCAPGTYTA 91
              | ||       : |   :  : : : :|| ||  | |  : |     || |  || | :|
Db         14 PEPG------NQCQISQEYYDKKAQMCCAKCPPGQYAKHFC-NKTSDTVCADCAAGMFTQ 66

Qy         92 LENHLRRCLSC-SRCRDEMFQVEISPCVVDRDTVCGCRKNQYREYWGETGFRCLNCSLCP 150
              : |||  |||| | | |: |||   |   :: || |  : |       :|    || |
Db         67 VWNHLHTCLSCSSSCSDD--QVETHNCTKKQNRVCACNADSYCALKLHSG----NCRQCM 120

Qy        151 NGTVNIPCQERQDTICHCHMGFFLKGAKC----ISCHDCKNKECEKLCPTRPSTGKDSQD 206
                          :  | || :  ::    : |  |                | | |:
Db        121 K------------LSKCGPGFGVARSRTSNGNVICSAC----------APGTFSDTTS 156

Qy        207 PGTTVLLPLVIVFGLCLASFASVVLACRYQRWKPKLYSIICGQSTLVKEGEPEL-----L 261
              | | |  |  |  | :  ||   |  :  |          ::  | : ||
Db        157 -STDVCRPHRICSILAIPGNASTDAVCASESPTPSAVP----RTIYVSQPEPTRSQPMDQ 211

Qy        262 VPAPGFNPTTTICFSSTPSSSP-----VSIPPYISCDRSNFGAV-------------AS 302
              | |  |  :  |||   |      :|:|  :    :  | :
Db        212 EPGPSQTPHIPVSLGSTPIIEPSITGGISLPIGLIVGLTTLGLLMLGLANCFILVQRKKK 271

Qy        303 PS---SETAPPHLKAGPILPGPPA----STHLCTPGPPAST 336
              ||    ||  |||   |       |       || |  | :|:
Db        272 PSCLQRETMVPHL---PDEKSQDAVGLEQQHLLTTAPSSSS 309


RESULT 12
Q9PW79
ID   Q9PW79      PRELIMINARY;      PRT;   368 AA.
AC   Q9PW79;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   TvbS3.
GN   TVB.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97100985; PubMed=8945512;
RA   Brojatsch J., Naughton J., Rolls M.M., Zingler K., Young J.A.;
RT   "CAR1, a TNFR-related protein, is a cellular receptor for cytopathic
RT   avian leukosis-sarcoma viruses and mediates apoptosis.";
RL   Cell 87:845-855(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Brojatsch J., Naughton J., Young J.A.T.;
RL   Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF161712; AAD47256.1; -.
DR   HSSP; O14763; 1D0G.
DR   InterPro; IPR001450; 4Fe4S_ferredoxin.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00531; death; 1.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00005; DEATH; 1.
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DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS00198; 4FE4S_FERREDOXIN; 1.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
DR   PROSITE; PS00652; TNFR_NGFR_1; 1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
SQ   SEQUENCE   368 AA;  41515 MW;  F558C225AB3750BB CRC64;

  Query Match             7.7%;  Score 200;  DB 13;  Length 368;
  Best Local Similarity   21.2%;  Pred. No. 1.1e-08;
  Matches   90;  Conservative   36;  Mismatches  130;  Indels  168;  Gaps   18;

Qy         61 KCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCLSCSRCRDEMFQVEISPCVVD 120
Db         45 KCPMGTYEAND------SIQCLPSKKDEYTEYPNDFPKCLGCRTCRED--QVEVSPCIPT  96

Qy        121 RDTVCGCRKNQYREYWGETGFRCL---NCSL-------CPNGTVNI-PCQERQDTICHCH 169
Db         97 RNTQCACKNGTF----------CLPDHPCEMCQKCQTECPKGQVRLAPCTQHSDLLC---  143

Qy        170 MGFFLKGAKCISCHDCKNKECEKLCPTRPSTGKDSQDPGTTVLLPLVIVFGLCLASFASV 229
Db        144 ------------------------------GPPLEISSSSSTLWIIITFTVLLAVILGL 172

Qy        230 VLA----CRYQR----------WKPK----------LYSIICGQSTLVKEGEPELLVPA 264
Db        173 VLVFWKRCSSRHHGAGDDGELSWKPSAVVNRLLQRLGIQDNRCNEQIYQNQQQQELLFTA 232

Qy        265 PGFNPTTTICFSSTPSSSPVSIPPYISCDRSNFGAVASPSSETAPPHLKAGPILPGPPAS 324
Db        233 QG-----------------------------------SEV--PH---GVEMEG----  245

Qy        325 THLCTPGPPASTH-----LCTPGPPASTHLCTPVQKWEASAPSAPDQLADADPATLYAVV 379
Db        246 TERRTPDPKVETQRKLVPVLGENPIALLH----------------------RSFNTFV 281

Qy        380 DGVPPSRWKELVRRLGLSEHEIERLELENGRHLREAQYSMLAAWRRRTPRREAT---LEL 436
Db        282 DYVPPPEWKRFGRALDLQENDLYLAE-QHDRVSCEPFYQMLNTWLNQQGSKASVNTLLET 340

Qy        437 LGRV 440
Db        341 LPRI 344


RESULT 13
Q98SM6
ID   Q98SM6      PRELIMINARY;      PRT;   651 AA.
AC   Q98SM6;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Death receptor 6.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Bridgham J.T., Johnson A.L.;
RT   "Expression of DR6 in the ovary.";
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF349908; AAK29666.2; -.
DR   HSSP; P19438; 1NCF.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00531; death; 1.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
DR   PROSITE; PS00652; TNFR_NGFR_1; 1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 1.
KW   Receptor.
SQ   SEQUENCE   651 AA;  71003 MW;  BDC95A600DAB2C2A CRC64;

  Query Match             7.7%;  Score 199.5;  DB 13;  Length 651;
  Best Local Similarity   22.9%;  Pred. No. 2.3e-08;
  Matches  125;  Conservative   57;  Mismatches  217;  Indels  147;  Gaps   30;

Qy         10 LLPLVLPALL----ADVYPAGVQGLVPHPGDLEKRESPCPQGKYNH---PQNSTICCTKC 62
Db          5 VLAAVLPLLVFLGTADAQPKLTS---------EQNAVSLPAGKYLHLDRATNQELICDKC 55

Qy         63 HKGTYLYNDCPGPGRDT--DCRVCAPGTYTALENHLRRCLSCSR-CRDEMFQVEISPCVV 119
Db         56 PAGTYVSKHCT---KSTLRECSPCPDGTFTKHENGIERCHPCRKPC--ELPMIEKTHCTA 110

Qy        120 DRDTVCGCRKNQYREYWGETGFRCLNCSLCPNG-TVNIPCQERQDTICH-CHMGFF---- 173
Db        111 LTDRECTCLSGTF-----QINDTCVPYTVCPVGWGVRKKGTETEDVRCKPCLRGTFSDVP 165

Qy        174 LKGAKCISCHDC--KN--------KECEKLC------PTRPSTGKDSQDPGTTVLLPLVI 217
Db        166 SSVMKCKTYTDCFGKNMVVVKPGTKESDNVCGSPASLPNTSLTSSDAQADGETYEAPPTA 225

Qy        218 VFGLCLASFASVVLACRYQRWKPKLYSIICGQSTLVKEGEPELLVPAPGFNPTTTICFSS 277
Db        226 YLPKGLNS---------------SVFDLSSSPAPRVSNGTAE----------PTVDYND 259

Qy        278 TPSSSPVSIPPYISCDRSNFGAVAS-------------PSSETAPPHLKAGPILP---GP 321
Db        260 TSANGTVGAPGSLS-SAGTAGQAQSYRHKHTSQAMGKQPAQEMAGGEKSSIPYRPPRRGP 318

Qy        322 P-ASTHLCTPGPPASTHL-----------------CTPGPPASTHLCTPVQKWEASAPSA 363
Db        319 PNVHQHP-----DINEHLPWMIVLFLLLVLVVIVVCSVRKSSRT-----LKKGPRQDPSA 368

Qy        364 PDQLADADPAT---------LYAV----VDGVPP------SRWKELVRRL-GLSEHEIER 403
Db        369 IVEKAIMKKSTTPTQNREKWIYYCNGHGIDILKPVAAQVGSQWKDIYQFLCNASEREV-- 426

Qy        404 LELENGRHL-REAQYSMLAAWRRRTPRREATLELLGRVLRDMDLLGCLENIEEALGGAAR 462
Db        427 AAFSNGYAADHERAYAALQHWTIRGP--EASLAQLISALRQHRRNDVVEKIRGLMEDTTP 484

Qy        463 LASEPR 468
Db        485 VQMQPQ 490


RESULT 14
O72761
ID   O72761      PRELIMINARY;      PRT;   322 AA.
AC   O72761;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   K2R protein.
GN   K2R.
OS   Cowpox virus (CPV).
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
OX   NCBI_TaxID=10243;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=GRI-90;
RX   MEDLINE=98229462; PubMed=9568042;
RA   Shchelkunov S.N., Safronov P.F., Totmenin A.V., Petrov N.A.,
RA   Ryazankina O.I., Gutorov V.V., Kotwal G.J.;
RT   "Species-specific differences in genome organization of cowpox,
RT   smallpox, and vaccinia viruses.";
RL   Virology 243:432-460(1998).
DR   EMBL; Y15035; CAA75300.1; -.
DR   HSSP; O14763; 1D0G.
DR   InterPro; IPR001368; TNFR_c6.
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DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
SQ   SEQUENCE   322 AA;  35412 MW;  774549278D156A9D CRC64;

  Query Match             7.3%;  Score 191;  DB 12;  Length 322;
  Best Local Similarity   31.4%;  Pred. No. 5.3e-08;
  Matches   49;  Conservative   18;  Mismatches   71;  Indels   18;  Gaps    7;

Qy         27 VQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCTKCHKGTYLYNDCPGPGRDTDCRVCAP 86
              | | ||:     |       |     ||   |: :|| :|  | |: : |     :| |  |
Db         18 VSGDVPY----EHINGKCNGTDYNSNSNN-LCCKQCDPGMYMTHSC-NTTSNTKCAKCPD 71

Qy         87 GTYTALENHLRRCLSC-SRCRDEMFQVEISPCVVDRDTVCGCRKNQYREYWGETGFR-CL 144
              ||:|:: ||:  |||| :|     |||   |   :|  | |     | |: |  | | |:
Db         72 GTPTSIPNHIPTCLSCRGKCSSN--QVETKSCSNTQDRECVCASGYYCEFEGSNGCRLCV 129

Qy        145 NCSLCPNGTVNIPCQERQDTIC--------HCHMGF 172
               : | :|       : | ||        |.| |
Db        130 PQTKCDSGYGVYGYSSKGDVICKKCPGNIDKCDMSF 165


RESULT 15
Q9PUS0
ID   Q9PUS0      PRELIMINARY;      PRT;   302 AA.
AC   Q9PUS0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Decoy TNF receptor.
OS   Salvelinus fontinalis (Brook trout) (Brook char).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC   Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.
OX   NCBI_TaxID=8038;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20111091; PubMed=10642582;
RA   Bobe J., Goetz F.W.;
RT   "A tumor necrosis factor decoy receptor homologue is up-regulated in
RT   the brook trout (Salvelinus fontinalis) ovary at the completion of
RT   ovulation.";
RL   Biol. Reprod. 62:420-426(2000).
DR   EMBL; AF156738; AAD56428.1; -.
DR   HSSP; O14763; 1D4V.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS01186; EGF_2; 1.
DR   PROSITE; PS00652; TNFR_NGFR_1; 1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 1.
KW   Receptor.
SQ   SEQUENCE   302 AA;  34037 MW;  E44C73477F05C3DF CRC64;

  Query Match             7.2%;  Score 187.5;  DB 13;  Length 302;
  Best Local Similarity   28.7%;  Pred. No. 9.7e-08;
  Matches   52;  Conservative   18;  Mismatches   60;  Indels   51;  Gaps   10;

Qy         56 TICCTKCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCLSCSRCRDEMFQVEIS 115
              :| | :|  ||||   |    | :||  |  | ||   ||: :|| || | :   ||
Db         33 SIVCDRCPPGTYLRAPCSAM-RKSDCAECPNGAYTEFWNHISKCLRCSMCAEN--QVVKQ 89

Qy        116 PCVVDRDTVCGCRKNQY--REYWGETGFRCLNCSLCPNG----TVNIPCQERQDTIC-HC 168
              |    :  | |::  |  ::|       |:    || |    |   |    ||| | | |
Db         90 ECSPSNNCECECKEGYYFNKKYEA-----CIKHKECPPGYGANTTGTP---HQDTECVQC 141

Qy        169 HMGFF----------------------LKG-----AKCISCHDCKNKE----CEKLCP 195
               ||:                     |||       | ||:| | ::      :: |
Db        142 QAGFYSEVSSAKATCLAQSNCKVGGLRVVLKGQDWHNTLCASCYDLKTRDGAEYLHEILP 201

Qy        196 T 196
              |
Db        202 T 202


Search completed: September 13, 2003, 07:05:34
Job time : 42 secs
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